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70 100 (54) Title: NUCLEIC ACID BASED MODULATORS OF GENE EXPRESSION

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NUCLEIC ACID BASED MODULATORS OF GENE EXPRESSION Background of the Invention

This invention relates to reagents useful as inhibitors of gene expression relating to diseases such as cancers, diabetes, obesity, Alzheimer's disease, cardiac diseases, agerelated diseases, and/or henatitis B infections and related conditions.

Summary of the Invention

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The invention features novel nucleic acid-based techniques [e.g., enzymatic nucleic acid molecules (ribozymes), antisense nucleic acids, 2-5A antisense chimeras, triplex

10. DNA, antisense nucleic acids containing RNA cleaving chemical groups (for example, Cook et al., U.S. Patent 5,359,051)] and methods for their use to modulate the expression of molecular targets impacting the development and progression of cancers, diabetes, obesity, Alzheimer's disease, cardiac diseases, age-related diseases, and/or hepatitis B infections and related conditions

15 In a preferred embodiment, the invention features novel nucleic acid-based techniques [e.g., enzymatic nucleic acid molecules (ribozymes), antisense nucleic acids, 2-5A antisense chimeras, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups (for exaple, Cook et al., U.S. Patent 5,359,051)] and methods for their use for inhibiting the expression of disease related genes, e.g., Protein-Tyrosine-Phosphatase-20 1b (PTP-1B, Genbank accession No. NM 002827), Methionine Aminopeptidase (MetAP-2, Genbank accession No. U29607), beta-Secretase (BACE, Genbank accession No. AF190725), Presenilin-1 (ps-1, Genbank accession No. L76517), Presenilin-2 (ps-2, Genbank accession No. L43964), Human Epidermal Growth Factor Receptor-2 (HER2/cerb2/neu, Genbank accession No. X03363), Phospholamban (PLN, Genbank accession No. 25 NM 002667), Telomerase (TERT, Genbank accession No. NM 003219) and Hepatitis B virus genes (HBV, Genbank accession No. AF100308.1). Such ribozymes can be used in a method for treatment of diseases caused by the expression of these genes in man and other animals, including other primates.

Thus, in an additional preferred embodiment, the invention features novel nucleic acid-based techniques such as enzymatic nucleic acid molecules and antisense molecules and methods for their use to down regulate or inhibit the expression of genes encoding Protein-Tyrosine-Phosphatase-1b (PTP-1B), Methionine Aminopeptidase (MetAP-2),

beta-Secretase (BACE), Presenilin-1 (ps-1), Presenilin-2 (ps-2), Human Epidermal Growth Factor Receptor-2 (HER2/c-erb2/neu), Phospholamban (PLN), Telomerase (hTERT) PKC alpha. and Hepatitis B (HBV) proteins. In particular, applicant describes the selection and function of nucleic acid molecules capable of cleaving RNAs encoded by these genes and their use to reduce levels of PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV proteins in various tissues to treat the diseases discussed herein. Such nucleic acid molecules are also useful for diagnostic uses.

In a preferred embodiment, the invention features the use of one or more of the nucleic acid-based techniques independently or in combination to inhibit the expression of the genes encoding PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV. Specifically, the invention features the use of nucleic acid-based techniques to specifically inhibit the expression of PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, PKC alpha, and/or HBV genes.

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In yet another preferred embodiment, the invention features the use of an enzymatic nucleic acid molecule, preferably in the hammerhead, NCH (Inozyme), G-cleaver, amberzyme, zinzyme, and/or DNAzyme motif, to inhibit the expression of PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, PKC alpha and/or HBV RNA.

Applicant indicates that these nucleic acid molecules are able to inhibit expression of PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, PKC alpha, and/or HBV genes. Those of ordinary skill in the art, will find that it is clear from the examples described that other nucleic acid molecules that inhibit target PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV encoding mRNAs may be readily designed and are within the scope of the invention.

By "inhibit" it is meant that the activity of target genes or level of mRNAs or equivalent RNAs encoding target genes is reduced below that observed in the absence of the nucleic acid molecules of the instant invention (e.g., enzymatic nucleic acid molecules), antisense nucleic acids, 2-5A antisense chimeras, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups). In one embodiment, inhibition with an enzymatic nucleic acid molecule preferably is below that level observed in the presence of an enzymatically attenuated nucleic acid molecule that is able to bind to the same site on the mRNA, but is unable to cleave that RNA. In another embodiment, inhibition with nucleic acid molecules, including enzymatic nucleic acid and antisense

molecules, is preferably greater than that observed in the presence of, for example, an oligonucleotide with scrambled sequence or with mismatches. In another embodiment, inhibition of target genes with the nucleic acid molecule of the instant invention is greater than in the presence of the nucleic acid molecule than in its absence. According to the invention, the activity of telomerase enzyme or the level of RNA encoding one or more portein subunits of the telomerase enzyme is inhibited if it is at least 10% less, 20% less, 50% less, 75% less or even not active or present at all, in the presence of a nucleic acid of the invention relative to the level in the absence of such a nucleic acid.

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By "enzymatic nucleic acid molecule" it is meant a nucleic acid molecule which has complementarity in a substrate binding region to a specified gene target, and also has an enzymatic activity which is active to specifically cleave target RNA. That is, the enzymatic nucleic acid molecule is able to intermolecularly cleave RNA and thereby inactivate a target RNA molecule. These complementary regions allow sufficient hybridization of the enzymatic nucleic acid molecule to the target RNA and thus permit cleavage. One hundred percent complementarity is preferred, but complementarity as low as 50-75% may also be useful in this invention. The nucleic acids may be modified at the base, sugar, and/or phosphate groups. The term enzymatic nucleic acid is used interchangeably with phrases such as ribozymes, catalytic RNA, enzymatic RNA, catalytic DNA, aptazyme or aptamer-binding ribozyme, regulatable ribozyme, catalytic oligonucleotides, nucleozyme, DNAzyme, RNA enzyme, endoribonuclease, endonuclease, minizyme, leadzyme, oligozyme or DNA enzyme. All of these terminologies describe nucleic acid molecules with enzymatic activity. The specific enzymatic nucleic acid molecules described in the instant application are not meant to be limiting and those skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it have a specific substrate binding site which is complementary to one or more of the target nucleic acid regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart a nucleic acid cleaving activity to the molecule (Cech et al., U.S. Patent No. 4,987,071; Cech et al., 1988, JAMA 260:20 3030-4).

By "nucleic acid molecule" as used herein is meant a molecule having nucleotides.

The nucleic acid can be single, double, or multiple stranded and may comprise modified or unmodified nucleotides or non-nucleotides or various mixtures and combinations thereof.

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An example of a nucleic acid molecule according to the invention is a gene which encodes for a macromolecule such as a protein.

By "enzymatic portion" or "catalytic domain" is meant that portion/region of the enzymatic nucleic acid molecule essential for cleavage of a nucleic acid substrate (for example see Figures 1-5).

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By "substrate binding arm" or "substrate binding domain" is meant that portion/region of a ribozyme which is complementary to (i.e., able to base-pair with) a portion of its substrate. Generally, such complementarity is 100%, but can be less if desired. For example, as few as 10 bases out of 14 may be base-paired. Such arms are shown generally in Figures 1-5. That is, these arms contain sequences within a ribozyme which are intended to bring ribozyme and target RNA together through complementary base-pairing interactions. The ribozyme of the invention may have binding arms that are contiguous or non-contiguous and may be of varying lengths. The length of the binding arm(s) are preferably greater than or equal to four nucleotides and of sufficient length to stably interact with the target RNA; specifically 12-100 nucleotides; more specifically 14-24 nucleotides long. If two binding arms are chosen, the design is such that the length of the binding arms are symmetrical (i.e., each of the binding arms is of the same length; e.g., five and five nucleotides, six and six nucleotides or seven and seven nucleotides long) or asymmetrical (i.e., the binding arms are of different length; e.g., six and three nucleotides; three and six nucleotides long; four and five nucleotides long; four and six nucleotides long; four and seven nucleotides long; and the like). Binding arms can be complementary to the specified substrate, to a portion of the indicated substrate, to the indicated substrate sequence and additional adjacent sequence, or a portion of the indicated sequence and additional adjacent sequence.

By "NCH" or "Inozyme" motif is meant, an enzymatic nucleic acid molecule comprising a motif as described in Ludwig et al., USSN No. 09/406,643, filed September 27, 1999, entitled "COMPOSITIONS HAVING RNA CLEAVING ACTIVITY", and International PCT publication Nos. WO 98/58058 and WO 98/58057, all incorporated by reference herein in their entirety, including the drawings.

By "G-cleaver" motif is meant, an enzymatic nucleic acid molecule comprising a motif as described in Eckstein *et al.*, International PCT publication No. WO 99/16871, incorporated by reference herein in its entirety, including the drawings.

By "zinzyme" motif is meant, a class II enzymatic nucleic acid molecule comprising a motif as described herein and in Beigelman et al., International PCT publication No. WO 99/55857, incorporated by reference herein in its entirety, including the drawings.

By "amberzyme" motif is meant, a class I enzymatic nucleic acid molecule comprising a motif as described herein and in Beigelman et al., International PCT publication No. WO 99/55857, incorporated by reference herein in its entirety, including the drawings.

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By 'DNAzyme' is meant, an enzymatic nucleic acid molecule lacking a ribonucleotide (2'-OH) group. In particular embodiments, the enzymatic nucleic acid molecule may have an attached linker(s) or other attached or associated groups, moieties, or chains containing one or more nucleotides with 2'-OH groups. A DNAzyme can be synthesized chemically or can be expressed by means of a single stranded DNA vector or equivalent thereof.

By "sufficient length" is meant an oligonucleotide of greater than or equal to 3 nucleotides that is of a length great enough to provide the intended function under the expected condition. For example, for binding arms of enzymatic nucleic acid "sufficient length" means that the binding arm sequence is long enough to provide stable binding to a target site under the expected binding conditions. Preferably, the binding arms are not so long as to prevent useful turnover.

By "stably interact" is meant, interaction of the oligonucleotides with target nucleic acid (e.g., by forming hydrogen bonds with complementary nucleotides in the target under physiological conditions).

By "equivalent" RNA to PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV is meant to include those naturally occurring RNA molecules having bomology (partial or complete) to PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV proteins or encoding for proteins with similar function as PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV in various organisms, including human, rodent, primate, rabbit, pig, protozoans, fungi, plants, and other microorganisms and parasites. The equivalent RNA sequence also includes in addition to the coding region, regions such as 5'-untranslated region, 3'-untranslated region, introns, intron-exon junction and the like in HBV.

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By "homology" is meant the nucleotide sequence of two or more nucleic acid molecules is nartially or completely identical.

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By "antisense nucleic acid", it is meant a non-enzymatic nucleic acid molecule that binds to target RNA by means of RNA-RNA or RNA-DNA or RNA-PNA (protein nucleic acid: Egholm et al., 1993 Nature 365, 566) interactions and alters the activity of the target RNA (for a review, see Stein and Cheng, 1993 Science 261, 1004 and Woolf et al., US patent No. 5,849,902). Typically, antisense molecules will be complementary to a target sequence along a single contiguous sequence of the antisense molecule. However, in certain embodiments, an antisense molecule may bind to substrate such that the substrate molecule forms a loop, and/or an antisense molecule may bind such that the antisense molecule forms a loop. Thus, the antisense molecule may be complementary to two (or even more) non-contiguous substrate sequences or two (or even more) non-contiguous sequence portions of an antisense molecule may be complementary to a target sequence or both. For a review of current antisense strategies, see Schmajuk et al., 1999, J. Biol. Chem., 274, 21783-21789, Delihas et al., 1997, Nature, 15, 751-753, Stein et al., 1997, Antisense N. A. Drug Dev., 7, 151, Crooke, 1998, Biotech. Genet. Eng. Rev., 15, 121-157, Crooke, 1997, Ad. Pharmacol., 40, 1-49. In addition, antisense DNA can be used to target RNA by means of DNA-RNA interactions, thereby activating RNase H, which digests the target RNA in the duplex. Antisense DNA can be synthesized chemically or can be expressed via the use of a single stranded DNA expression vector or the equivalent thereof.

By "2-5A antisense chimera" it is meant, an antisense oligonucleotide containing a 5'-phosphorylated 2'-5'-linked adenylate residue. These chimeras bind to target RNA in a sequence-specific manner and activate a cellular 2-5A-dependent ribonuclease which, in turn, cleaves the target RNA (Torrence et al., 1993 Proc. Natl. Acad. Sci. USA 90, 1300).

By "triplex DNA" it is meant an oligonucleotide that can bind to a double-stranded DNA in a sequence-specific manner to form a triple-strand helix. Formation of such triple helix structure has been shown to inhibit transcription of the targeted gene (Duval-Valentin et al., 1992, Proc. Natl. Acad. Sci. USA, 89, 504).

By "gene" it is meant a nucleic acid that encodes a RNA.

By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another RNA sequence by either traditional Watson-Crick or other non-traditional types. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its target or complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., ribozyme cleavage, antisense or triple helix inhibition. Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner et al., 1987, CSH Symp. Quant. Biol. LII pp.123-133; Frier et al., 1986, Proc. Nat. Acad. Sci. USA 83:9373-9377; Turner et al., 1987, J. Am. Chem. Soc. 109:3783-3785). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule which can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary). "Perfectly complementary" means that all the contiguous residues in a second nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence.

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At least seven basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds in trans (and thus can cleave other RNA molecules) under physiological conditions. Table I summarizes some of the characteristics of these ribozymes. In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor of gene expression, with the specificity of inhibition depending not only on the base-pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches,

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or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme.

The enzymatic nucleic acid molecule that cleave the specified sites in PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV-specific RNAs represent a novel therapeutic approach to treat a variety of pathologic indications, including, HBV infection, hepatitis, hepatocellular carcinoma, tumorigenesis, cirrhosis, liver failure, cancers including breast, ovarian, prostate, and esophogeal cancer, tumorigenesis, retinopathy, arthritis, psoriasis, female reproduction, restinosis, certain infectious diseases, transplant rejection and autoimmune disease such as multiple sclerosis, lupus, and AIDS, age related diseases such as macular degeneration and skin ulceration, Alzheimer's disease, dementia, diabetes, obesity and any other condition related to the level of PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV in a cell or tissue.

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In one of the preferred embodiments of the inventions described herein, the enzymatic nucleic acid molecule is formed in a hammerhead or hairpin motif, but may also be formed in the motif of a hepatitis delta virus, group I intron, group II intron or RNase P 15 RNA (in association with an RNA guide sequence), Neurospora VS RNA, DNAzvmes. NCH cleaving motifs, or G-cleavers. Examples of such hammerhead motifs are described by Drevfus, supra. Rossi et al., 1992, AIDS Research and Human Retroviruses 8, 183. Examples of hairpin motifs are described by Hampel et al., EP0360257, Hampel and Tritz, 1989 Biochemistry 28, 4929, Feldstein et al., 1989, Gene 82, 53, Haseloff and Gerlach, 20 1989, Gene, 82, 43, Hampel et al., 1990 Nucleic Acids Res. 18, 299; and Chowrira & McSwiggen, US. Patent No. 5,631,359. The hepatitis delta virus motif is described by Perrotta and Been, 1992 Biochemistry 31, 16. The RNase P motif is described by Guerrier-Takada et al., 1983 Cell 35, 849; Forster and Altman, 1990, Science 249, 783; and Li and Altman, 1996, Nucleic Acids Res. 24, 835. The Neurospora VS RNA 25 ribozyme motif is described by Collins (Saville and Collins, 1990 Cell 61, 685-696; Saville and Collins, 1991 Proc. Natl. Acad. Sci. USA 88, 8826-8830; Collins and Olive, 1993 Biochemistry 32, 2795-2799; and Guo and Collins, 1995, EMBO. J. 14, 363). Group II introns are described by Griffin et al., 1995, Chem. Biol. 2, 761; Michels and Pyle, 1995, Biochemistry 34, 2965; and Pyle et al., International PCT Publication No. WO 96/22689. 30 The Group I intron is described by Cech et al., U.S. Patent 4,987,071. DNAzymes are described by Usman et al., International PCT Publication No. WO 95/11304; Chartrand et

al., 1995, NAR 23, 4092; Breaker et al., 1995, Chem. Bio. 2, 655; and Santoro et al., 1997, PNAS 94, 4262. NCH cleaving motifs are described in Ludwig & Sproat, International PCT Publication No. WO 98/58058; and G-cleavers are described in Kore et al., 1998, Nucleic Acids Research 26, 4116-4120 and Eckstein et al., International PCT Publication No. WO 99/16871. Additional motifs include the Aptazyme (Breaker et al., WO 98/43993), Amberzyme (Class I motif; Figure 3; Beigelman et al., International PCT publication No. WO 99/55857) and Zinzyme (Beigelman et al., International PCT publication No. WO 99/55857), all these references are incorporated by reference herein in their totalities, including drawings and can also be used in the present invention. These specific motifs are not limiting in the invention and those skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule (Cech et al., U.S. Patent No. 4.987.071).

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In preferred embodiments of the present invention, a nucleic acid molecule, e.g., an antisense molecule, a triplex DNA, or a ribozyme, is 13 to 100 nucleotides in length, e.g., in specific embodiments 35, 36, 37, or 38 nucleotides in length (e.g., for particular ribozymes or antisense). In particular embodiments, the nucleic acid molecule is 15-100, 17-100, 20-100, 21-100, 23-100, 25-100, 27-100, 30-100, 32-100, 35-100, 40-100, 50-100, 60-100, 70-100, or 80-100 nucleotides in length. Instead of 100 nucleotides being the upper limit on the length ranges specified above, the upper limit of the length range can be, for example, 30, 40, 50, 60, 70, or 80 nucleotides. Thus, for any of the length ranges, the length range for particular embodiments has lower limit as specified, with an upper limit as specified which is greater than the lower limit. For example, in a particular embodiment, the length range can be 35-50 nucleotides in length. All such ranges are expressly included. Also in particular embodiments, a nucleic acid molecule can have a length with is any of the lengths specified above, for example, 21 nucleotides in length.

In a preferred embodiment, the invention provides a method for producing a class of nucleic acid-based gene inhibiting agents which exhibit a high degree of specificity for the RNA of a desired target. For example, the enzymatic nucleic acid molecule is preferably targeted to a highly conserved sequence region of target RNAs encoding PTP-1B, MetAP-

2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV proteins (specifically PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV RNA) such that specific treatment of a disease or condition can be provided with either one or several nucleic acid molecules of the invention. Such nucleic acid molecules can be delivered exogenously to specific tissue or cellular targets as required. Alternatively, the nucleic acid molecules (e.g., ribozymes and antisense) can be expressed from DNA and/or RNA vectors that are delivered to specific cells.

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As used in herein "cell" is used in its usual biological sense, and does not refer to an entire multicellular organism, e.g., specifically does not refer to a human. The cell may be present in an organism which may be a human but is preferably a non-human multicellular organism, e.g., birds, plants and mammals such as cows, sheep, apes, monkeys, swine, dogs, and cats. The cell may be prokaryotic (e.g., bacterial cell) or eukaryotic (e.g., mammalian or plant cell).

By "PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV proteins" is meant, a protein or a mutant protein derivative thereof, comprising sequence expressed and/or encoded by PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, genes and/or the HBV genome respectively.

By "highly conserved sequence region" is meant a nucleotide sequence of one or more regions in a target gene does not vary significantly from one generation to the other or from one biological system to the other.

The enzymatic nucleic acid-based inhibitors of PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV expression are useful for the prevention of the diseases and conditions including HBV infection, hepatitis, hepatocellular carcinoma, tumorigenesis, cirrhosis, liver failure, cancers including breast, ovarian, prostate, and esophogeal cancer, tumorigenesis, retinopathy, arthritis, psoriasis, female reproduction, restinosis, certain infectious diseases, transplant rejection and autoimmune disease such as multiple sclerosis, lupus, and AIDS, age related diseases such as macular degeneration and skin ulceration, Alzheimer's disease, dementia, diabetes, obesity and any other condition related to the level of PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV in a cell or tissue. and any other diseases or conditions that are related to the levels of PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV in a cell or tissue.

By "related" is meant that the reduction of PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV expression (specifically PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV genes) RNA levels and thus reduction in the level of the respective protein will relieve, to some extent, the symptoms of the disease or condition.

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The nucleic acid-based inhibitors of the invention are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells or tissues. The nucleic acid or nucleic acid complexes can be locally administered to relevant tissues ex vivo, or in vivo through injection, infusion pump or stent, with or without their incorporation in biopolymers. In preferred embodiments, the enzymatic nucleic acid inhibitors comprise sequences, which are complementary to the substrate sequences in Tables 3-31, 33, 34, 36-43, 56, 58, 59, 62, 63. Examples of such enzymatic nucleic acid molecules also are shown in Tables 3-29, 31, 33, 34, 37-43, 56, 58, 59, 62, 63. Examples of such enzymatic nucleic acid molecules consist essentially of sequences defined in these tables.

In yet another embodiment, the invention features antisense nucleic acid molecules including sequences complementary to the substrate sequences shown in Tables 3-31, 33, 34, 36, 37-43, 56, 58, 59, 62, 63. Such nucleic acid molecules can include sequences as shown for the binding arms of the enzymatic nucleic acid molecules in Tables 3-29, 31, 33, 34, 37-43, 56, 58, 59, 62, 63. Similarly, triplex molecules can be provided targeted to the corresponding DNA target regions, and containing the DNA equivalent of a target sequence or a sequence complementary to the specified target (substrate) sequence. Typically, antisense molecules will be complementary to a target sequence along a single contiguous sequence of the antisense molecule. However, in certain embodiments, an antisense molecule may bind to substrate such that the substrate molecule forms a loop, and/or an antisense molecule may bind such that the antisense molecule forms a loop. Thus, the antisense molecule may be complementary to two (or even more) noncontiguous substrate sequences or two (or even more) non-contiguous sequence portions of an antisense molecule may be complementary to a target sequence or both.

In another aspect, the invention provides mammalian cells containing one or more nucleic acid molecules and/or expression vectors of this invention. The one or more nucleic acid molecules may independently be targeted to the same or different sites.

By "consists essentially of" is meant that the active nucleic acid molecule of the invention, for example, an enzymatic nucleic acid molecule, contains an enzymatic center or core equivalent to those in the examples, and binding arms able to bind mRNA such that cleavage at the target site occurs. Other sequences may be present which do not interfere with such cleavage. Thus, a core region may, for example, include one or more loop or stem-loop structures, which do not prevent enzymatic activity. "X" in the sequences in Tables 3, 4, 9, 10, 13, 14, 18, 19, 24, 25, 33, 34, 37, 38, 63 can be such a loop. A core sequence for a hammerhead ribozyme can be CUGAUGAG X CGAA where X=GCCGUUAGGC or other stem II region as specifically or generally known in the art.

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In another aspect of the invention, ribozymes or antisense molecules that interact with target RNA molecules and inhibit PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV (specifically PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV RNA) activity are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors are preferably DNA plasmids or viral vectors. Ribozyme or antisense expressing viral vectors could be constructed based on. but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. Preferably, the recombinant vectors capable of expressing the ribozymes or antisense are delivered as described above, and persist in target cells. Alternatively, viral vectors may be used that provide for transient expression of ribozymes or antisense. Such vectors might be reneatedly administered as necessary. Once expressed, the ribozymes or antisense bind to the target RNA and inhibit its function or expression. Delivery of ribozyme or antisense expressing vectors could be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from the patient followed by reintroduction into the patient, or by any other means that would allow for introduction into the desired target cell. Antisense DNA can be expressed via the use of a single stranded DNA intracellular expression vector.

By RNA is meant a molecule comprising at least one ribonucleotide residue. By "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2' position of a β -D-ribo-furanose moiety.

By "vectors" is meant any nucleic acid- and/or viral-based technique used to deliver a desired nucleic acid. By "patient" is meant an organism, which is a donor or recipient of explanted cells or the cells themselves. "Patient" also refers to an organism to which the nucleic acid molecules of the invention can be administered. Preferably, a patient is a mammal or mammalian cells. More preferably, a patient is a human or human cells.

The nucleic acid molecules of the instant invention, individually, or in combination or in conjunction with other drugs, can be used to treat diseases or conditions discussed above. For example, to treat a disease or condition associated with PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV, the patient may be treated, or other appropriate cells may be treated, as is evident to those skilled in the art, individually or in combination with one or more drugs under conditions suitable for the treatment.

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In a further embodiment, the described molecules, such as antisense or ribozymes, can be used in combination with other known treatments to treat conditions or diseases discussed above. For example, the described molecules could be used in combination with one or more known therapeutic agents to treat HBV infection, hepatitis, hepatocellular carcinoma, tumorigenesis, cirrhosis, liver failure, cancers including breast, ovarian, prostate, and esophogeal cancer, tumorigenesis, retinopathy, arthritis, psoriasis, female reproduction, restinosis, certain infectious diseases, transplant rejection and autoimmune disease such as multiple sclerosis, lupus, and AIDS, age related diseases such as macular degeneration and skin ulceration. Alzheimer's disease, dementia, diabetes, and/or obesity.

In another preferred embodiment, the invention features nucleic acid-based inhibitors (e.g., enzymatic nucleic acid molecules (ribozymes), antisense nucleic acids, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups) and methods for their use to down regulate or inhibit the expression of RNA (e.g., PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV) capable of progression and/or maintenance of HBV infection, hepatitis, hepatocellular carcinoma, tumorigenesis, cirrhosis, liver failure, cancers including breast, ovarian, prostate, and esophogeal cancer, tumorigenesis, retinopathy, arthritis, psoriasis, female reproduction, restinosis, certain infectious diseases, transplant rejection and autoimmune disease such as multiple sclerosis, lupus, and AIDS, age related diseases such as macular degeneration and skin ulceration, Alzheimer's disease, dementia, diabetes, and/or obesity.

In another preferred embodiment, the invention features nucleic acid-based techniques (e.g., enzymatic nucleic acid molecules (ribozymes), antisense nucleic acids, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups) and methods for their use to down regulate or inhibit the expression of PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV RNA expression.

By "comprising" is meant including, but not limited to, whatever follows the word "comprising". Thus, use of the term "comprising" indicates that the listed elements are required or mandatory, but that other elements are optional and may or may not be present. By "consisting of" is meant including, and limited to, whatever follows the phrase "consisting of". Thus, the phrase "consisting of" indicates that the listed elements are required or mandatory, and that no other elements may be present. By "consisting essentially of" is meant including any elements listed after the phrase, and limited to other elements that do not interfere with or contribute to the activity or action specified in the disclosure for the listed elements. Thus, the phrase "consisting essentially of" indicates 15 that the listed elements are required or mandatory, but that other elements are optional and may or may not be present depending upon whether or not they affect the activity or action of the listed elements.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

Description Of The Preferred Embodiments

The drawings will first briefly be described.

Drawings:

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Figure 1 shows the secondary structure model for seven different classes of enzymatic nucleic acid molecules. Arrow indicates the site of cleavage. ----- indicate the target sequence. Lines interspersed with dots are meant to indicate tertiary interactions. - is meant to indicate base-paired interaction. Group I Intron: P1-P9.0 represent various stem-loop structures (Cech et al., 1994, Nature Struc. Bio., 1, 273). RNase P (M1RNA): EGS represents external guide sequence (Forster et al., 1990, Science, 249, 783; Pace et al., 1990, J. Biol. Chem., 265, 3587). Group II Intron: 5'SS means 5' splice site; 3'SS means 3'-splice site: IBS means intron binding site; EBS means exon binding site (Pyle et

al., 1994, Biochemistry, 33, 2716). VS RNA: I-VI are meant to indicate six stem-loop structures; shaded regions are meant to indicate tertiary interaction (Collins, International PCT Publication No. WO 96/19577). HDV Ribozyme: I-IV are meant to indicate four stem-loop structures (Been et al., US Patent No. 5,625,047). Hammerhead Ribozvme: I-III are meant to indicate three stem-loop structures; stems I-III can be of any length and may be symmetrical or asymmetrical (Usman et al., 1996, Curr. Op. Struct. Bio., 1, 527). Halrpin Ribozyme: Helix 1, 4 and 5 can be of any length; Helix 2 is between 3 and 8 base-pairs long; Y is a pyrimidine; Helix 2 (H2) is provided with a least 4 base pairs (i.e., n is 1, 2, 3 or 4) and helix 5 can be optionally provided of length 2 or more bases (preferably 3 - 20 bases, i.e., m is from 1 - 20 or more). Helix 2 and helix 5 may be 10 covalently linked by one or more bases (i.e., r is ≥ 1 base). Helix 1, 4 or 5 may also be extended by 2 or more base pairs (e.g., 4 - 20 base pairs) to stabilize the ribozyme structure and preferably is a protein binding site. In each instance, each N and N' independently is any normal or modified base and each dash represents a potential basepairing interaction. These nucleotides may be modified at the sugar, base or phosphate. 15 Complete base-pairing is not required in the helices, but is preferred. Helix 1 and 4 can be of any size (i.e., o and p is each independently from 0 to any number, e.g., 20) as long as some base-pairing is maintained. Essential bases are shown as specific bases in the structure, but those in the art will recognize that one or more may be modified chemically (abasic, base, sugar and/or phosphate modifications) or replaced with another base without 20 significant effect. Helix 4 can be formed from two separate molecules, i.e., without a connecting loop. The connecting loop when present may be a ribonucleotide with or without modifications to its base, sugar or phosphate. "q" ≥ is 2 bases. The connecting loop can also be replaced with a non-nucleotide linker molecule. H refers to bases A. U. or C. Y refers to pyrimidine bases. " refers to a covalent bond. (Burke et al., 1996, 25 Nucleic Acids & Mol. Biol., 10, 129; Chowrira et al., US Patent No. 5,631,359).

Figure 2 shows examples of chemically stabilized ribozyme motifs. HH Rz, represents hammerhead ribozyme motif (Usman et al., 1996, Curr. Op. Struct. Bio., 1, 527); NCH Rz represents the NCH ribozyme motif (described herein and in Ludwig & Sproat, International PCT Publication No. WO 98/58058); G-Cleaver, represents G-cleaver ribozyme motif (Kore et al., 1998, Nucleic Acids Research, 26, 4116-4120). N or

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n, represent independently a nucleotide which may be same or different and have complementarity to each other; r1, represents ribo-Inosine nucleotide; arrow indicates the site of cleavage within the target. Position 4 of the HH Rz and the NCH Rz is shown as having 2'-C-allyl modification, but those skilled in the art will recognize that this position can be modified with other modifications well known in the art, so long as such modifications do not significantly inhibit the activity of the ribozyme.

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Figure 3 shows an example of the Amberzyme ribozyme motif that is chemically stabilized (see, for example, Beigelman et al., International PCT publication No. WO 99/55857; also referred to as Class I Motif). The Amberzyme motif is a class of enzymatic nucleic acid molecules that do not require the presence of a ribonucleotide (2'-OH) group for activity.

Figure 4 shows an example of the Zinzyme A ribozyme motif that is chemically stabilized (see, for example, International PCT publication No. WO 99/55857; also referred to as Class A Motif). The Zinzyme motif is a class of enzymatic nucleic acid molecules that do not require the presence of a ribonucleotide (2'-OH) group for activity.

 $\label{eq:Figure 5} \textbf{Figure 5 shows an example of a DNAzyme motif described by Santoro et al., 1997, PNAS, 94, 4262.}$

Figure 6 is a diagrammatic representation of the hammerhead ribozyme motif known in the art and the NCH motif. Stem II can be 2 base-pair long, preferably, 2, 3, 4, 5, 6, 7, 8, and 10 base-pairs long. Each N and N' is independently any base or non-nucleotide as used herein; X is adenosine, cytidine or uridine; Stem I-III are meant to indicate three stem-loop structures; stems I-III can be of any length and may be symmetrical or asymmetrical (Usman et al., 1996, Curr. Op. Struct. Bio., 1, 527); arrow indicates the site of cleavage in the target RNA; Rz refers to ribozyme; Loop II may be present or absent. If Loop II is present it is greater than or equal to three nucleotides, preferably four nucleotides. The Loop II sequence is preferably 5'-GAAA-3' or 5'-GUUA-3'.

Figure 7 shows examples of chemically stabilized ribozyme motifs. HH Rz, represents hammerhead ribozyme motif (Usman et al., 1996, Curr. Op. Struct. Bio., 1, 527); NCH-Inosine Rz represents the NCH ribozyme motif with riboinosine at 15.1 position; NCH-Xylo Rz represents the NCH ribozyme with xylo inosine at 15.1 position. N or n, represent independently a nucleotide which may be same or different and may have

complementarity to each other; rI, represents ribo-Inosine nucleotide; xI represent xyloinosine; arrow indicates the site of cleavage within the target. Position 4 of the HH Rz and
the NCH Rzs is shown as having 2'-C-allyl modification, but those skilled in the art will
recognize that this position can be modified with other modifications well known in the
art, so long as such modifications do not significantly inhibit the activity of the ribozyme.

Figure 8 is a graphical representation of data showing inhibition of cell proliferation mediated by NCH and HH ribozymes targeted against HER2/neu/ErbB2 gene. Untreated, refers to cells not treated with ribozymes; HH RZ refers to hammerhead ribozyme; NCX RZ refers to the NCH ribozymes of the invention; IA refers to catalytically inactive or attenuated ribozyme used as a control.

Figure 9 is a schematic diagram of the process for the synthesis of beta-Dxylofuranosyl hypoxantine 3'-phosphoramidite.

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Figure 10 displays a schematic representation of NTP synthesis using nucleoside substrates.

Figure 11 shows a scheme for an in vitro selection method. A pool of nucleic acid molecules is generated with a random core region and one or more region(s) with a defined sequence. These nucleic acid molecules are bound to a column containing immobilized oligonucleotide with a defined sequence, where the defined sequence is complementary to region(s) of defined sequence of nucleic acid molecules in the pool. Those nucleic acid molecules capable of cleaving the immobilized oligonucleotide (target) in the column are isolated and converted to complementary DNA (cDNA), followed by transcription using NTPs to form a new nucleic acid pool.

Figure 12 shows a scheme for a two column in vitro selection method. A pool of nucleic acid molecules is generated with a random core and two flanking regions (region A and region B) with defined sequences. The pool is passed through a column which has immobilized oligonucleotides with regions A' and B' that are complementary to regions A and B of the nucleic acid molecules in the pool, respectively. The column is subjected to conditions sufficient to facilitate cleavage of the immobilized oligonucleotide target. The molecules in the pool that cleave the target (active molecules) have A' region of the target bound to their A region, whereas the B region is free. The column is washed to isolate the active molecules with the bound A' region of the target. This pool of active molecules may also contain some molecules that are not active to cleave the target (inactive

molecules) but have dissociated from the column. To separate the contaminating inactive molecules from the active molecules, the pool is passed through a second column (column 2) which contains immobilized oligonucleotides with the A' sequence but not the B' sequence. The inactive molecules will bind to column 2 but the active molecules will not bind to column 2 because their A region is occupied by the A' region of the target oligonucleotide from column 1. Column 2 is washed to isolate the active molecules for further processing as described in the scheme shown in Figure 11.

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Figure 13 is a diagram of a novel 48 nucleotide enzymatic nucleic acid motif which was identified using in vitro methods described in the instant invention. The molecule shown is only exemplary. The 5' and 3' terminal nucleotides (referring to the nucleotides of the substrate binding arms rather than merely the single terminal nucleotide on the 5' and 3' ends) can be varied so long as those portions can base-pair with target substrate sequence. In addition, the guanosine (G) shown at the cleavage site of the substrate can be changed to other nucleotides so long as the change does not eliminate the ability of enzymatic nucleic acid molecules to cleave the target sequence. Substitutions in the nucleic acid molecule and/or in the substrate sequence can be readily tested, for example, as described herein.

Figure 14 is a schematic diagram of HCV luciferase assay used to demonstrate efficacy of class I enzymatic nucleic acid molecule motif.

Figure 15 is a graph indicating the dose curve of an enzymatic nucleic acid molecule targeting site 146 on HCV RNA.

Figure 16 is a bar graph showing enzymatic nucleic acid molecules targeting 4 sites within the HCV RNA are able to reduce RNA levels in cells.

Figure 17 shows secondary structures and cleavage rates for characterized Class II
25 enzymatic nucleic acid motifs.

Figure 18 is a diagram of a novel 35 nucleotide enzymatic nucleic acid motif which was identified using in vitro methods described in the instant invention. The molecule shown is only exemplary. The 5' and 3' terminal nucleotides (referring to the nucleotides of the substrate binding arms rather than merely the single terminal nucleotide on the 5' and 3' ends) can be varied so long as those portions can base-pair with target substrate sequence. In addition, the guanosine (G) shown at the cleavage site of the substrate can be changed to other nucleotides so long as the change does not eliminate the ability of

enzymatic nucleic acid molecules to cleave the target sequence. Substitutions in the nucleic acid molecule and/or in the substrate sequence can be readily tested, for example, as described herein.

Figure 19 is a bar graph showing substrate specificities for Class II (zinzyme) 5 $\,$ ribozymes.

Figure 20 is a bar graph showing Class II enzymatic nucleic acid molecules targeting 10 representative sites within the HER2 RNA in a cellular proliferation screen.

Figure 21 is a synthetic scheme outlining the synthesis of 5-[3aminopropynyl(propyl)]uridine 5'-triphosphates and 4-imidazoleaceticacid conjugates.

Figure 22 is a synthetic scheme outlining the synthesis of 5-[3-(N-4imidazoleacetyl)aminopropynyl(propyl)]uridine 5'-triphosphates.

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Figure 23 is a synthetic scheme outlining the synthesis of carboxylate tethered uridine 5'-triphosphoates.

Figure 24 is a synthetic scheme outlining the synthesis of 5-(3-aminoalkyl) and 5-[3(N-succinvl)aminopropyl] functionalized cytidines.

Figure 25 is a diagram of a class I ribozyme stem truncation and loop replacement analysis.

Figure 26 is a diagram of class I ribozymes with truncated stem(s) and/or nonnucleotide linkers used in loop structures.

Figure 27 is a diagram of "no-ribo" class II ribozymes.

Figure 28 is a graph showing cleavage reactions with class II ribozymes under differing divalent metal concentrations.

Figure 29 is a diagram of differing class II ribozymes with varying ribo content and their relative rates of catalysis.

Figure 30 is a graph showing class II ribozyme (zinzyme) mediated reduction of HER2 RNA in SKBR3 breast carcinoma cells. Cells were treated with 100 nm, and 200 nm of zinzyme (RPI 18656) targeting site 972 of HER2 RNA and a corresponding scrambled attenuated control complexed with 2.5 μg/ml of lipid. Active zinzymes and scrambled attenuated controls were compared to untreated cells after 24 hours post treatment.

Figure 31 is a graph showing class II ribozyme (zinzyme) mediated dose response anti-prolferation assay in SKBR3 breast carcinoma cells. Cells were treated with 100 nm, and 200 nm of zinzyme (RPI 18656) targeting site 972 of HER2 RNA and a corresponding scrambled attenuated control complexed with 2.0 µg/ml of lipid. Active zinzymes and scrambled attenuated controls were compared to untreated cells after 24 hours post treatment.

Figure 32 is a graph which shows the dose dependent reduction of HER2 RNA in SKOV-3 cells treated with RPI 19293 from 0 to 100 nM with 5.0 μg/ml of cationic lipid.

Figure 33 is a graph which shows the dose dependent reduction of HER2 RNA and inhibition of cellular proliferation in SKBR-3 cells treated with RPI 19293 from 0 to 400 nM with 5.0 ue/ml of cationic lipid.

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Figure 34 shows a non-limiting example of the replacement of a 2'-O-methyl 5'-CA-3' with a ribo G in the class II (zinzyme) motif. The representative motif shown for the purpose of the figure is a "seven-ribo" zinzyme motif, however, the interchangeability of a G and a CA in the position shown in Figure 25 of the class II (zinzyme) motif extends to any combination of 2-O-methyl and ribo residues. For instance, a 2'-O-methyl G can replace the 2'-O-methyl 5'-CA-3' and vise versa.

Figure 35 is a graph which shows a screen of class II ribozymes (zinzymes) targeting site 972 of HER2 RNA which contain ribo-G reductions (RPI 19727 = no ribo, RPI 19728 = one ribo, RPI 19293 = two ribo, RPI 19729 = three ribo, RPI 19730 = four ribo, 19731 = five ribo, and RPI 19292 = seven ribo) for anti-proliferative activity in SKBR3 cells.

Figure 36 summarizes the results of functional group modification studies in which various nucleoside analogs were tested for activity in the NCH ribozyme motif. $K_{\rm rel}$ values describe the cleavage values of a given substituent at position 15.1 relative the Inosine at position 15.1 (I-15.1).

Figure 37 summarizes reported functional group modification studies performed at the A 15.1 residue in the A-15.1 \cdot U-16.1 context of NUH cleaving ribozymes. K_{rel} values describe the cleavage values of a given substituent at position 15.1 relative the adenosine at position 15.1 (A-15.1).

Mechanism of action of Nucleic Acid Molecules of the Invention

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Antisense: Antisense molecules may be modified or unmodified RNA, DNA, or mixed polymer oligonucleotides and primarily function by specifically binding to matching sequences resulting in inhibition of peptide synthesis (Wu-Pong, Nov 1994. 5 BioPharm, 20-33). The antisense oligonucleotide binds to target RNA by Watson Crick base-pairing and blocks gene expression by preventing ribosomal translation of the bound sequences either by steric blocking or by activating RNase H enzyme. Antisense molecules may also alter protein synthesis by interfering with RNA processing or transport from the nucleus into the cytoplasm (Mukhopadhyay & Roth, 1996, Crit. Rev. in Oncogenesis 7, 151-190).

In addition, binding of single stranded DNA to RNA may result in nuclease degradation of the heteroduplex (Wu-Pong, supra; Crooke, supra). To date, the only backbone modified DNA chemistry which will act as substrates for RNase H are phosphorothioates, phosphorodithioates, and borontrifluoridates. Recently, it has been reported that 2'-arabino and 2'-fluoro arabino- containing oligos can also activate RNase H activity.

A number of antisense molecules have been described that utilize novel configurations of chemically modified nucleotides, secondary structure, and/or RNase H substrate domains (Woolf et al., International PCT Publication No. WO 98/13526; Thompson et al., International PCT Publication No. WO 99/54459; Hartmann et al., International PCT Publication No. WO 00/17346) all of these are incorporated by reference herein in their entirety.

Antisense DNA can be used to target RNA by means of DNA-RNA interactions, thereby activating RNase H, which digests the target RNA in the duplex. Antisense DNA can be chemically synthesized or can be expressed via the use of a single stranded DNA intracellular expression vector or the equivalent thereof.

Triplex Forming Oligonucleotides (TFO): Single stranded DNA may be designed to bind to genomic DNA in a sequence specific manner. TFOs are comprised of pyrimidinerich oligonucleotides which bind DNA helices through Hoogsteen Base-pairing (Wu-Pong, supra). The resulting triple helix composed of the DNA sense, DNA antisense, and TFO disrupts RNA synthesis by RNA polymerase. The TFO mechanism may result in gene expression or cell death since binding may be irreversible (Mukhopadhyay & Roth, supra)

2'-5' Oligoadenvlates: The 2-5 A system is an interferon-mediated mechanism for RNA degradation found in higher vertebrates (Mitra et al., 1996, Proc Nat Acad Sci USA 93, 6780-6785). Two types of enzymes, 2-5A synthetase and RNase L, are required for RNA cleavage. The 2-5A synthetases require double stranded RNA to form 2'-5' oligoadenylates (2-5A). 2-5A then acts as an allosteric effector for utilizing RNase L which has the ability to cleave single stranded RNA. The ability to form 2-5A structures with double stranded RNA makes this system particularly useful for inhibition of viral replication.

(2'-5') oligoadenylate structures may be covalently linked to antisense molecules to form chimeric oligonucleotides capable of RNA cleavage (Torrence, supra). These molecules putatively bind and activate a 2-5A dependent RNase, the oligonucleotide/enzyme complex then binds to a target RNA molecule which can then be cleaved by the RNase enzyme. The covalent attachment of 2'-5' oligoadenylate structures is not limited to antisense applications, and can be further elaborated to include attachment to nucleic acid molecules of the instant invention.

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Enzymatic Nucleic Acid: Seven basic varieties of naturally-occurring enzymatic RNAs are presently known. In addition, several *in vitro* selection (evolution) strategies (Orgel, 1979, Proc. R. Soc. London, B 205, 435) have been used to evolve new nucleic acid catalysts capable of catalyzing cleavage and ligation of phosphodiester linkages (Joyce, 1989, Gene, 82, 83-87; Beaudry et al., 1992, Science 257, 635-641; Joyce, 1992, Scientific American 267, 90-97; Breaker et al., 1994, TIBTECH 12, 268; Bartel et al., 1993, Science 261:1411-1418; Szostak, 1993, TIBS 17, 89-93; Kumar et al., 1995, FASEB J., 9, 1183; Breaker, 1996, Curr. Op. Biotech., 7, 442; Santoro et al., 1997, Proc. Natl. Acad. Sci., 94, 4262; Tang et al., 1997, RNA 3, 914; Nakamaye & Eckstein, 1994, supra; Long & Uhlenbeck, 1994, supra; Ishizaka et al., 1995, supra; Vaish et al., 1997, Biochemistry 36, 6495; all of these are incorporated by reference herein). Each can catalyze a series of reactions including the hydrolysis of phosphodiester bonds in trans (and thus can cleave other RNA molecules) under physiological conditions.

In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of an enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target

RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

Nucleic acid molecules of this invention will block to some extent PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV protein expression and can be used to treat disease or diagnose disease associated with the levels of PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV.

The enzymatic nature of a ribozyme has significant advantages, such as the concentration of ribozyme necessary to affect a therapeutic treatment is low. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base-pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can be chosen to completely eliminate catalytic activity of a ribozyme.

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Nucleic acid molecules having an endonuclease enzymatic activity are able to repeatedly cleave other separate RNA molecules in a nucleotide base sequence-specific manner. Such enzymatic nucleic acid molecules can be targeted to virtually any RNA transcript, and achieve efficient cleavage in vitro (Zaug et al., 324, Nature, 429 1986; Uhlenbeck, 1987 Nature, 328, 596; Kim et al., 84 Proc. Natl. Acad. Sci. USA, 8788, 1987; Dreyfus, 1988, Einstein Quart. J. Bio. Med., 6, 92; Haseloff and Gerlach, 334 Nature, 585, 1988; Cech, 260 JAMA, 3030, 1988; Jefferies et al., 17 Nucleic Acids Research, 1371, 1989; and Santoro et al., 1997 supra).

Because of their sequence specificity, trans-cleaving ribozymes show promise as therapeutic agents for human disease (Usman & McSwiggen, 1995 Ann. Rep. Med. Chem. 30, 285-294; Christoffersen and Marr, 1995 J. Med. Chem. 38, 2023-2037). Ribozymes can be designed to cleave specific RNA targets within the background of cellular RNA. Such a cleavage event renders the RNA non-functional and abrogates protein expression from that RNA. In this manner, synthesis of a protein associated with a disease state can be selectively inhibited (Warashina et al., 1999, Chemistry and Biology, 6, 237-250.

The nucleic acid molecules of the instant invention are also referred to as GeneBloc™ reagents, which are essentially nucleic acid molecules (e.g.; ribozymes, antisense) canable of down-regulating gene expression.

5 Target sites

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Targets for useful ribozymes and antisense nucleic acids can be determined as disclosed in Draper et al., WO 93/23569; Sullivan et al., WO 93/23057; Thompson et al.. WO 94/02595; Draper et al., WO 95/04818; McSwiggen et al., US Patent No. 5.525.468. and all hereby incorporated in their entireties by reference herein. Other examples include the following PCT applications, which concern inactivation of expression of diseaserelated genes: WO 95/23225, WO 95/13380, WO 94/02595, all incorporated by reference herein. Rather than repeat the guidance provided in those documents here, below are provided specific examples of such methods, not limiting to those in the art. Ribozymes and antisense to such targets are designed as described in those applications and synthesized to be tested in vitro and in vivo, as also described. The sequence of human PTP-1B, MetAP-2, BACE, ps-1, ps-2, HER2, PLN, TERT, and/or HBV RNAs (for example, GenBank accession Nos. (PTP-1B., NM 002827), (MetAP-2, U29607), (BACE, AF190725), (ps-1, L76517), (ps-2, L43964), (HER2/c-erb2/neu, X03363), (PLN, NM 002667), (TERT, NM 003219) and (HBV, AF100308.1, HBV strain 2-18; additionally, other HBV strains can be screened by one skilled in the art, see Table 35 for other possible strains) were screened for optimal enzymatic nucleic acid and antisense target sites using a computer-folding algorithm. Antisense, hammerhead, DNAzyme, NCH (Inozyme), amberzyme, zinzyme or G-Cleaver ribozyme binding/cleavage sites were identified. These sites are shown in Tables 3-29, 31, 33, 34, 37-43, 56, 58, 59, 62, 63 (all sequences are 5' to 3' in the tables; X can be any base-paired sequence, the actual sequence is not relevant here). The nucleotide base position is noted in the Tables as that site to be cleaved by the designated type of enzymatic nucleic acid molecule. Table 36 shows substrate positions selected from Renbo et al., 1987, Sci. Sin., 30, 507, used in Draner, US natent No. 6.017,756 entitled "METHOD AND REAGENT FOR INHIBITING HEPATITIS B VIRUS REPLICATION" and Draper et al., International 30 PCT publication No. WO 93/23569, filed April 29, 1993, entitled "METHOD AND REAGENT FOR INHIBITING VIRAL REPLICATION". While human sequences can be

screened and enzymatic nucleic acid molecule and/or antisense thereafter designed, as discussed in Stinchcomb *et al.*, WO 95/23225, mouse targeted ribozymes may be useful to test efficacy of action of the enzymatic nucleic acid molecule and/or antisense prior to testine in humans.

Antisense, hammerhead, DNAzyme, NCH (Inozyme), amberzyme, zinzyme or G-Cleaver ribozyme binding/cleavage sites were identified, as discussed above. The nucleic acid molecules were individually analyzed by computer folding (Jaeger et al., 1989 Proc. Natl. Acad. Sci. USA, 86, 7706) to assess whether the sequences fold into the appropriate secondary structure. Those nucleic acid molecules with unfavorable intramolecular interactions such as between the binding arms and the catalytic core were eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity.

Antisense, hammerhead, DNAzyme, NCH, amberzyme, zinzyme or G-Cleaver ribozyme binding/cleavage sites were identified and were designed to anneal to various sites in the RNA target. The binding arms are complementary to the target site sequences described above. The nucleic acid molecules were chemically synthesized. The method of synthesis used follows the procedure for normal DNA/RNA synthesis as described below and in Usman et al., 1987 J. Am. Chem. Soc., 109, 7845; Scaringe et al., 1990 Nucleic Acids Res., 18, 5433; Wincott et al., 1995 Nucleic Acids Res., 23, 2677-2684; and Caruthers et al., 1992, Methods in Enzymology 211,3-19.

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Synthesis of Nucleic acid Molecules

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs ("small refers to nucleic acid motifs no more than 100 nucleotides in length, preferably no more than 80 nucleotides in length, and most preferably no more than 50 nucleotides in length; e.g., antisense oligonucleotides, hammerhead or the NCH ribozymes) are preferably used for exogenous delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of RNA structure. Exemplary molecules of the instant invention are chemically synthesized, and others can similarly be synthesized.

Oligonucleotides (e.g.; antisense GeneBlocs) are synthesized using protocols known in the art as described in Caruthers et al., 1992, Methods in Enzymology 211, 3-19, Thompson et al., International PCT Publication No. WO 99/54459, Wincott et al., 1995. Nucleic Acids Res. 23, 2677-2684, Wincott et al., 1997, Methods Mol. Bio., 74, 59, Brennan et al., 1998, Biotechnol Bioeng., 61, 33-45, and Brennan, US patent No. 5 6.001.311. All of these references are incorporated herein by reference. The synthesis of oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 µmol scale protocol with a 2.5 min coupling step for 2'-O-10 methylated nucleotides and a 45 sec coupling step for 2'-deoxy nucleotides. Table II outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 µmol scale can be performed on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 µL of 0.11 M = 6.6 µmol) of 2'-O-methyl 15 phosphoramidite and a 105-fold excess of S-ethyl tetrazole (60 μ L of 0.25 M = 15 μ mol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'hydroxyl. A 22-fold excess (40 μ L of 0.11 M = 4.4 μ mol) of deoxy phosphoramidite and a 70-fold excess of S-ethyl tetrazole (40 µL of 0.25 M = 10 µmol) can be used in each coupling cycle of deoxy residues relative to polymer-bound 5'-hydroxyl. Average 20 coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% N-methyl imidazole in THF (ABI) and 10% acetic 25 anhydride/10% 2,6-lutidine in THF (ABI); and oxidation solution is 16.9 mM I2, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-30 1,2-Benzodithiol-3-one 1,1-dioxide, 0.05 M in acetonitrile) is used.

Deprotection of the antisense oligonucleotides is performed as follows: the polymerbound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to -20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H2O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder.

The method of synthesis used for normal RNA including certain enzymatic nucleic acid molecules follows the procedure as described in Usman et al., 1987, J. Am. Chem. Soc., 109, 7845; Scaringe et al., 1990, Nucleic Acids Res., 18, 5433; and Wincott et al., 10 1995, Nucleic Acids Res. 23, 2677-2684 Wincott et al., 1997, Methods Mol. Bio., 74, 59, and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. 15 synthesizer using a 0.2 μmol scale protocol with a 7.5 min coupling step for alkylsilyl protected nucleotides and a 2.5 min coupling step for 2'-O-methylated nucleotides. Table II outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 µmol scale can be done on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 μ L of 0.11 M = 6.6 μ mol) of 2'-O-methyl 20 phosphoramidite and a 75-fold excess of S-ethyl tetrazole (60 μ L of 0.25 M = 15 μ mol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'hydroxyl. A 66-fold excess (120 µL of 0.11 M = 13.2 µmol) of alkylsilyl (ribo) protected phosphoramidite and a 150-fold excess of S-ethyl tetrazole (120 µL of 0.25 M = 30 µmol) can be used in each coupling cycle of ribo residues relative to polymer-bound 5'-hydroxyl. 25 Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% N-methyl imidazole in THF (ABI) and 10% acetic 30 anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution is 16.9 mM I2, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade

acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide0.05 M in acetonitrile) is used.

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Deprotection of the RNA is performed using either a two-pot or one-pot protocol. For the two-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to –20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H2O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder. The base deprotected oligoribonucleotide is resuspended in anhydrous TEA/HF/NMP solution (300 µL of a solution of 1.5 mL N-methylpyrrolidinone, 750 µL TEA and 1 mL TEA-3HF to provide a 1.4 M HF concentration) and heated to 65 °C. After 1.5 h, the oligomer is quenched with 1.5 M NH₄HCO₃.

Alternatively, for the one-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 33% ethanolic methylamine/DMSO: 1/1 (0.8 mL) at 65 °C for 15 min. The vial is brought to r.t. TEA-3HF (0.1 mL) is added and the vial is heated at 65 °C for 15 min. The sample is cooled at -20 °C and then quenched with 1.5 M NH₄HCO₃.

For purification of the trityl-on oligomers, the quenched NH₄HCO₃ solution is loaded onto a C-18 containing cartridge that had been prewashed with acetonitrile followed by 50 mM TEAA. After washing the loaded cartridge with water, the RNA is detritylated with 0.5% TFA for 13 min. The cartridge is then washed again with water, salt exchanged with 1 M NaCl and washed with water again. The oligonucleotide is then eluted with 30% acetonitrile.

Inactive hammerhead ribozymes or binding attenuated control (BAC) oligonucleotides) are synthesized by substituting a U for G₅ and a U for A₁4 (numbering from Hertel, K. J., et al., 1992, <u>Nucleic Acids Res.</u>, 20, 3252). Similarly, one or more nucleotide substitutions can be introduced in other enzymatic nucleic acid molecules to inactivate the molecule and such molecules can serve as a negative control.

The average stepwise coupling yields are typically >98% (Wincott et al., 1995

Nucleic Acids Res. 23, 2677-2684). Those of ordinary skill in the art will recognize that
the scale of synthesis can be adapted to be larger or smaller than the example described
above including but not limited to 96-well format, all that is important is the ratio of

chemicals used in the reaction.

Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together post-synthetically, for example, by ligation (Moore et al., 1992, Science 256, 9923; Draper et al., International PCT publication No. WO 93/23569; Shabarova et al., 1991, Nucleic Acids Research 19, 4247; Bellon et al., 1997, Nucleosides & Nucleotides, 16, 951; Bellon et al., 1997, Bioconiugate Chem. 8, 204).

The nucleic acid molecules of the present invention are modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-flouro, 2'-C-methyl, 2'-H (for a review see Usman and Cedergren, 1992, TIBS 17, 34; Usman et al., 1994, Nucleic Acids Symp. Ser. 31, 163). Ribozymes are purified by gel electrophoresis using general methods or are purified by high pressure liquid chromatography (HPLC; see Wincott et al., supra, the totality of which is hereby incomorated herein by reference) and are re-suspended in water.

The sequences of the ribozymes and antisense constructs that are chemically synthesized, useful in this study, are shown in Tables 3-31, 33, 34, 37-43, 56, 58, 59, 62, 63. Those in the art will recognize that these sequences are representative only of many more such sequences where the enzymatic portion of the ribozyme (all but the binding arms) is altered to affect activity. The ribozyme and antisense construct sequences listed in Tables 3-31, 33, 34, 37-43, 56, 58, 59, 62, 63 may be formed of ribonucleotides or other nucleotides or non-nucleotides. Such ribozymes with enzymatic activity are equivalent to the ribozymes described specifically in the Tables.

Optimizing Activity of the nucleic acid molecule of the invention.

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Chemically synthesizing nucleic acid molecules with modifications (base, sugar and/or phosphate) that prevent their degradation by scrum ribonucleases may increase their potency (see e.g., Eckstein et al., International Publication No. WO 92/07065; Perrault et al., 1990 Nature 344, 565; Pieken et al., 1991, Science 253, 314; Usman and Cedergren, 1992, Trends in Biochem. Sci. 17, 334; Usman et al., International Publication No. WO 93/15187; Rossi et al., International Publication No. WO 91/03162; Sproat, US Patent No.

5,334,711; and Burgin et al., supra; all of these describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of the nucleic acid molecules herein and are all hereby incorporated by reference herein). Modifications which enhance their efficacy in cells, and removal of bases from nucleic acid molecules to shorten oligonucleotide synthesis times and reduce chemical requirements are desired.

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There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into nucleic acid molecules (e.g., enzymatic nucleic acid molecules) without significantly effecting catalysis and with significant enhancement in their nuclease stability and efficacy. Enzymatic nucleic acid molecules are modified to enhance stability and/or enhance catalytic activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-O-allyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992 TIBS 17, 34; Usman et al., 1994 Nucleic Acids Symp. Ser. 31, 163; Burgin et al., 1996 Biochemistry 35, 14090). Sugar modification of enzymatic nucleic acid molecules have been extensively described in the art (see Eckstein et al., International Publication PCT No. WO 92/07065; Perrault et al. Nature 1990, 344, 565-568; Pieken et al. Science 1991, 253, 314-317; Usman and Cedergren, Trends in Biochem. Sci. 1992, 17, 334-339; Usman et al. International Publication PCT No. WO 93/15187; Sproat, US Patent No. 5,334,711 and Beigelman et al., 1995 J. Biol. Chem. 270, 25702; all of the references are hereby incorporated in their totality by reference herein). Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into enzymatic nucleic acid molecules without inhibiting catalysis, and are incorporated by reference herein. The 2'-position of the sugar in a nucleotide present in the nucleic acid molecules of the instant invention which tolerates substitution is selected from the group comprising -H, -OH, -COOH, -CONH2, -CONHR1, -CONR1R2, -NH2, -NHR1, -NR1R2, -NHCOR1, -SH, SR1, -F, -ONH2, -ONHR1, -ONR1R2, -NHOH, -NHOR1, -NR2OH, -NR2OR1, substituted or unsubstituted C1-C10 straight chain or branched alkyl, substituted or unsubstituted C2-C10 straight chain or branched alkenyl, substituted or unsubstituted C2-C10 straight chain or branched alkynyl, substituted or unsubstituted C1-C10 straight chain or branched alkoxy, substituted or unsubstituted C2-C10 straight chain or branched alkenyloxy, and substituted or unsubstituted C2-C10 straight chain or branched alkynyloxy. The substituents for sugar 2'

position preferably are independently halogen, cyano, amino, carboxy, ester, ether, carboxamide, hydroxy, or mercapto. R^1 and R^2 can be substituted or unsubstituted alkyl, alkenyl, or alkynyl groups, where the substituents are independently halogen, cyano, amino, carboxy, ester, ether, carboxamide, hydroxy, or mercapto.

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In view of such teachings, similar modifications can be used as described herein to modify the nucleic acid molecules of the instant invention. Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into ribozymes without inhibiting catalysis, and are incorporated by reference herein. In view of such teachings, similar modifications can be used as described herein to modify the nucleic acid molecules of the instant invention.

Some of the non-limiting examples of base modifications that can be introduced into enzymatic nucleic acids without significantly effecting their catalytic activity include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyluracil, dihydrouridine, naphthyl, aminophenyl, 5-alkyleytidines (e.g., 5-methylcytidine), 5-alkyluridines (e.g., ribothynidine), 5-halouridine (e.g., 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (e.g. 6-methylluridine) and others (Burgin et al., 1996, Biochemistry, 35, 14090). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents; such bases may be used within the catalytic core of the enzyme and/or in the substrate-binding regions.

The nucleic acid bases can be hypoxanthin-9-yl, or a functional equivalent thereof, in position^{15.1} of the ribozyme; the base at other positions may be guanin-9-yl, hypoxanthin-9-yl or 7-deazaguanin-9-yl in positions 5, 8 and 12 in the ribozyme; adenin-9-yl, 2,6-diaminopurin-9-yl, purin-9-yl or 7-deaza adenin-9-yl in position 6, 9, 13 and 14; uracil-1-yl, uracil-5-yl, thymin-1-yl or 5-propynyluracil-1-yl in position 4; cytosin-1-yl, 5-methylcytosin-1-yl, or 5-propynylcytosin-1-yl in position 3; and adenin-9-yl, cytosin-1-yl, guanin-9-yl, uracil-1-yl, uracil-5-yl, hypoxanthin-9-yl, thymin-1-yl, 5-methylcytosin-1-yl, 2,6-diaminopurin-9-yl, purin-9-yl, 7-deaza adenin-9-yl, 7-deazaguanin-9-yl, 5
30 propynylcytosin-1-yl, 5-propynyluracil-1-yl, isoguanin-9-yl, 2-aminopurin-9-yl, 6-methyluracil-1-yl, 4-thiouracil-1-yl, 2-pyrimidone-1-yl, quinazoline-2,4-dione-1-yl, xanthin-9-yl, N²-dimethylguanin-9-yl, or a functional equivalent thereof in position 7. The

base at position 15.1 is preferably hypoxanthin-9-yl or an analog where no hydrogen bond can form between any group at the 2 position of the base and the 2-oxo group of C^{16.1}.

Preferably, B is not guanin-9-yl in position 15.1.

In particular, the invention features modified ribozymes having a base substitution selected from pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene. 3-methyluracil, dihydrouracil, naphthyl, 6-methyl-uracil and aminophenyl.

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While chemical modification of oligonucleotide internucleotide linkages with phosphorothioate, phosphorothioate, and/or 5'-methylphosphonate linkages improves stability, too many of these modifications may cause some toxicity. Therefore, when designing nucleic acid molecules, the amount of these internucleotide linkages should be minimized. The reduction in the concentration of these linkages should lower toxicity resulting in increased efficacy and higher specificity of these molecules.

Nucleic acid molecules having chemical modifications which maintain or enhance activity are provided. Such nucleic acid molecules are also generally more resistant to nucleases than unmodified nucleic acid. Thus, in a cell and/or in vivo the activity may not be significantly lowered. Therapeutic nucleic acid molecules delivered exogenously must optimally be stable within cells until translation of the target RNA has been inhibited long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Clearly, nucleic acid molecules must be resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of RNA and DNA (Wincott et al., 1995 Nucleic Acids Res. 23, 2677; Caruthers et al., 1992, Methods in Enzymology 211,3-19 (all are incorporated by reference herein) have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

Use of these the nucleic acid-based molecules of the invention will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple antisense or enzymatic nucleic acid molecules targeted to different genes, nucleic acid molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations of molecules (including different motifs) and/or other chemical or biological molecules). The treatment of patients with nucleic acid molecules may also include combinations of different types of nucleic acid molecules.

Therapeutic nucleic acid molecules (e.g., enzymatic nucleic acid molecules and antisense nucleic acid molecules) delivered exogenously must optimally be stable within cells until translation of the target RNA has been inhibited long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Clearly, these nucleic acid molecules must be resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of nucleic acid molecules described in the instant invention and in the art have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

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By "enhanced enzymatic activity" is meant to include activity measured in cells and/or in vivo where the activity is a reflection of both catalytic activity and ribozyme stability. In this invention, the product of these properties is increased or not significantly (less than 10-fold) decreased in vivo compared to an all RNA ribozyme or all DNA enzyme.

In yet another preferred embodiment, nucleic acid catalysts having chemical modifications which maintain or enhance enzymatic activity are provided. Such nucleic acid catalysts are also generally more resistant to nucleases than unmodified nucleic acid. Thus, in a cell and/or in vivo the activity may not be significantly lowered. As exemplified herein such ribozymes are useful in a cell and/or in vivo even if activity over all is reduced 10 fold (Burgin et al., 1996, Biochemistry, 35, 14090). Such ribozymes herein are said to "maintain" the enzymatic activity of an all RNA ribozyme.

In another aspect the nucleic acid molecules comprise a 5' and/or a 3'- cap structure.

By "cap structure" is meant chemical modifications, which have been incorporated at either terminus of the oligonucleotide (see, for example, Wincott et al., WO 97/26270, incorporated by reference herein). These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and may help in delivery and/or localization within a cell. The cap may be present at the 5'-terminus (5'-cap) or at the 3'-terminal (3'-cap) or may be present on both termini. In non-limiting examples: the 5'-cap is selected from the group comprising inverted abasic residue (moiety); 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide, 4'-thio nucleotide; carbocyclic nucleotide; 1,5-

anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; threo-pentofuranosyl nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 3'-2'-inverted abasic moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphorodithioate; or bridging or non-bridging methylphosphonate moiety (for more details, see Wincott et al., International PCT publication No. WO 97/26270, incorporated by reference herein).

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In yet another preferred embodiment, the 3'-cap is selected from a group comprising, 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,2-aminodecyl phosphate; 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminodecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alphanucleotide; modified base nucleotide; phosphorodithioate; threo-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moieties (for more details see Beaucage and Iyer, 1993, Tetrahedron 49, 1925; incorporated by reference herein).

An "alkyl" group refers to a saturated aliphatic hydrocarbon, including straightchain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12
carbons. More preferably it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4
carbons. The alkyl group may be substituted or unsubstituted. When substituted the
substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO2 or N(CH3)2,
amino, or SH. The term also includes alkenyl groups which are unsaturated hydrocarbon
groups containing at least one carbon-carbon double bond, including straight-chain,
branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons.
More preferably it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4
carbons. The alkenyl group may be substituted or unsubstituted. When substituted the

substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO2, halogen, N(CH3)2, amino, or SH. The term "alkyl" also includes alkynyl groups which have an unsaturated hydrocarbon group containing at least one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably it is a lower alkynyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkynyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO2 or N(CH3)2, amino or SH.

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Such alkyl groups may also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group which has at least one ring having a conjugated pi electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The preferred substitutent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an -C(O)-OR, where R is either alkyl, aryl, alkylaryl or hydrogen.

By "nucleotide" as used herein is as recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a nucleotide sugar moiety. Nucleotides generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see, for example, Usman and McSwiggen, supra; Eckstein et al., International PCT Publication No. WO 92/07065; Usman et al., International PCT Publication No. WO 93/15187;

Uhlman & Peyman, supra, all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach et al., 1994, Nucleic Acids Res. 22, 2183. Some of the non-limiting examples of base modifications that can be introduced into nucleic acid molecules include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkyletidines (e.g., 5-methylcytidine), 5-alkyluridines (e.g., ribothymidine), 5-halouridine (e.g., 6-methyluridine), propyne, and others (Burgin et al., 1996, Biochemistry, 35, 14090; Uhlman & Peyman, supra).

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By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents; such bases may be used at any position, for example, within the catalytic core of an enzymatic nucleic acid molecule and/or in the substrate-binding regions of the nucleic acid molecule. Such modified nucleotides include dideoxynucleotides which have pharmaceutical utility well known in the art, as well as utility in basic molecular biology methods such as sequencing.

In a preferred embodiment, the invention features modified ribozymes with phosphate backbone modifications comprising one or more phosphorothioate, phosphorodithioate, methylphosphonate, morpholino, amidate carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and/or alkylsilyl, substitutions. For a review of oligonucleotide backbone modifications, see Hunziker and Leumann, 1995, Nucleic Acid Analogues: Synthesis and Properties, in Modern Synthetic Methods, VCH, 331-417, and Mesmaeker et al., 1994, Novel Backbone Replacements for Oligonucleotides, in Carbohydrate Modifications in Antisense Research, ACS, 24-39. These references are hereby incorporated by reference herein.

By "abasic" is meant sugar moieties lacking a base or having other chemical groups in place of a base at the 1' position, (for more details, see Wincott *et al.*, International PCT publication No. WO 97/26270).

By "unmodified nucleoside" or "unmodified nucleotide" is meant one of the bases adenine, cytosine, guanine, thymine, uracil joined to the 1' carbon of β -D-ribo-furanose.

By "modified nucleoside" or "modified nucleotide" is meant any nucleotide base which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate.

In connection with 2'-modified nucleotides as described for the present invention, by "amino" is meant 2'-NH₂ or 2'-O-NH₂, which may be modified or unmodified. Such modified groups are described, for example, in Eckstein et al., U.S. Patent 5,672,695 and Matulic-Adamic et al., WO 98/28317, which are both incorporated by reference in their entireties.

Various modifications to nucleic acid (e.g., antisense and ribozyme) structure can be made to enhance the utility of these molecules. Such modifications will enhance shelf-life, half-life in vitro, stability, and ease of introduction of such oligonucleotides to the target site, e.g., to enhance penetration of cellular membranes, and confer the ability to recognize and bind to targeted cells.

Use of these molecules will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple ribozymes targeted to different genes, ribozymes coupled with known small molecule inhibitors, or intermittent treatment with combinations of ribozymes (including different ribozyme motifs) and/or other chemical or biological molecules). The treatment of patients with nucleic acid molecules may also include combinations of different types of nucleic acid molecules. Therapies may be devised which include a mixture of ribozymes (including different ribozyme motifs), antisense and/or 2-5A chimera molecules to one or more targets to alleviate symptoms of a disease.

Administration of Nucleic Acid Molecules

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Methods for the delivery of nucleic acid molecules are described in Akhtar et al., 1992, Trends Cell Bio., 2, 139; and Delivery Strategies for Antisense Oligonucleotide Therapeutics, ed. Akhtar, 1995 which are both incorporated herein by reference. Sullivan et al., PCT WO 94/02595, further describes the general methods for delivery of enzymatic RNA molecules. These protocols may be utilized for the delivery of virtually any nucleic acid molecule. Nucleic acid molecules may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels,

cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, nucleic acid molecules may be directly delivered ex vivo to cells or tissues with or without the aforementioned vehicles. Alternatively, the nucleic acid/vehicle combination is locally delivered by direct injection or by use of a catheter, infusion numn or stent. Many examples in the art describe CNS delivery methods of oligonucleotides by osmotic pump, (see Chun et al., 1998, Neuroscience Letters, 257, 135-138, D'Aldin et al., 1998, Mol. Brain Research, 55, 151-164, Dryden et al., 1998, J. Endocrinol., 157, 169-175, Ghirnikar et al., 1998, Neuroscience Letters, 247, 21-24) or direct infusion (Broaddus et al., 1997, Neurosurg. Focus, 3, article 4). Other routes of delivery include, but are not limited to oral (tablet or pill form) and/or intrathecal delivery (Gold, 1997, Neuroscience, 76, 1153-1158). For a comprehensive review on drug delivery strategies including broad coverage of CNS delivery, see Jain, Drug Delivery Systems: Technologies and Commercial Opportunities, Decision Resources, 1998. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of nucleic acid delivery and administration are provided in Sullivan et al., supra, Draper et al., PCT WO93/23569; Beigelman et al., PCT WO99/05094, and Klimuk et al., PCT WO99/04819 all of which are incorporated by reference herein.

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The molecules of the instant invention can be used as pharmaceutical agents.

Pharmaceutical agents prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state in a patient.

The negatively charged polynucleotides of the invention can be administered (e.g., RNA, DNA or protein) and introduced into a patient by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a liposome delivery mechanism, standard protocols for formation of liposomes can be followed. The compositions of the present invention may also be formulated and used as tablets, capsules or elixirs for oral administration; suppositories for rectal administration; sterile solutions; suspensions for injectable administration; and the other compositions known in the art.

The present invention also includes pharmaceutically acceptable formulations of the compounds described. These formulations include salts of the above compounds, e.g., acid addition salts, for example, salts of hydrochloric, hydrobromic, acetic acid, and benzene sulfonic acid.

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A pharmacological composition or formulation refers to a composition or formulation in a form suitable for administration, e.g., systemic administration, into a cell or patient, preferably a human. Suitable forms, in part, depend upon the use or the route of entry, for example, oral, transdermal, or by injection. Such forms should not prevent the composition or formulation from reaching a target cell (i.e., a cell to which the negatively charged polymer is desired to be delivered to). For example, pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms which prevent the composition or formulation from exerting its effect.

By "systemic administration" is meant in vivo systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body. Administration routes which lead to systemic absorption include, without limitations: intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes expose the desired negatively charged polymers, e.g., nucleic acids, to an accessible diseased tissue. The rate of entry of a drug into the circulation has been shown to be a function of molecular weight or size. The use of a liposome or other drug carrier comprising the compounds of the instant invention can potentially localize the drug, for example, in certain tissue types, such as the tissues of the reticular endothelial system (RES). A liposome formulation which can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This approach may provide enhanced delivery of the drug to target cells by taking advantage of the specificity of macrophage and lymphocyte immune recognition of ahnormal cells, such as cancer cells.

By pharmaceutically acceptable formulation is meant, a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the instant invention in the physical location most suitable for their desired activity. Nonlimiting examples of agents suitable for formulation with the nucleic acid molecules of the instant invention include: P-glycoprotein inhibitors (such as Pluronic P85) which can enhance

entry of drugs into the CNS (Jolliet-Riant and Tillement, 1999, Fundam. Clin. Pharmacol., 13, 16-26); biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery after intracerebral implantation (Emerich, DF et al., 1999, Cell Transplant, 8, 47-58) Alkermes, Inc. Cambridge, MA; and loaded nanoparticles, such as those made of polybutyleyanoacrylate, which can deliver drugs across the blood brain barrier and can alter neuronal uptake mechanisms (Prog Neuropsychopharmacol Biol Psychiatry, 23, 941-949, 1999). Other non-limiting examples of delivery strategies for the nucleic acid molecules of the instant invention include material described in Boado et al., 1998, J. Pharm. Sci., 87, 1308-1315; Tyler et al., 1999, FEBS Lett., 421, 280-284; Pardridge et al., 1995, PNAS USA., 92, 5592-5596; Boado, 1995, Adv. Drug Delivery Rev., 15, 73-107; Aldrian-Herrada et al., 1998, Nucleic Acids Res., 26, 4910-4916; and Tyler et al., 1999, PNAS USA., 96, 7053-7058.

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The invention also features the use of the composition comprising surface-modified linosomes containing poly (ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes). These formulations offer a method for increasing the 15 accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic et al. Chem. Rev. 1995, 95, 2601-2627; Ishiwata et al., Chem. Pharm. Bull. 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably 20 by extravasation and capture in the neovascularized target tissues (Lasic et al., Science 1995, 267, 1275-1276; Oku et al., 1995, Biochim. Biophys. Acta, 1238, 86-90). The longcirculating liposomes enhance the pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu et al., J. Biol. Chem. 1995, 42, 24864-24870; Choi 25 et al., International PCT Publication No. WO 96/10391; Ansell et al., International PCT Publication No. WO 96/10390; Holland et al., International PCT Publication No. WO 96/10392; all of which are incorporated herein by reference). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically 30 aggressive MPS tissues such as the liver and spleen.

The present invention also includes compositions prepared for storage or administration which include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A.R. Gennaro edit. 1985) hereby incorporated by reference herein. For example, preservatives, stabilizers, dyes and flavoring agents may be provided. These include sodium benzoate, sorbic acid and esters of *p*-hydroxybenzoic acid. In addition, antioxidants and suspending agents may be used.

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A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent medication, and other factors which those skilled in the medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer.

The nucleic acid molecules of the present invention may also be administered to a patient in combination with other therapeutic compounds to increase the overall therapeutic effect. The use of multiple compounds to treat an indication may increase the beneficial effects while reducing the presence of side effects.

Alternatively, certain of the nucleic acid molecules of the instant invention can be expressed within cells from eukaryotic promoters (e.g., Izant and Weintraub, 1985, Science, 229, 345; McGarry and Lindquist, 1986, Proc. Natl. Acad. Sci., USA, 83, 399;

Scanlon et al., 1991, Proc. Natl. Acad. Sci. USA, 88, 10591-5; Kashani-Sabet et al., 1992, Antisense Res. Dev., 2, 3-15; Dropulic et al., 1992, J. Virol., 66, 1432-41; Weerasinghe et al., 1991, J. Virol., 65, 5531-4; Ojwang et al., 1992, Proc. Natl. Acad. Sci. USA, 89, 10802-6; Chen et al., 1992, Nucleic Acids Res., 20, 4581-9; Sarver et al., 1990 Science, 247, 1222-1225; Thompson et al., 1995, Nucleic Acids Res., 23, 2259; Good et al., 1997, Gene Therapy, 4, 45; all of these references are hereby incorporated herein, in their totalities, by reference). Those skilled in the art realize that any nucleic acid can be expressed in eukaryotic cells from the appropriate DNA/RNA vector. The activity of such

nucleic acids can be augmented by their release from the primary transcript by a ribozyme (Draper et al., PCT WO 93/23569, and Sullivan et al., PCT WO 94/02595; Ohkawa et al., 1992, Nucleic Acids Symp. Ser., 27, 15-6; Taira et al., 1991, Nucleic Acids Res., 19, 5125-30; Ventura et al., 1993, Nucleic Acids Res., 21, 3249-55; Chowrira et al., 1994, J. Biol. Chem., 269, 25856; all of these references are hereby incorporated in their totality by reference herein).

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In another aspect of the invention, RNA molecules of the present invention are preferably expressed from transcription units (see, for example, Couture et al., 1996, TIG., 12, 510) inserted into DNA or RNA vectors. The recombinant vectors are preferably DNA plasmids or viral vectors. Ribozyme expressing viral vectors could be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. Preferably, the recombinant vectors capable of expressing the nucleic acid molecules are delivered as described above, and persist in target cells. Alternatively, viral vectors may be used that provide for transient expression of nucleic acid molecules. Such vectors might be repeatedly administered as necessary. Once expressed, the nucleic acid molecule binds to the target mRNA. Delivery of nucleic acid molecule expressing vectors could be systemic, such as by intravenous or intra-muscular administration, by administration to target cells ex-planted from the patient followed by reintroduction into the patient, or by any other means that would allow for introduction into the desired target cell (for a review see Couture et al., 1996, TIG., 12, 510).

In one aspect, the invention features an expression vector comprising a nucleic acid sequence encoding at least one of the nucleic acid molecules of the instant invention is disclosed. The nucleic acid sequence encoding the nucleic acid molecule of the instant invention is operably linked in a manner which allows expression of that nucleic acid molecule.

In another aspect the invention features an expression vector comprising: a) a transcription initiation region (e.g., eukaryotic pol I, II or III initiation region); b) a transcription termination region (e.g., eukaryotic pol I, II or III termination region); c) a nucleic acid sequence encoding at least one of the nucleic acid catalyst of the instant invention; and wherein said sequence is operably linked to said initiation region and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. The vector may optionally include an open reading frame (ORF) for a

protein operably linked on the 5' side or the 3'-side of the sequence encoding the nucleic acid catalyst of the invention; and/or an intron (intervening sequences).

Transcription of the nucleic acid molecule sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990, Proc. Natl. Acad. Sci. U.S.A. 87, 6743-7; Gao and Huang 1993, Nucleic Acids Res., 21, 2867-72; 10 Lieber et al., 1993, Methods Enzymol., 217, 47-66; Zhou et al., 1990, Mol. Cell. Biol., 10, 4529-37). All of these references are incorporated by reference herein. Several investigators have demonstrated that nucleic acid molecules, such as ribozymes expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet et al., 1992, Antisense Res. Dev., 2, 3-15; Ojwang et al., 1992, Proc. Natl. Acad. Sci. USA, 89, 15 10802-6; Chen et al., 1992, Nucleic Acids Res., 20, 4581-9; Yu et al., 1993, Proc. Natl. Acad. Sci. U.S.A., 90, 6340-4; L'Huillier et al., 1992, EMBO J., 11, 4411-8; Lisziewicz et al., 1993, Proc. Natl. Acad. Sci. U. S. A, 90, 8000-4; Thompson et al., 1995, Nucleic Acids Res., 23, 2259; Sullenger & Cech, 1993, Science, 262, 1566). More specifically, transcription units such as the ones derived from genes encoding U6 small nuclear 20 (snRNA), transfer RNA (tRNA) and adenovirus VA RNA are useful in generating high concentrations of desired RNA molecules such as ribozymes in cells (Thompson et al.. supra; Couture and Stinchcomb, 1996, supra; Noonberg et al., 1994, Nucleic Acid Res., 22, 2830; Noonberg et al., US Patent No. 5,624,803; Good et al., 1997, Gene Ther., 4, 45; Beigelman et al., International PCT Publication No. WO 96/18736; all of these 25 publications are incorporated by reference herein. The above ribozyme transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or 30 alphavirus vectors) (for a review see Couture and Stinchcomb, 1996, supra).

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In yet another aspect, the invention features an expression vector comprising nucleic acid sequence encoding at least one of the nucleic acid molecules of the invention. in a manner which allows expression of that nucleic acid molecule. The expression vector comprises in one embodiment; a) a transcription initiation region; b) a transcription termination region; c) a nucleic acid sequence encoding at least one said nucleic acid molecule; and wherein said sequence is operably linked to said initiation region and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. In another preferred embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an open reading frame; d) a nucleic acid sequence encoding at least one said nucleic acid molecule. wherein said sequence is operably linked to the 3'-end of said open reading frame; and wherein said sequence is operably linked to said initiation region, said open reading frame and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. In yet another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) a nucleic acid sequence encoding at least one said nucleic acid molecule; and wherein said sequence is operably linked to said initiation region, said intron and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. In another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) an open reading frame; e) a nucleic acid sequence encoding at least one said nucleic acid molecule, wherein said sequence is operably linked to the 3'-end of said open reading frame; and wherein said sequence is operably linked to said initiation region, said intron, said open reading frame and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule.

Examples:

The following are non-limiting examples showing the selection, isolation, synthesis and activity of nucleic acids of the instant invention.

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Example 1: Telomerase

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The ribonucleoprotein enzyme telomerase consists of an RNA template subunit and one or more protein subunits including telomerase reverse transcriptase (TERT), which function together to direct the synthesis of telomeres. Telomeres exist as non-nucleosome 5 DNA/protein complexes at the physical ends of eukaryotic chromosomes. These capping structures maintain chromosome stability and replicative potential (Zakian, V. A., 1995. Science, 270, 1601-1607). Telomere structure is characterized by tandem repeats of conserved DNA sequences rich in G-C base pairs. Additional conserved telomere elements include a terminal 3'-overhang in the G-rich strand and non-histone structural proteins that are complexed with telomeric DNA in the nucleus. (Blackburn, "E., 1990, JBC., 265, 5919-5921.). Observed shortening of telomeres coincides with the onset of cellular senescence in most somatic cell lines lacking significant levels of telomerase. This finding has had a profound impact on our views concerning the mechanisms of aging, age related disease, and cancer.

Conventional DNA polymerases are unable to fully replicate the ends of linear chromosomes (Watson, J. D., 1972, Nature, 239, 197-201). This inability stems from the 3' G-rich overhang that is a product of ribonuclease cleavage of the RNA primer used in DNA replication. The overhang prevents DNA polymerase replication since the recessed C-rich parent strand cannot be used as a template. Telomerase overcomes this limitation by extending the 3' end of the chromosome using deoxyribonucleotides as substrates and a sequence within the telomerase RNA subunit as a template. (Lingner, J., 1995, Science, 269, 1533-1534). As such, telomerase is considered a reverse transcriptase that is responsible for telomere maintenance.

Telomerase was first discovered by in Tetrahymena thermophila in 1985 (Greider,

C. W., 1995. Cell. 43, 405-413). The RNA subunits and their respective genes were later discovered and characterized in protozoa, budding yeast, and mammals. Genetic studies of these genes confirmed the role of telomerase RNA (TR) in determining telomere sequence by mutating genes which encode the telomeric RNA (Yu, G. L., 1990, Nature, 344, 126-132), (Singer, M. S., 1994, Science, 266, 404-409), (Blasco, M. A., 1995, Science, 269, 1267-1270). These studies showed that telomerase activity parallels TR expression in protozoa, yeast and mice. However, the expression of human telomerase RNA (hTR) does not correlate well with telomerase activity in mammalian cells. Many

human tissues express hTR but are devoid of telomerase activity (Feng, J., 1995, Science, 269, 1236-1241). Knockout mice, in which the mTR gene has been deleted from germline cells, have been shown to be viable for at least six generations. Cells from later generations of these mice showed chromosomal abnormalities consistent with telomere degradation, indicating that mTR is necessary for telomere length maintenance, but is not required for embryonic development, oncogenic transformation, or tumor formation in mice (Blasco, M. A., 1997, Cell, 91, 25-34).

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The first catalytically active subunit of telomerase (p123) was isolated from Euplotes aediculatus along with another subunit (p43) and a 66-kD RNA subunit (Linger, J., 1996, Proc. Natl. Acad. Sci., 93, 10712-10717). Subsequent studies revealed telomerase 10 catalytic subunit homologs from fission yeast (Est2p) and human genes (TRT1). The human homolog, TRT1 encoding hTERT, expressed mRNA with a strong correlation to telomerase activity in human cells (Nakamura, T. M., 1997, Science, 277, 955-959). Reconstitution of telomerase activity with in vitro transcribed and translated hTERT and hTR, either co-synthesized or simply mixed, demonstrated that hTERT and hTR represent 15 the minimal components of telomerase. Furthermore, transient expression of hTERT in normal diploid human cells restored telomerase activity, demonstrating that hTERT is the only component necessary to restore telomerase activity in normal human cells (Weinrich, S. L., 1997, Nature Genetics, 17, 498-502). The introduction of telomerase into normal human cells using hTERT expression via transfection has resulted in the extension of life 20 span in these cells. Such findings indicate that telomere loss in the absence of telomerase is the "mitotic clock" that controls the replicative potential of a cell prior to senescence (Bodnar, A. G., 1998, Science, 279, 349-352).

Expression of telomerase is observed in germ cell and most cancer cell lines. These "immortal" cell lines continue to divide without shortening of their telomeres (Kim, N. W., 1994, Science, 266, 2011-2015). A model of tumor progression has evolved from these findings, suggesting a role for telomerase expression in malignant transformation. Successful malignant transformation in human cells was accomplished for the first time by ectopic expression of hTERT in combination with two oncogenes, SV40 large-T and Hras. Injection of nude mice with cells expressing these oncogenes and hTERT resulted in 30 rapid growth of tumors. These observations indicate that hTERT mediated telomere

maintenance is essential for the formation of human tumor cells (Hahn, W. C., 1999, Nature, 400, 464-468).

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Various methods have been developed to assay telomerase activity in vitro. The most widely used method to characterize telomerase activity is the telomeric repeat amplification protocol (TRAP). TRAP utilizes RT-PCR of cellular extracts to measure telomerase activity by making the amount of PCR target dependant upon the biochemical activity of the enzyme (Kim, N. W., 1997, Nucleic Acids Research, 25, 2595-2597, which is incorporated by reference herein).

A method based on Kim is as follows. Briefly, for the telomerase assay, 2µg of protein extract is used. The extract is assayed in 50µl of reaction mixture containing 0.1 µg TS substrate primer (5'-AATCCGTCGAGCAGAGTT-3', end-labeled using alpha-²²P-ATP and T4 polynucleotide kinase), 0.1µg ACX return primer(5'-GCGCGG[CTTACC]₃ CTAACC-3'), 0.1 µg NT internal control primer (5'-ATCGCTTCTCGGCCTTTT-3'), 0.01 micromol TSNT internal control template (5'-

15 AATCCGTCGAGCAGAGTTAAAAGGCCGAGAACGAT-3'), 50 μM each

deoxynucleoside triphosphate, 2 U of Taq DNA polymerase, and 2 μ l CHAPS protein extract, all in 1X TRAP buffer (20 mM Tris (pH 8.3), 68 mM KCl, 1.5 mM MgCl₂, 1 mM EGTA, 0.05% Tween 20). Each reaction is placed in a thermocycler block preheated to 30 C and incubated at 30 C for 10 minutes, then cycled for 27 cycles of 94 degrees C for 30 seconds, 60 degrees C for 30 seconds. Reaction products are separated on a denaturing 8% polyacrylamide gel, followed by drying of the gel and autoradiography. The internal control (to control for possible Taq polymerase inhibition) generates a band of 36 nt. Comparison of radioactive signal integrated (e.g., by phorphorimager analysis) for telomerase-extended bands with the radioactive signal from a reaction performed with a known amount of quantification standard template (termed R8; 5'-AATCCGTCGAGCAGAGTTAG [GGTTAG]₇-3) allows expression of telomerase activity as an absolute value. The absolute value = TPG (total product generated) =(TP-TPf)/TI]/[(R8-B)/R]) x 100, where TP = telomerase products from test extract, TPf =

 $TPI)TIJ[(R8-B)RI)] \times 100, \ where \ TP = telomerase \ products \ from \ test \ extract, \ TPi = telomerase \ products \ from \ a heat-inactivated \ (75\ C, 10\ minutes) \ extract \ reaction, \ TI = the signal \ from \ the internal \ control, \ R8 = the signal \ from \ the \ R8 \ qualification \ standard \ template \ reaction, \ B = signal \ from \ a \ lysis \ buffer-only \ blank \ reaction, \ and \ RI = the \ internal \ control \ value \ for \ the \ reaction \ containing \ R8 \ template \ and \ NT \ and \ TSNT \ control \ primers.$

TPG values of 0-10,000 are possible, with the linear range being from approximately 1 to 1000 TPG. The range of 1 to 1000 TPG encompasses the minimum and maximum levels of telomerase activity in most tumor samples tested, while non-tumor cells most often have no telomerase activity (TPG approximately zero).

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Telomerase activity may also be assayed as follows. Samples to be assayed for telomerase activity are prepared by extraction into CHAPS lysis buffer (10mM Tris pH 7.5, 1mM MgCl₂, 1mM EGTA, 0.1 mM PMSF, 5mM -mercaptoethanol, 1mM DTT, 0.5% 3-[(3-cholamidopropyl)-dimethyl-amino]-1- propanesulfonate (CHAPS), 10% glycerol and 40 U/ml RNAse inhibitor (Promega, Madison, WL, U.S.A.). Cells are suspended in CHAPS lysis buffer and incubated on ice for 30 minutes, which allows lysis of 90-100% of cells. Lysate is then transferred to polyallomer centrifuge tubes and spun at $100,000 \times g$ for 1 hour at 4 degrees C. The supernatant is the protein extract, and concentration ranges of 4-10 $\mu g/\mu l$ are suitable for telomerase assay. Extracts may be concentrated if necessary using a Microcon Microfilter 30 (Amicron, Beverly, MA U.S.A.) according to the manufactureris instructions. Extracts may be stored frozen at -80 degrees C until assayed.

A variety of animal models have been designed to assay telomerase activity in vivo. Inhibition of telomerase activity has been analyzed in rats via cell proliferation studies with MNU (N-methyl-N-nitosurea) induced mammary carcinomas in response to treatment with 4-(hydroxyphenyl)retinamide (4-HPR), a known inhibitor of mammary carcinogenesis in animal models and premenopausal women (Bednarek, A., 1999, Carcinogenesis, 20, 879-883). Additional studies have focused on the up-regulation of telomerase in transformed cell lines from animal and human model systems (Zhang, P. B., 1998, Leuk. Res., 22, 509-516), (Chadeneau, C., 1995, Oncogene, 11, 893-898), (Greenberg, R., 1999, Oncogene, 18, 1219-1226).

Human cell culture studies have been established to assay inhibition of telomerase activity in human carcinomas responding to various therapeutics. A human breast cancer model for studying telomerase inhibitors is described (Raymond, E., 1999, Br. J. Cancer, 80, 1332-1341). Human studies of telomerase expression as related to various other cancers are described including cervical cancer (Nakano, K., 1998, Am. J. Pathol, 153, 857-864), endometrial cancer (Kyo, S., 1999, Int. J. Cancer, 80, 60-63), meningeal carcinoma (Kleinschmidt-DeMasters, B. K., 1998, J. Neurol. Sci., 161, 124-134), lung

carcinoma (Yashima, K., 1997, Cancer Reseach, 57, 2372-2377), testicular cancer in response to cisplatin (Burger, A. M., 1997, Eur. J. Cancer, 33, 638-644), and ovarian carcinoma (Counter, C. M., 1994, Proc. Natl. Acad. Sci., 91, 2900-2904).

Particular degenerative and disease states that can be associated with telomerase

5 expression modulation include but are not limited to:

<u>Cancer</u>: Almost all human tumors have detectable telomerase activity (Shay, J. W., 1997, Eur. J. Cancer, 33, 787-791). Treatment with telomerase inhibitors may provide effective cancer therapy with minimal side effects in normal somatic cells that lack telomerase activity. The therapeutic potential exists for the treatment of a wide variety of cancer types.

<u>Restinosis</u>: Telomerase inhibition in vascular smooth muscle cells may inhibit restinosis by limiting proliferation of these cells.

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Infectious disease: Telomerase inhibition in infectious cell types that express telomerase activity may provide selective anti-infectious agent activity. Such treatment may prove especially effective in protozoan-based infection such as Giardia and Lesh Meniesis

<u>Transplant rejection</u>: Telomerase inhibition in endothelial cell types may demonstrate selective immunnosuppressant activity. Activation of telomerase in transplant cells could benefit grafting success through increased proliferative potential.

<u>Autoimmune disease</u>: Telomerase modulation in various immune cells may prove beneficial in treating diseases such as multiple sclerosis, lupus, and AIDS.

Age related disease: Activation of telomerase expression in cells at or nearing senescence as a result of advanced age or premature aging could benefit conditions such as macular degeneration, skin ulceration, and rheumatoid arthritis.

The present body of knowledge in telomerase research indicates the need for methods to assay telomerase activity and for compounds that can regulate telomerase expression for research, diagnostic, trait alteration, animal health and therapeutic use.

Gemcytabine and cyclophosphamide are non-limiting examples of chemotherapeutic agents that can be combined with or used in conjunction with the nucleic acid molecules (e.g. ribozymes and antisense molecules) of the instant invention. Those skilled in the art will recognize that other drugs such as anti-cancer compounds and therapies can be similarly be readily combined with the nucleic acid molecules of the instant invention

(e.g. ribozymes and antisense molecules) and are hence within the scope of the instant invention. Such compounds and therapies are well known in the art (see for example Cancer: Principles and Pranctice of Oncology, Volumes 1 and 2, eds Devita, V.T., Hellman, S., and Rosenberg, S.A., J.B. Lippincott Company, Philadelphia, USA; incorporated herein by reference) and include, without limitations, antifolates; fluoropyrimidines; cytarabine; purine analogs; adenosine analogs; amsacrine; topoisomerase I inhibitors; anthrapyrazoles; retinoids; antibiotics such as bleomycin, anthacyclins, mitomycin C, dactinomycin, and mithramycin; hexamethylmelamine; dacarbazine: 1-asperginase: platinum analogs; alkylating agents such as nitrogen mustard, 10 melphalan, chlorambucil, busulfan, ifosfamide, 4-hydroperoxycyclophosphamide, nitrosoureas, thiotepa; plant derived compounds such as vinca alkaloids, epipodophyllotoxins, taxol; Tomaxifen; radiation therapy; surgery; nutritional supplements; gene therapy; radiotherapy such as 3D-CRT; immunotoxin therapy such as ricin, monoclonal antibodies herceptin; and the like. For combination therapy, the nucleic acids of the invention are prepared in one of two ways. First, the agents are physically 15 combined in a preparation of nucleic acid and chemotherapeutic agent, such as a mixture of a nucleic acid of the invention encapsulated in liposomes and ifosfamide in a solution for intravenous administration, wherein both agents are present in a therapeutically effective concentration (e.g., ifosfamide in solution to deliver 1000-1250 mg/m²/day and liposome-associated nucleic acid of the invention in the same solution to deliver 0.1-100 20 mg/kg/day). Alternatively, the agents are administered separately but simultaneously in their respective effective doses (e.g., 1000-1250 mg/m²/d ifosfamide and 0.1 to 100 mg/kg/day nucleic acid of the invention).

Gaeta et al., US patents No. 5,760,062; 5,767,278; 5,770,613 have described small

25 molecule inhibitors of human telomerase RNA (hTR) subunit.

Blasco et al., 1995, Science, 269, 1267-1270 describe the synthesis and testing of antisense oligonucleotides targeted against a specific region of the mouse telomerase RNA (mTR) subunit and reported reduction in telomerase activity in mice.

Bisoffi et al., 1998, Eur. J. Cancer, 34, 1242-1249 have studied the down regulation of human telomerase activity by a retrovirus vector expressing antisense RNA targeted against the hTR RNA.

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Norton et al., 1996, Nature Biotechnology, 14, 615-619 have reported the use of a peptide nucleic acid (PNA) molecule targeting hTR RNA to down regulate telomerase activity in human immortal breast epithelial cells.

Yokoyama et al., 1998, Cancer Research, 58, 5406-5410 have reported the synthesis and testing of hammerhead ribozyme constructs targeting hTR RNA resulting in a decrease in the telomerase activity in Ishikawa cells.

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Henderson, European Patent Application No. 666,313-A2 describes methods of identifying and cloning hTR gene for use in gene therapy approaches for creating aberrant telomeric sequences in transfected human tumor cells. A ribozyme based gene therapy approach to inhibit the expression of hTR gene is described as well. The intended result of such therapies involves incurred genetic instability based on non-native telomeric sequences resulting in rapid cell death of the treated cells.

West et al., US patent No. 5,489,508 describe methods for determining telomere length and telomerase activity in cells. Inhibitors of hTR RNA, including oligonucleotides and/or small molecules are described.

These foregoing approaches of targeting the telomerase RNA subunit (TR) may not be very beneficial, because as demonstrated by Feng et al., (Feng, J., 1995, Science, 269, 1236-1241), telomerase activity in humans does not correlate well to hTR concentration.

Collins et al., International PCT publication No. WO 98/01542 describes assays for the detection of telomerase activity. Four human telomerase subunit proteins are described called p140, p105, p48 and p43. In addition, hybridization probes and primers are described as inhibitors of telomerase gene function. Antibody based inhibitors of telomerase protein subunits are described.

A more attractive approach to telomerase regulation would involve the regulation of human telomerase by modulating the expression of the protein subunits of the enzyme, preferably the reverse transcriptase (hTERT) subunit. Based of reconstitution experiments, hTERT and hTR represent the minimal components of telomerase. Since hTR expression does not correlate well with telomerase activity in human cells and since many human cells express hTR without telomerase activity, targeting hTERT may prove more beneficial than targeting hTR. hTERT is the only component necessary to restore 30 telomerase activity in normal human cells. A study in which the three major subunits of telomerase (hTR, TP1, and hTERT were assayed in normal and malignant endometrial

tissues determined that hTERT is a rate limiting determinant of enzymatic activity of human telomerase (Kyo, S., 1999, Int. J. Cancer, 80, 60-63). Additional protein subunits that have been isolated most likely serve only a structural role in telomerase activity, but may be important in enhancing the activity of the telomerase enzyme. As such, hTERT is one of the better targets for the ectopic regulation of telomerase activity.

Cech et al., International PCT publication No. WO 98/14593 describe compositions and methods related to hTERT for diagnosis, prognosis and treatment of human diseases, for altering proliferative capacity in cells and organisms, and for screening compounds and treatments with potential use as human therapeutics.

Cech et al., International PCT publication No. WO 98/14592 describe nucleic acid and amino acid sequences encoding various telomerase protein subunits and motifs of Euplotes aediculatus, and related sequences from Schizosaccharomyces, Saccharomyces sequences, and human telomerase. The polypeptides comprising telomeric subunits and functional polypeptides and ribonucleoproteins that contain these subunits are described as well. Cech et al., International PCT Publication No. WO 98/14592, mentions in general terms the the possibility of using antisense and ribozymes to down regulate the expression of human telomerase reverse transcriptase enzyme.

Identification of Potential Target Sites in Human TERT RNA

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The sequence of human TERT was screened for accessible sites using a computer folding algorithm. Regions of the RNA that did not form secondary folding structures and contained potential ribozyme and/or antisense binding/cleavage sites were identified. The sequences of these cleavage sites are shown in Tables 13-17.

25 Selection of Enzymatic Nucleic Acid Cleavage Sites in Human TERT RNA

To test whether the sites predicted by the computer-based RNA folding algorithm corresponded to accessible sites in TERT RNA, 10 hammerhead ribozyme and three G-Cleaver ribozyme sites were selected for further analysis (Table 17). Ribozyme target sites were chosen by analyzing sequences of Human TERT (Nakamura et al., 1997 Science 277, 955-959; Genbank sequence accession number: NM_003219) and prioritizing the sites on the basis of folding. Ribozymes were designed that could bind each target and were individually analyzed by computer folding (Christoffersen et al.,

1994 J. Mol. Struc. Theochem, 311, 273; Jaeger et al., 1989, Proc. Natl. Acad. Sci. USA, 86, 7706) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable intramolecular interactions between the binding arms and the catalytic core were eliminated from consideration. As noted below, varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 bases on each arm are able to bind to, or otherwise interact with, the target RNA.

Chemical Synthesis and Purification of Ribozymes for Efficient Cleavage of TERT RNA

Ribozymes were designed to anneal to various sites in the RNA message. The binding arms are complementary to the target site sequences described above. The ribozymes were chemically synthesized. The method of synthesis used followed the procedure for normal RNA synthesis as described above and in Usman et al., (1987 J. Am. Chem. Soc., 109, 7845), Scaringe et al., (1990 Nucleic Acids Res., 18, 5433) and Wincott et al., supra, and made use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The average stepwise coupling yields were >98%.

Ribozymes were also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbeck, 1989, Methods Enzymol. 180, 51). Ribozymes were purified by gel electrophoresis using general methods or were purified by high pressure liquid chromatography (HPLC; See Wincott et al., supra; the totality of which is hereby incorporated herein by reference) and were resuspended in water. The sequences of the chemically synthesized ribozymes used in this study are shown below in Table 13-17.

Ribozyme Cleavage of TERT RNA Target in vitro

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Ribozymes targeted to the human TERT RNA are designed and synthesized as described above. These ribozymes can be tested for cleavage activity in vitro, for example using the following procedure. The target sequences and the nucleotide location within the TERT RNA are given in Tables 13-17.

Cleavage Reactions: Full-length or partially full-length, internally-labeled target RNA for ribozyme cleavage assay is prepared by in vitro transcription in the presence of [a-32p] CTP, passed over a G 50 Sephadex column by spin chromatography and used as

substrate RNA without further purification. Alternately, substrates are $5^{t.32}P$ -end labeled using T4 polynucleotide kinase enzyme. Assays are performed by pre-warming $15~\mu l$ of a 2X concentration of purified ribozyme in ribozyme cleavage buffer (50 mM Tris-HCl, pH 7.5 at $37^{\circ}C$, 10~mM MgCl₂) and the cleavage reaction was initiated by adding the 2X ribozyme mix to an equal volume ($15~\mu l$) of substrate RNA (maximum of 1-5 nM; 5~x 10^5 to 1~x 10^7 cpm) that was also pre-warmed in cleavage buffer. As an initial screen, assays are carried out for 1~h our at $37^{\circ}C$ using a final concentration of either 40~nM or 1~mM ribozyme, i.e., ribozyme excess. The reaction is quenched by the addition of an equal volume ($30~\mu l$) of 95% formamide, 20~mM EDTA, 0.05% bromophenol blue and 0.05% xylene cyanol after which the sample is heated to $95^{\circ}C$ for 2~minutes, quick chilled and loaded onto a denaturing polyacrylamide gel. Substrate RNA and the specific RNA cleavage products generated by ribozyme cleavage are visualized on an autoradiograph of the gel. The percentage of cleavage is determined by Phosphor Imager quantitation of bands representing the intact substrate and the cleavage products.

Example 2: PTP-1B

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Protein tyrosine phosphorylation and dephosphorylation are important mechanisms in the regulation of signal transduction pathways that control the processes of cell growth, proliferation, and differentiation (Fantl, W. J., 1993, Annu. Rev. Biochem., 62, 453-481). 20 Cooperative enzyme classes regulate protein tyrosine phosphorylation and dephosphorylation events. These broad classes of enzymes consist of the protein tyrosine kinases (PTKs) and protein tyrosine phosphatases (PTPs). PTKs and PTPs can exist as both receptor-type transmembrane proteins and as cytoplasmic protein enzymes. Receptor tyrosine kinases propagate signal transduction events via extracellular receptor-ligand 25 interactions that result in the activation of the tyrosine kinase portion of the PTK in the cytoplasmic domain. Receptor-like transmembrane PTPs function through extracellular ligand binding that modulates dephosphorylation of intracellular phosphotyrosine proteins via cytoplasmic phosphatase domains. Cytoplasmic PTKs and PTPs exert enzymatic activity without receptor-mediated ligand interactions, however, phosphorylation can 30 regulate the activity of these enzymes.

Protein tyrosine phosphatase IB, a cytoplasmic PTP, was the first PTP to be isolated in homogeneous form (Tonks, N. K., 1988, J. Biol. Chem., 263, 6722-6730), characterized (Tonks, N. K., 1988, J. Biol. Chem., 263, 6731-6737), and sequenced (Charbonneau, H., 1989, Biochemistry, 86, 5252-5256). Cytoplasmic and receptor-like PTPs both share a catalytic domain characterized by eleven conserved amino acids containing cysteine and arginine residues that are critical for phosphatase activity (Streuli, M., 1990, EMBO, 9, 2399-2407). A cysteine residue at position 215 is responsible for the covalent attachment of phosphate to the enzyme (Guan, K., 1991, J. Biol. Chem., 266, 17026-17030). The crystal structure of human PTP1B defined the phosphate binding site of the enzyme as a glycine rich cleft at the surface of the molecule with cysteine 215 positioned at the base of this cleft. The location of cysteine 215 and the shape of the cleft provide specificity of PTPase activity for tyrosine residues but not for serine or threonine residues (Barford, D., 1994, Science, 263, 1397-1404).

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Receptor tyrosine kinase and protein tyrosine phosphatase localization plays a key role in the regulation of phosphotyrosine mediated signal transduction. PTP-IB activity and specificity against a panel of receptor tyrosine kinases demonstrated clear differences between substrates, suggesting that cellular compartmentalization is a determinant in defining the activity and function of the enzyme (Lammers, R., 1993, J. Biol. Chem., 268, 22456-22462). Experiments have indicated that PTP-IB is localized predominantly in the endoplasmic reticulum via its 35 amino acid carboxyterminal sequence. PTP-IB is also tightly associated with microsomal membranes with its catalytic phosphatase domain oriented towards the cytoplasm (Francioni, J. V., 1992, Cell. 68, 545-560).

PTP-1B has been identified as a negative regulator of the insulin response. PTP-1B is widely expressed in insulin sensitive tissues (Goldstein, B. J., 1993, Receptor, 3, 1-15).

Isolated PTP-1B dephosphorylates the insulin receptor in vitro (Tonks, N. K., 1988, J. Biol. Chem., 263, 6731-6737). PTP-1B dephosphorylation of multiple phosphotyrosine residues of the insulin receptor proceeds sequentially and with specificity for the three tyrosine residues that are critical for receptor autoactivation (Ramachandran, C., 1992, Biochemistry, 31, 4232-4238). In addition to insulin receptor dephosphorylation, PTP-1B also dephosphorylates the insulin related subtrate 1 (IRS-1), a principal substrate of the insulin receptor (Lammers, R., 1993, J. Biol. Chem., 268, 22456-22462).

Microinjection of PTP1B into Xenopus occytes results in the inhibition of insulin stimulated tyrosine phosphorylation of endogenous proteins, including the β -subunit of the insulin and insulin-like growth factor receptor proteins. The resulting 3 to 5 fold increase over endogenous PTPase activity also blocks the activation of an 86 peptide kinase (Cicirelli, M. F., 1990, Proc, Natl. Acad. Sci., 87, 5514-5518). Inactivation of recombinant rat PTP-1B with antibody immunoprecipitation results in the dramatic increase in insulin stimulated DNA synthesis and phosphatidylinositol 3'-kinase activity. Insulin stimulated receptor autophosphorylation and insulin receptor substrate 1 tyrosine phosphorylation are increased dramatically as well through PTP-1B inhibition (Ahmad, F., 1995, J. Biol. Chem., 270, 20503-20508).

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Increased PTP-1B expression correlates with insulin resistance in hyperglycemic cultured fibroblasts. In this study, desensitized insulin receptor function was observed via impaired insulin-induced autophosphorylation of the receptor. Treatment with insulin sensitivity normalizing thiazolidine derivatives resulted in the amelioration of the hyperglycemic insulin resistance via a normalization in PTP-1B expression (Maegawa, H., 1995, J. Biol. Chem., 270, 7724-7730). A murine model of insulin resistance with a knockout of the hetrerotrimeric GTP-binding protein subunit Giα2 provides a type 2 diabetis phenotype that correlates with the increased expression of PTP-1B (Moxam, C. M., 1996, Nature, 379, 840-844).

PTP-1B interacts directly with the activated insulin receptor β -subunit. An inactive homolog of PTP-1B was used to precipitate the activated insulin receptor in both purified receptor preparations and whole-cell lysates. Phosphorylation of the insulin receptor's triple tyrosine residues in the kinase domain is necessary for PTP-1B interaction. Furthermore, insulin stimulates tyrosine phosphorylation of PTP-1B (Seely, B. L., 1996, Diabetes, 45, 1379-1385). A similar study confirmed the direct interaction of PTP-1B with the insulin receptor β -subunit as well as the required multiple phosphorylation sites within the receptor and PTP-1B (Bandyopadhyay, D., J. Biol. Chem., 272, 1639-1645).

Knockout mice lacking the PTP-1B gene (both homozygous PTP-1B-4- and heterozygous PTP-1B+5) have been used to study the specific role of PTP-1B relating to insulin action in vivo. The resulting PTP-1B deficient mice were healthy and, in the fed state, had lower blood glucose and circulating insulin levels that were half that of their

PTP-1B^{+/+} expressing littermates. These PTP-1B deficient mice demonstrated enhanced insulin sensitivity in glucose and insulin tolerance tests. At the physiological level, the PTP-1B deficient mice showed increased phosphorylation of the insulin receptor after insulin administration. When fed a high fat diet, the PTP-1B deficient mice were resistant to weight gain and remained insulin sensitive as opposed to normal PTP-1B expressing mice, who rapidly gained weight and become insulin resistant (Elchebly, M., 1999, Science, 283, 1544-1548). As such, modulation of PTP-1B expression could be used to regulate autophosphorylation of the insulin receptor and increase insulin sensitivity *in vivo*. This modulation could prove beneficial in the treatment of insulin related disease states.

In light of the above findings, particular disease states that involve PTP-1B expression include but are not limited to:

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<u>Diabetes</u>: Both type 1 and type 2 diabetes may be treated by modulation of PTP-1B expression. Type 2 diabetes correlates to desensitized insulin receptor function (White et al., 1994). Disruption of the PTP-1B dephosphorylation of the insulin receptor in vivo manifests in insulin sensitivity and increased insulin receptor autophosphorylation (Elchebly et al., 1999). Insulin dependant diabetes, type 1, may respond to PTP-1B modulation through increased insulin sensitivity.

Obesity: Elchebly et al., 1999, demonstrated that PTP-1B deficient mice were resistant to weight gain when fed a high fat diet compared to normal PTP-1B expressing mice. This finding suggests that PTP-1B modulation may be beneficial in the treatment of obesity. Ahmad et al., 1997, Metab. Clin. Exp., 46, 1140-1145, describe reduced PTPs in adipose tissue and improved insulin sensitivity in obese subjects following weight loss.

Troglitazone is a non-limiting example of a pharmaceutical agent that can be combined with or used in conjunction with the nucleic acid molecules (e.g. ribozymes and antisense molecules) of the instant invention. Those skilled in the art will recognize that other drugs such as anti-diabetes and anti-obesity compounds and therapies can be similarly be readily combined with the nucleic acid molecules of the instant invention (e.g. ribozymes and antisense molecules) are hence within the scope of the instant invention.

Methods have been developed to assay PTP-1B activity.

Maegawa et al., 1995, J. Biol. Chem., 270, 7724-7730, describe a tissue culture model in which Rat 1 fibroblasts expressing human insulin receptors can be used to model

hyperglycemia induced insulin resistance. Maegawa et al. also describe assays to measure PTPase activity using labeled phosphorylated insulin receptors and by immunoenzymatic techniques.

Moxham et al., 1996, Nature, 379, 840-844, describe a murine animal and tissue culture model employing Gio2 deficiency to study hyperinsulinaemia, impaired glucose tolerance and resistance to insulin in vivo. Assays for PTPase activity and tyrosine phosphorylation of insulin-receptor substrate 1 are described.

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Khandelwal et al., 1995, Molecular and Cellular Biochemistry, 153, 87-94, describe four different animal models for studying insulin dependent and insulin resistant diabetes mellitus. These models were used to study the effect of vanadate, an insulin mimetic and PTPase inhibitor, on the insulin-stimulated phosphorylation of the insulin receptor and its tyrosine kinase actitivity.

Wang et al., 1999, Biochim. Biophys. Acta, 1431, 14-23, describe fluorescein monophosphates as fluorogenic substrates for PTPs.

Various methods and compounds have been developed to inhibit protein tyrosine phosphatase activity.

Wrobel et al., 1999, J. Med. Chem., 42, 3199-3202, describe PTP-1B inhibition and antihyperglycemic activity in the ob/ob mouse model by 11-arylbenzo[b]naphtho[2,3-d]furans and arylbenzo[b]naphtho[2,3-d]thiophenes.

Andersen et al., International PCT publication No. WO 98/DK407 describe the preparation of thienopyridzinones and thienochromenones as modulators of PTPases.

Taing et al., 1999, Biochemistry, 38, 3793-3803, describe potent and highly selective inhibitors of PTP-1B comprising an array of bis(aryldifluorophosphonates).

Ham et al., 1999, Bioorg. Med. Chem. Lett., 9, 185-186, describe selective
25 inactivation of PTP-1B by a sulfone analog of naphthoquinone.

Desmarais et al., 1999, Biochem, J., 337, 219-223, describe [Difluro(phosphono)methyl]phenylalanine-containing peptide inhibitors of PTPs.

Taylor et al., 1998, Bioorg. Med. Chcm., 6, 2235, describe potent non-peptidyl inhibitors of PTP-1B.

Kotoris et al., 1998, Bioorg. Med. Chem. Lett., 8, 3275-3280, describe novel phosphate mimetics for the design of non-peptidyl inhibitors of PTPs.

Groves et al., 1998, Biochemistry, 37, 17773-17783, describe the structural basis for PTP-1B inhibition by the phosphotyrosine peptide mimetics

(difluoronaphthylmethyl)phosphonic acid and the fluoromalonyl tyrosines with complexed crystal structures.

Yao et al., 1998, Bioorgl Med. Chem., 6, 1799-1810, describe the structure-based design and synthesis of small molecule PTP-1B inhibitors comprising novel naphthyldifluoromethyl phosphonic acids 1 and 2.

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Taylor et al., 1998, Bioorg. Med. Chem., 6, 1457-1468, describe potent non-peptidyl inhibitors of PTP-1B.

10 Desmarais et al., 1998, Arch. Biochem. Biophys., 354, 225-231, describe inhibition of PTP-1B and CD45 by sulfotyrosyl peptides.

Mjalli et al., application US 96-766114, cont. in part of US patent No. 543,630, describe the preparation of heterocyclic compounds as modulators of proteins with phosphotyrosine recognition units.

15 Wang et al., 1998, Bioorg. Med. Chem. Lett., 8, 345-350, describe naphthalenebis[α,α-difluoromethylenephosphonates] as potent inhibitors of PTPs.

Rice et al., 1997, Biochemistry, 36, 15965-15974, describe a targeted library of small molecule tyrosine and dual-specificity phosphatase inhibitors with random side chain variation from a rational core design.

Olefsky, International PCT publication No. WO 97/US2752 describes a method and phosphopeptides used for the treatment of insulin resistance based on the association of PTP-1B with the activated insulin receptor. Also included is a method for determining whether a compound inhibits PTP-1B binding to the insulin receptor.

Huyer et al., 1997, J. Biol. Chem., 272, 843-851, describe the mechanism of inhibition of PTPases by vanadate and pervanadate.

Burke $et\ al.$, 1996, Biochemistry, 35, 15989-15996, describe the structure-based design of PTP-1B inhibitors.

Tonks et al., International PCT publication No. WO 97/US13016, describe substrate-trapping protein PTPase mutants for identification of tyrosine-phosphorylated protein substrates and their clinical uses.

The human genome is thought to contain up to 100 PTPases, each varying slightly in chemistry but vastly in function. Compounds designed to inhibit PTP-1B activity specifically by covalent binding to or modification of PTP-1B have the potential for multiple side effects. Conventional drug substances that will potently suppress PTP-1B activity with few or no side effects from interaction with other PTPs are difficult to envision. A more attractive approach to PTP-1B modulation would involve the specific regulation of PTP-1B expression with oligonucleotides.

Identification of Potential Target Sites in Human PTP-1B RNA

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with, the target RNA.

The sequence of human PTP-1B was screened for accessible sites using a computer folding algorithm. Regions of the RNA that did not form secondary folding structures and contained potential ribozyme and/or antisense binding/cleavage sites were identified. The sequences of these cleavage sites are shown in Tables 3-8.

Selection of Enzymatic Nucleic Acid Cleavage Sites in Human PTP-1B RNA

To test whether the sites predicted by the computer-based RNA folding algorithm corresponded to accessible sites in PTP-1B RNA, 10 hammerhead ribozyme, five NCH and three G-Cleaver ribozyme sites were selected for further analysis (Table 8). Ribozyme target sites were chosen by analyzing sequences of Human PTP-1B (Genbank accession number M33689) and prioritizing the sites on the basis of folding. Ribozymes were designed that could bind each target and were individually analyzed by computer folding (Christoffersen et al., 1994 J. Mol. Struc. Theochem, 311, 273; Jaeger et al., 1989, Proc. Natl. Acad. Sci. USA, 86, 7706) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable intramolecular interactions between the binding arms and the catalytic core were eliminated from consideration. As noted below, varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 bases on each arm are able to bind to, or otherwise interact

Chemical Synthesis and Purification of Ribozymes for Efficient Cleavage of PTP-1B RNA

Ribozymes were designed to anneal to various sites in the RNA message. The binding arms are complementary to the target site sequences described above. The ribozymes were chemically synthesized. The method of synthesis used followed the procedure for normal RNA synthesis as described above and in Usman et al., (1987 J. Am. Chem. Soc., 109, 7845), Scaringe et al., (1990 Nucleic Acids Res., 18, 5433) and Wincott et al., supra, and made use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The average stepwise coupling yields were >98%.

Ribozymes were also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbeck, 1989, Methods Enzymol. 180, 51). Ribozymes were purified by gel electrophoresis using general methods or were purified by high pressure liquid chromatography (HPLC; see Wincott et al., supra; the totality of which is hereby incorporated herein by reference) and were resuspended in water. The sequences of the chemically synthesized ribozymes used in this study are shown below in **Tables 3-8**.

Ribozyme Cleavage of PTP-1B RNA Target in vitro

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Ribozymes targeted to the human PTP-1B RNA are designed and synthesized as described above. These ribozymes can be tested for cleavage activity in vitro, for example, using the following procedure. The target sequences and the nucleotide location within the PTP-1B RNA are given in Tables 3-8.

Cleavage Reactions: Full-length or partially full-length, internally-labeled target RNA for ribozyme cleavage assay is prepared by *in vitro* transcription in the presence of $[\alpha^{-32}p]$ CTP, passed over a G 50 Sephadex column by spin chromatography and used as substrate RNA without further purification. Alternately, substrates are $5^{\cdot-32}P$ -end labeled using T4 polynucleotide kinase enzyme. Assays are performed by pre-warming a 2X concentration of purified ribozyme in ribozyme cleavage buffer (50 mM Tris-HCl, pH 7.5 at 37°C, 10 mM MgCl₂) and the cleavage reaction was initiated by adding the 2X ribozyme mix to an equal volume of substrate RNA (maximum of 1-5 nM) that was also pre-warmed in cleavage buffer. As an initial screen, assays are carried out for 1 hour at 37° C using a final concentration of either 40 nM or 1 mM ribozyme, *i.e.*, ribozyme excess.

The reaction is quenched by the addition of an equal volume of 95% formamide, 20 mM EDTA, 0.05% bromophenol blue and 0.05% xylene cyanol after which the sample is heated to 95°C for 2 minutes, quick chilled and loaded onto a denaturing polyacrylamide gel. Substrate RNA and the specific RNA cleavage products generated by ribozyme cleavage are visualized on an autoradiograph of the gel. The percentage of cleavage is determined by Phosphor Imager[®] quantitation of bands representing the intact substrate and the cleavage products.

Example 3: MetAP-2

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Methionyl aminopeptidases are metalloproteases that are known to possess posttranslational enzymatic activity by hydrolytically cleaving amino-terminal methionine
residues from nascent peptide substrates in a non-processive manner (Kendall, R. L., 1992,
J. Biol. Chem., 267, 20667-20673). This family of enzymes is divided into two classes
(type 1 and type 2) based on differences in sequence, although the overall structure of the
two classes are similar (Liu, S., 1998, Science, 282, 1324-1327). Methionine
aminopeptidase expression appears to be involved in the control of cellular proliferation.
Deletion of the MetAP gene from E. Coli is lethal (Chang, S. Y., 1989, J. Bacteriol., 171,
4071-4072). In Saccharomyces cerevisiae, deletion of the gene that codes for either
MetAP-1 or 2 results in a slow growth phenotype while deletion of both genes is lethal (Li,
X., 1995, Proc. Natl. Acad. Sci., 92, 12357-12361). (Human methionine aminopeptidase1, MetAP-1, accession No. P53582).

The aminopeptidase function of this class of enzymes may serve a regulatory role in activating signal peptides in conjunction with N-myristoyl transferase (NMT) activity. NMT is expressed from a lethal gene in yeast (Duronio, R. J., 1989, Science, 243, 796-800). NMT is responsible for amino-terminal ligation of myristic acid onto nascent peptides and cannot act on peptides with an amino-terminal methionine residue (Resh, M. D., 1996, Cell. Signal., 8, 403-412). Myristoylation of proteins correlates to intracellular localization events that may determine why certain signaling proteins are dependent on NMT for activity (Taunton, J., 1997, Chemistry & Biology, 4, 493-496). Protein tyrosine kinase Src is dependant on myristoylation for activity and has been identified as an unstream regulator of human vascular endothelial growth factor (VEGF) expression

through hypoxic induction in solid tumors (Mukhopadhyay, D., 1995, Nature, 375, 577-581). MetAPs may therefore regulate the activation of signal peptides (such as VEGF) through cotranslational modification of nascent peptides with NMT. Disruption of protein myristovlation by MetAP inhibition could result in the improper localization of signaling proteins resulting in inhibition of cell growth. (Human N-myristoyltransferase. hNMT. accession No. AF043324.)

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Fumagillin, a sesquiterpene diepoxide metabolite of the fungus Aspergillus fumigatus, and a related compound TNP-470, are strong inhibitors of growth in cultured endothelial cells. The antiproliferative and angiostatic activity of fumagillin was originally 10 discovered by the serendipitous contamination of Aspergillus fumigatus in an endothelial cell culture dish in which cells closest to the fungal colony displayed growth inhibition. Synthetic analogs of fumagillin were later synthesized resulting in the discovery of TNP-470, which is 50 times more potent of an inhibitor than fumagillin and is less toxic in mice (Ingber, D., 1990, Nature, 348, 555-557). Treatment of endothelial cells with these compounds results in late G1 phase arrest. TNP-470 inhibits the signaling pathway of retinoblastoma gene product phosphorylation, cyclin dependent kinases cdk2 and cdk4 activation, and cyclins E and A expression (Abe, J., 1994, Cancer Res., 54, 3407-3412). TNP-470 has also been shown to potently inhibit endothelial cell proliferation induced by the growth factors VEGF and bFGF (Toi, M., 1994, Oncology Reports, 1, 423-426).

fumagillin and related compounds that demonstrate antiproliferative activity in endothelial cells. The use of affinity chromatography with a fumagillin-biotin conjugate resulted in the isolation of a 67-kDa mammalian protein through covalent interaction with the bound substrate. Analysis of digested peptide fragments from the isolated protein revealed MetAP-2 as the covalently bound substrate. Subsequent growth inhibition studies in yeast 25 utilizing MetAP-1 and MetAP-2 deletion strains determined that MetAP-2 is selectively inhibited by fumagillin in vivo (Sin, N., 1997, Proc. Natl. Acad. Sci., 94, 6099-6103). A similar study with TNP-470 and ovalicin, another potent inhibitor of neovascularization, determined that MetAP-2 is the molecular target for these fumagillin-related compounds (Griffith, E. C., 1997, Chemistry & Biology, 4, 461-471).

The bifunctional protein MetAP-2 has been identified as the molecular target for

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MetAP-2 expression correlates with cellular growth. Non-dividing cells in culture have no detectable levels of the 67-kDa MetAP-2 protein by immunoassay. MetAP-2 has been shown to affect translational initiation by association with eukaryotic initiation factor 2α (eIF-2 α) (Ray, M. K., 1992, Proc. Natl. Acad. Sci., 89, 539-543). The binding of MetAP-2 with eIF-2 α inhibits the heme-regulated inhibitor kinase (HRI) phosphorylation of eIF-2 α in vitro in reticulocyte lysates (Datta, B., 1988, Proc. Natl. Acad. Sci., 85, 3324-3328). MetAP-2/eIF-2 α binding results in the partial reversal of protein synthesis inhibition by double stranded RNA dependent kinase mediated phosphorylation in vivo (Wu, S., 1996, Biochemistry, 35, 8275-8280). Griffith et al. also determined that covalent binding of TNP-470 and ovalicin, while potently inhibiting methionine aminopeptidase type 2 activity specifically, did not affect the regulatory activity of MetAP-2 on eIF-2 α . This finding by Griffith et al. rules out the possibility that control of eIF-2 α phosphorylation by MetAP-2 is responsible for the inhibition of endothelial cell proliferation by furnagillin related compounds.

Particular angiogenesis related degenerative and disease states that can be associated with MetAP expression modulation include but are not limited to:

<u>Cancer</u>: Solid tumors are unable to grow or metastasize without the formation of new blood vessels (Hanahan, D., 1996, Cell, 86, 353-364). Inhibition of angiogenesis via

MetAP modulation can potentially be used to treat a wide variety of cancers.

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<u>Diabetic retinopathy and age related macular degeneration</u>: Ocular neovascularization is observed in diabetic retinopathy, which is mediated by up-regulation of VEGF (Adamis, A. P., 1994, Amer. J. Ophthal., 118, 445-450). The requirement of protein kinase Src in hypoxia induced VEGF expression (Mukhopadhyay, D., 1995, Nature, 375, 577-581) indicates that MetAP modulation of aminopeptidase activity can potentially be used to treat conditions involving ocular neovascularization.

Arthritis: The ingrowth of a vascular pannus in arthritis may be mediated by the overexpression of angiogenic factors from infiltrating inflammatory cells, macrophages, and immune cells (Peacock, D. J., 1992, J. exp. Med., 175, 1135-1138). Angiogenesis inhibition through MetAP modulation can potentially be used to treat arthritis.

<u>Psoriasis</u>: Angiogenesis has been implicated in psoriasis due to overexpression of the angiogenic polypeptide interleukin-8 and decreased expression of the angiogenesis inhibitor thrombospondin (Nickoloff, B. J., 1994, Amer. J. Pathol. 44, 820-828).

Angiogenesis inhibition through MetAP modulation can potentially be used to treat psoriasis.

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<u>Female reproduction</u>: Angiogenesis in the female reproductive system has been implicated in several disorders of the reproductive tract (Reynolds, L. P., 1992, FASEB, 6, 886-892). Modulation of angiogenesis through control of MetAP may have various applications in the area of female reproduction and fertility.

Various methods have been developed to assay MetAP activity.

Griffith et al., 1998, Proc. Natl. Acad. Sci., 95, 15183-15188, describe an enzymatic assay for MetAP-2 activity in vitro and an endothelial cell culture proliferation assay for MetAP-2 activity in vivo.

Weber et al., 1999, International PCT publication No. WO 98/US-21231 describe novel fluorescent reporter molecules and an enzymatic assay that can be used for determining the activity of MetAP-2 for drug screening and determining the chemosensitivity of human cancer cells to treatment with chemotherapeutic drugs.

Larrabee, J. A. et al., 1999, Anal. Biochem, 269, 194-198, describe the use of a highpressure liquid chromatographic (HPLC) method for assaying MetAP-2 activity with application to the study of enzymic inactivation.

Quantitative methods have been developed to assay the efficacy of antiangiogenic therapies.

Wantanabe et al., 1992, Molec. Biol. Cell, 3, 324a, describe the quantitation of angiogenic peptides (bFGF) in human serum as a prognostic test for breast cancer.

Nguyen et al., 1994, J. Natn. Cancer Inst., 86, 356-361, describe the quantitation of angiogenic peptides (bFGF) in the urine of patients with a wide spectrum of cancers.

Li et al., 1994, The Lancet, 344, 82-86, describe the quantitation of angiogenic peptides (bFGF) in the cerebrospinal fluid of children with brain tumors. This work also describes determining the extent of neovascularization in histological sections by utilizing microvessel count.

The present body of knowledge in angiogenesis research indicates the need for compounds that can modulate MetAP activity for research, diagnostic, trait alteration. animal health and therapeutic use.

Griffith et al., International PCT publication No. WO 9856372 describe small molecule inhibitors of MetAP2 and uses thereof. 5

D'Amato et al., International PCT publication No. WO 9805293 describe the use of AGM-1470 (TNP-470) as an angiogenesis inhibitor for use in regulating the female reproductive system and for treating diseases of the reproductive tissue.

Davidson et al., US patent No. 5,801,146 describe a compound and method for 10 inhibiting angiogenesis using mammalian kringle 5 protein.

Cao et al., US patent No. 5,854,221 describe a protein-based endothelial cell proliferation inhibitor and its method of use.

Chang et al., US patent No. 5,888,796 describe a clone of a nucleotide sequence encoding a protein having two functions comprising methionine aminopeptidase activity and anti eIF-2 phosphorylation activity.

Wang et al., 1998, Proc. Am. Assoc. Cancer Res., 39, 98 (abstr.) describe blocked proliferation of human endothelial cells by human MetAP-2 antisense oligonucleotides.

A rat corneal model has been developed to study ribozyme inhibition of VEGF receptor-mediated angiogenesis (Pavco, P. A., 1999, Nucleic Acids Research, 27, 2569-2577). A similar study employing MetAP-2 inhibition could be used to study ribozyme based inhibition of MetAP-2 induced angiogenesis in vivo.

Identification of Potential Target Sites in Human MetAP-2 RNA

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The sequence of human MetAP-2 was screened for accessible sites using a computer-folding algorithm. Regions of the RNA that did not form secondary folding structures and contained potential ribozyme and/or antisense binding/cleavage sites were identified. The sequences of these cleavage sites are shown in Tables 9-12.

Selection of Enzymatic Nucleic Acid Cleavage Sites in Human MetAP-2 RNA

To test whether the sites predicted by the computer-based RNA folding algorithm corresponded to accessible sites in MetAP-2 RNA, 11 hammerhead ribozyme, 4 NCH and three G-Cleaver ribozyme sites were selected for further analysis (Table 12). Ribozyme

target sites were chosen by analyzing sequences of Human MetAP-2 (Genbank accession number HSU29607) and prioritizing the sites on the basis of folding. Ribozymes were designed that could bind each target and were individually analyzed by computer folding (Christoffersen et al., 1994 J. Mol. Struc. Theochem, 311, 273; Jaeger et al., 1989, Proc. Natl. Acad. Sci. USA, 86, 7706) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable intramolecular interactions between the binding arms and the catalytic core were eliminated from consideration. As noted below, varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 bases on each arm are able to bind to, or otherwise interact with, the target RNA.

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Chemical Synthesis and Purification of Ribozymes for Efficient Cleavage of MetAP-2 RNA

Ribozymes were designed to anneal to various sites in the RNA message. The binding arms are complementary to the target site sequences described above. The ribozymes were chemically synthesized. The method of synthesis used followed the procedure for normal RNA synthesis as described above and in Usman et al., (1987 J. Am. Chem. Soc., 109, 7845), Scaringe et al., (1990 Nucleic Acids Res., 18, 5433) and Wincott et al., supra, and made use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The average stepwise coupling yields were >98%.

Ribozymes were also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbeck, 1989, Methods Enzymol. 180, 51). Ribozymes were purified by gel electrophoresis using general methods or were purified by high pressure liquid chromatography (HPLC; see Wincott et al., supra; the totality of which is hereby incorporated herein by reference) and were resuspended in water. The sequences of the chemically synthesized ribozymes used in this study are shown below in **Table 9-12**.

Ribozyme Cleavage of MetAP-2 RNA Target in vitro

Ribozymes targeted to the human MetAP-2 RNA are designed and synthesized as described above. These ribozymes can be tested for cleavage activity in vitro, for

example, using the following procedure. The target sequences and the nucleotide location within the MetAP-2 RNA are given in Tables 9-12.

Cleavage Reactions: Full-length or partially full-length, internally-labeled target RNA for ribozyme cleavage assay is prepared by in vitro transcription in the presence of [a-32p] CTP, passed over a G 50 Sephadex column by spin chromatography and used as substrate RNA without further purification. Alternately, substrates are 5'-32P-end labeled using T4 polynucleotide kinase enzyme. Assays are performed by pre-warming a 2X concentration of purified ribozyme in ribozyme cleavage buffer (50 mM Tris-HCl, pH 7.5 at 37°C, 10 mM MgCl₂) and the cleavage reaction was initiated by adding the 2X ribozyme mix to an equal volume of substrate RNA (maximum of 1-5 nM) that was also pre-warmed in cleavage buffer. As an initial screen, assays are carried out for 1 hour at 37°C using a final concentration of either 40 nM or 1 mM ribozyme, i.e., ribozyme excess. The reaction is quenched by the addition of an equal volume of 95% formamide, 20 mM EDTA, 0.05% bromophenol blue and 0.05% xylene cyanol after which the sample is heated to 95°C for 2 minutes, quick chilled and loaded onto a denaturing polyacrylamide gel. Substrate RNA and the specific RNA cleavage products generated by ribozyme cleavage are visualized on an autoradiograph of the gel. The percentage of cleavage is determined by Phosphor Imager® quantitation of bands representing the intact substrate and the cleavage products.

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Example 4: BACE, ps-1, ps-2

Alzheimer's disease (AD) is a progressive, degenerative disease of the brain which affects approximately 4 million people in the United States alone. An estimated 14 million Americans will have Alzheimer's disease by the middle of the next century if no cure or definitive prevention of the disease is found. Nearly one out of ten people over age 65 and nearly half of those over 85 have Alzheimer's disease. Alzheimer's disease is not confined to the elderly, a small percentage of people in their 30's and 40's are afflicted with early onset AD. Alzheimer's disease is the most common form of dementia, and amounts to the third most expensive disease in the US following heart disease and cancer. An estimated 100 billion dollars are spent annually on Alzheimer's disease (National Alzheimer's Association, 1999).

Alzheimer's disease is characterized by the progressive formation of insoluble plaques and vascular deposits in the brain consisting of the 4 kD amyloid β peptide (Aβ). These plaques are characterized by dystrophic neurites that show profound synaptic loss, neurofibrillary tangle formation, and gliosis. Aß arises from the proteolytic cleavage of the large type I transmembrane protein, β-amyloid precursor protein (APP) (Kang et al., 1987, Nature, 325, 733). Processing of APP to generate AB requires two sites of cleavage by a β-secretase and a γ-secretase. β-secretase cleavage of APP results in the cytoplasmic release of a 100 kD soluble amino-terminal fragment, APPsB, leaving behind a 12 kD transmembrane carboxy-terminal fragment, C99. Alternately, APP can be cleaved by a \alphasecretase to generate cytoplasmic APPsa and transmembrane C83 fragments. Both remaining transmembrane fragments, C99 and C83, can be further cleaved by a ysecretase, leading to the release and secretion of Alzheimer's related Aß and a nonpathogenic peptide, p3, respectively (Vassar et al., 1999, Science, 286, 735-741). Early onset familial Alzheimer's disease is characterized by mutant APP protein with a Met to Leu substitution at position P1, characterized as the "Swedish" familial mutation (Mullan et al., 1992, Nature Genet., 1, 345). This APP mutation is characterized by a dramatic enhancement in β-secretase cleavage (Citron et al., 1992, Nature, 360, 672).

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The identification of β-secretase, and γ-secretase constituents involved in the release of β-amyloid protein is of primary importance in the development of treatment strategies for Alzheimer's disease. Characterization of α-secretase is also important in this regard since α-secretase cleavage may compete with β-secretase cleavage resulting in non-pathogenic vs. pathogenic protein production. Involvement of the two metalloproteases, ADAM 10, and TACE has been demonstrated in α-cleavage of AAP (Buxbaum et al., 1999, J. Biol. Chem., 273, 27765, and Lammich et al., 1999, Proc. Natl. Acad. Sci. U.S.A., 96, 3922). Studies of γ-secretase activity have demonstrated presenilin dependence (De Stooper et al., 1998, Nature, 391, 387, and De Stooper et al., 1999, Nature, 398, 518), and as such, presenilins have been proposed as γ-secretase even though presenilin does not present proteolytic activity (Wolfe et al., 1999, Nature, 398, 513).

Recently, Vassar et al., 1999, supra reported β-secretase cleavage of AAP by the transmembrane aspartic protease beta site APP cleaving enzyme, BACE. While other potential candidates for β-secretase have been proposed (for review see Evin et al., 1999, Proc. Natl. Acad. Sci. U.S.A., 96, 3922), none have demonstrated the full range of characteristics expected from this enzyme. Vassar et al. supra, demonstrate that BACE expression and localization are as expected for β-secretase, that BACE overexpression in cells results in increased β-secretase cleavage of APP and Swedish APP, that isolated BACE demonstrates site specific proteolytic activity on APP derived peptide substrates, and that antisense mediated endogenous BACE inhibition results in dramatically reduced β-secretase activity.

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Current treatment strategies for Alzheimer's disease rely on either the prevention or the alleviation of symptoms and/or the slowing down of disease progression. Two drugs approved in the treatment of Alzheimer's, donepezil (Aricept®) and tacrine (Cognex®), both cholinomimetics, attempt to slow the loss of cognitive ability by increasing the amount of acetylcholine available to the brain. Antioxidant therapy through the use of antioxidant compounds such as alpha-tocopherol (vitamin E), melatonin, and selegeline (Eldepryl®) attempt to slow disease progression by minimizing free radical damage. Estrogen replacement therapy is thought to incur a possible preventative benefit in the development of Alzheimer's disease based on limited data. The use of anti-inflammatory drugs may be associated with a reduced risk of Alzheimer's as well. Calcium channel blockers such as Nimodipine® are considered to have a potential benefit in treating Alzheimer's disease due to protection of nerve cells from calcium overload, thereby prolonging nerve cell survival. Nootropic compounds, such as acetyl-L-carnitine (Alcar®) and insulin, have been proposed to have some benefit in treating Alzheimer's due to enhancement of cognitive and memory function based on cellular metabolism.

Whereby the above treatment strategies may all improve quality of life in Alzheimer's patients, there exists an unmet need in the comprehensive treatment and prevention of this disease. As such, there exists the need for therapeutics effective in reversing the physiological changes associated with Alzheimer's disease, specifically, therapeutics that can eliminate and/or reverse the deposition of amyloid β peptide. The use of compounds to modulate the expression of proteases that are instrumental in the

release of amyloid β peptide, namely β -secretase (BACE), and γ -secretase (presenilin), is of therapeutic significance.

Tsai et al., 1999, Book of Abstrasts, 218th ACS National Meeting, New Orleans, Aug 22-26, describe substrate-based alpha-aminoisobutyric acid derivatives of difluoro ketone pentidomimetic inhibitors of amyloid β peptide through γ-secretase inhibition.

Czech et al., International PCT publication No. WO/9921886, describe peptides capable of inhibiting the interaction between presentlins and the β -amyloid peptide or its precursor for therapeutic use.

Fournier et al., International PCT publication No. WO/9916874, describe human brain proteins capable of interacting with presentilins and cDNAs encoding them toward therapeutic use.

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St. George-Hyslop et al., International PCT publication No. WO/9727296, describe genes for proteins that interact with presenilins and their role in Alzheimer's disease toward theraneutic use.

Vassar et al., 1999, Science, 286, 735-741, describe specific antisense oligonucleotides targeting BACE, used for inhibition studies of endogenous BACE expression in 101 cells and APPsw cells via lipid mediated transfection.

Vassar et al., 1999, Science, 286, 735-741, describe a cell culture model for studying BACE inhibition. Specific antisense nucleic acid molecules targeting BACE mRNA were used for inhibition studies of endogenous BACE expression in 101 cells and APPsw (Swedish type amyloid precursor protein expressing) cells via lipid mediated transfection. Antisense treatment resulted in dramatic reduction of both BACE mRNA by Northern blot analysis, and APPsβsw ("Swedish" type β-secretase cleavage product) by ELISA, with maximum inhibition of both parameters at 75-80%. This model was also used to study the effect of BACE inhibition on amyloid β-peptide production in APPsw cells.

Games et al., 1995, Nature, 373, 523-527, describe a transgenic mouse model in which mutant human familial type APP (Phe 717 instead of Val) is overexpressed. This model results in mice that progressively develop many of the pathological hallmarks of Alzheimer's disease, and as such, provides a model for testing therapeutic drugs.

Particular degenerative and disease states that can be associated with BACE expression modulation include but are not limited to Alzheimer's disease and dementia.

Donepezil, tacrine, selegeline, and acetyl-L-carnitine are non-limiting examples of pharmaceutical agents that can be combined with or used in conjunction with the nucleic acid molecules (e.g. ribozymes and antisense molecules) of the instant invention. Those skilled in the art will recognize that other drugs such as diuretic and antihypertensive compounds and therapies can be similarly be readily combined with the nucleic acid molecules of the instant invention (e.g. ribozymes and antisense molecules) are hence within the scope of the instant invention.

Identification of Potential Target Sites in Human BACE RNA

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The sequence of human BACE was screened for accessible sites using a computerfolding algorithm. Regions of the RNA that did not form secondary folding structures and contained potential ribozyme and/or antisense binding/cleavage sites were identified. The sequences of these cleavage sites are shown in Tables 18-23.

15 Selection of Enzymatic Nucleic Acid Cleavage Sites in Human BACE RNA

Ribozyme target sites were chosen by analyzing sequences of Human BACE (Genbank sequence accession number: AF190725) and prioritizing the sites on the basis of folding. Ribozymes were designed that could bind each target and were individually analyzed by computer folding (Christoffersen et al., 1994 J. Mol. Struc. Theochem, 311, 273; Jaeger et al., 1989, Proc. Natl. Acad. Sci. USA, 86, 7706) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable intramolecular interactions between the binding arms and the catalytic core were eliminated from consideration. As noted below, varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 bases on each arm are able to bind to, or otherwise interact with, the target RNA.

Chemical Synthesis and Purification of Ribozymes and Antisense for Efficient Cleavage and/or blocking of BACE RNA

Ribozymes and antisense constructs were designed to anneal to various sites in the RNA message. The binding arms of the ribozymes are complementary to the target site sequences described above, while the antisense constructs are fully complimentary to the target site sequences described above. The ribozymes and antisense constructs were

chemically synthesized. The method of synthesis used followed the procedure for normal RNA synthesis as described above and in Usman et al., (1987 J. Am. Chem. Soc., 109. 7845), Scaringe et al., (1990 Nucleic Acids Res., 18, 5433) and Wincott et al., supra, and made use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The average stepwise coupling yields were >98%.

Ribozymes and antisense constructs were also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbeck, 1989, Methods Enzymol, 180, 51). Ribozymes and antisense constructs were purified by gel electrophoresis using general methods or were purified by high pressure liquid chromatography (HPLC; See Wincott et al., supra; the totality of which is hereby incorporated herein by reference) and were resuspended in water. The sequences of the chemically synthesized ribozymes and antisense constructs used in this study are shown below in Table 18-23.

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Rihozyme Cleavage of BACE RNA Target in vitro

Ribozymes targeted to the human BACE RNA are designed and synthesized as described above. These ribozymes can be tested for cleavage activity in vitro, for example, using the following procedure. The target sequences and the nucleotide location within the BACE RNA are given in Tables 18-23.

Cleavage Reactions: Full-length or partially full-length, internally-labeled target RNA for ribozyme cleavage assay is prepared by in vitro transcription in the presence of [a-32p] CTP, passed over a G 50 Sephadex column by spin chromatography and used as substrate RNA without further purification. Alternately, substrates are 5'-32P-end labeled using T4 polynucleotide kinase enzyme. Assays are performed by pre-warming a 2X concentration of purified ribozyme in ribozyme cleavage buffer (50 mM Tris-HCl, pH 7.5 at 37°C, 10 mM MgCl2) and the cleavage reaction was initiated by adding the 2X ribozyme mix to an equal volume of substrate RNA (maximum of 1-5 nM) that was also pre-warmed in cleavage buffer. As an initial screen, assays are carried out for 1 hour at 37°C using a final concentration of either 40 nM or 1 mM ribozyme, i.e., ribozyme excess.

The reaction is quenched by the addition of an equal volume of 95% formamide, 20 mM

EDTA, 0.05% bromophenol blue and 0.05% xylene cyanol after which the sample is heated to 95°C for 2 minutes, quick chilled and loaded onto a denaturing polyacrylamide gel. Substrate RNA and the specific RNA cleavage products generated by ribozyme cleavage are visualized on an autoradiograph of the gel. The percentage of cleavage is determined by Phosphor Imager[®] quantitation of bands representing the intact substrate and the cleavage products.

Example 5: Phospholamban

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Cardiac disease leading to heart failure is the leading cause of combined morbidity and mortality in the developed world. Nearly twenty million people worldwide suffer from heart failure related disease. An estimated five million Americans are afflicted with congestive heart failure (CHF), with 400,000 new cases diagnosed each year. In the US, cardiac disease associated failure results in approximately 40,000 deaths per year, and is associated with an additional 250,000 deaths (Harnish, 1999, Drug & Market Development, 10, 114-119). Heart failure related disease represents a major public health issue due to an overall increase in prevalence and incidence in aging populations with a greater proportion of survivors of acute myocardial infarction (AMI) (Kannel et al., 1994, Br. Heart. J., 72 (suppl), 3). Heart failure related disease represents the most common teason for hospitalization of elderly patients in the US. The resulting life expectancy of these patients is less than that of many common cancers, with five year survival rates for men and women at only 25% and 38% respectively, and with one year mortality rates for severe heart failure at 50% (Ho et al., 1993, Circulation, 88, 107).

Heart disease is characterized by a progressive decrease in cardiac output resulting from insufficient pumping activity of the diseased heart. The resulting venous back-pressure results in peripheral and pulmonary dysfunctional congestion. The heart responds to a variety of mechanical, hemodynamic, hormonal, and pathological stimuli by increasing muscle mass in response to an increased demand for cardiac output. The resulting transformation of heart tissue (myocardial hypertrophy) can arise as a result of genetic, physiologic, and environmental factors, and represents an early indication of clinical heart disease and an important risk factor for subsequent heart failure (Hunter and Chien, 1999, New England J. of Medicine, 99, 313-322).

Coronary heart disease is a predominant factor in the development of the cardiac disease state, along with prior AMI, hypertension, diabetes mellitus, and valvular heart disease. Diagnosis of cardiac disease includes determination of coronary heart disease associated left ventricular systolic dysfunction (LVSD) and/or left ventricular diastolic dysfunction (LVDD) by echocaardiographic imaging (Cleland, 1997, Dis Management Health Outcomes, 1, 169). Promising diagnosis may also rely on assaying atrial natriuretic peptide (ANP) and brain natriuretic peptide (BNP) concentrations. ANP and BNP levels are indicative of the level of ventricular dysfunction (Davidson et al., 1996, Am. J. Cardiol., 77, 828).

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Current treatment strategies for cardiac disease associated failure are varied.

Diuretics are often used to reduce pulmonary edema and dyspnea in patients with fluid overload, and are usually used in conjunction with angiotensin converting enzyme (ACE) inhibitors for vasodilation. Digoxin is another popular choice for treating cardiac disease as an inontropic agent, however, doubts remain concerning the long-term efficacy and safety of Digoxin (Harnish, 1999, Drug & Market Development, 10, 114-119). Carvedilol, a beta-blocker, has been introduced to complement the above treatments in order to slow down the progression of cardiac disease. Antiarrhythmic agents can be used in order to reduce the risk of sudden death in patients suffering from cardiac disease. Lastly, heart transplants have been effective in the treatment of patients with advanced stages of cardiac disease, however, the limited supply of donor hearts greatly limits the scope of this treatment to the broad population (Harnish, 1999, Drug & Market Development, 10, 114-119).

Whereby the above treatment strategies can all improve morbidity and mortality associated with cardiac disease, the only existing definitive approach to curing the diseased heart is replacement by transplant. Even a healthy, transplanted heart can become diseased in response to the various stresses of mechanical, hemodynamic, hormonal, and pathological stimuli associated with extrinsic risk factors. As such there exists the need for therapeutics effective in reversing the physiological changes associated with cardiac disease.

Myocardial hypertrophy and apoptosis are the underlying degenerative process associated with cardiac hypertrophy and failure. A variety of signaling pathways are involved in the progression of myocardial hypertrophy and myocardial apoptosis. Genetic studies have been instrumental in elucidating these pathways and their involvement in cardiac disease through in vitro assays of cardiac muscle cells and in vivo studies of genetically engineered animals.

Studies in which the expression of specific genes have been altered in cardiac myocytes have shown that specific peptide hormones, growth factors, and cytokines can activate various features of the hypertrophic response (Hunter and Chien, 1999, New England J of Medicine, 99, 313-322). Particular substances that have been characterized from these studies include potential therapeutic and molecular targets involved in heart failure. Hunter et al., in Chien, KR, ed. Molecular basis of heart disease: a companion to Braunwald's Heart Disease, Philadelphia: W.B. Saunders, 1999:211-250, describe classes of therapeutic and molecular targets involved in heart failure including:

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- Endothelin 1 and angiotensin II receptor antagonists, and antagonists of ras, p38, and e-iun N-terminal kinase (JNK) for inhibition of pathologic hypertrophy.
- Insulin like growth factor I and growth hormone receptor stimulation for promotion of physiologic hypertrophy.
 - 3. beta-1-adrenergic receptor blockers for inhibition of neurohumoral over stimulation.
 - Phospholamban and Sarcolipin small molecule inhibitors for relief of sarcoplasmic reticulum calcium ATPase inhibition to provide enhancement of myocardial contractile and relaxation responses.
- Small molecule inhibitors of β-adrenergic receptor kinase to counteract the desensitization of G protein coupled receptor kinases in order to provide enhancement of myocardial contractile and relaxation responses.
 - Enhancement of angiogenic growth factors (VEGF, FGF-5) for relief of energy deprivation in cardiac tissues.
- Promoters of myocyte survival including gp 130 ligands (cardiotrophin 1), and Neuregulin for the inhibition of apoptosis of myocytes.
 - Inhibitors of apoptosis such as Caspase inhibitors for the inhibition of apoptosis of myocytes.
 - 9. Inhibitors of cytokines such as TNF-alpha for the inhibition of apoptosis of myocytes.
 - Congestive heart failure, heart failure, dilated cardiomyopathy and pressure overload hypertrophy are nonlimiting examples of disorders and disease states that can be associated with the above classes of molecular targets.

The failure of cardiac contractile performance leading to cardiac disorders and disease, governed by impairment of cardiac excitation/contraction coupling, points to the importance of the signaling pathways involved in this process. The release and uptake of cytosolic Ca2+ by the sarcoplasmic reticulum plays an integral role in each cycle of cardiac contraction and excitation (Minamisawa et al., 1999, Cell, 99, 313-322). The process of Ca2+ reuptake is mediated by the cardiac sarcoplasmic reticulum Ca2+ ATPase (SERCA2a). SERCA2a activity is regulated by phospholamban, a p52 muscle specific sarcoplasmic reticulum phosphoprotein (Koss et al., 1996, Circ. Res., 79, 1059-1063, and Simmerman et al., 1998, Physiol. Rev., 78, 921-947). In its active, unphosphorylated state, phospholamban is a potent inhibitor of SERCA2a activity. Phosphorylation of phospholamban at serine 16 by cyclic AMP-dependent protein kinase (PKA) or calmodulin kinase, results in the inhibition of phospholamban interaction with SERCA2a. This phosphorylation event is predominantly responsible for the proportional increase in the rate of Ca2+ uptake into the sarcoplasmic reticulum and resultant ventricular relaxation (Tada et al., 1982, Mol. Cell. Biochem., 46, 73-95, and Luo et al., 1998, J. Biol. Chem., 273, 4734-4739).

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Since a proportional decrease in Ca²⁺ uptake is a hallmark feature of heart failure (Sordahl et al., 1973, Am. J. Physiol., 224, 497-502) and since an increase in the relative ratio of phospholamban to SERCA2a is an important determinant of sarcoplasmic reticulum dysfunction in heart failure (Hasenfuss, 1998, Cardiovasc. Res., 37, 279-289), the targeting of phospholamban and related regulatory factors as therapeutic targets for heart disorders should prove valuable for cardiac indications.

Pystynen et al., International PCT publication No. WO 99/00132, describe bisethers of 1-oxa, aza and thianaphthalen-2-ones as small molecule inhibitors of phospholamban for increasing coronary flow via direct dilation of the coronary arteries.

Pystynen *et al.*, International PCT publication No. WO 99/15523, describe bisethers of 1-oxa, aza and thianaphthalen-2-ones as small molecule inhibitors of phospholamban that are useful for treating heart failure.

The efficacy of the above mentioned treatment strategies is limited. Small molecule inhibition of a molecular target is often limited by toxicity, which can restrict dosing and overall efficacy.

He et al., 1999, Circulation, 100, 974-980, describe endogenous expression of mutant phospholamban and phospholamban antisense RNA to investigate the corresponding effect on SERCA2a activity and cardiac myocyte contractility.

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A more attractive approach to the treatment of heart disease would involve the use of ribozymes and/or antisense constructs to modulate the expression of target molecules involved in heart failure. The use of nucleic acid molecules of the instant invention permits highly specific regulation of the molecular targets of interest, including phospholamban (PLN) (GenBank accession No. NM 002667), sarcolipin (SLN) (GenBank accession No. NM 003063), angiotensin II receptor (GenBank accession No. U20860), endothelin 1 receptor (GenBank accession No. NM 001957), K-ras (GenBank 10 accession No. NM 004985), p38 (GenBank accession No. AF092535), c-jun N-terminal kinase (GenBank accession No. NM 002750, L31951, NM 002753), growth hormone receptor (GenBank accession No. NM_000163), insulin-like growth factor I receptor (GenBank accession No. NM 000875), beta-1-adrenergic receptor (GenBank accession No. NM 000024), \(\beta\)1-adrenergic receptor kinase (GenBank accession No. NM 001619, 15 NM 005160), VEGF receptor (GenBank accession No. U43368, M27281 X15997), fibroblast growth factor 5 (GenBank accession No. NM 004464), cardiotrophin I (GenBank accession No. NM 001330), neuregulin (GenBank accession No. AF009227), TNF-alpha (GenBank accession No. X02910 X02159), PI3 kinase (GenBank accession No. NM 006218, NM 006219, U86453, NM_002649, M61906), and AKT kinase 20 (GenBank accession No. NM 005163, M77198).

Various methods have been developed to assay phospholamban activity in vitro and in vivo. Holt et al., 1999, J. Mol. Cell. Cardiol., 31, 645-656, describe a cell culture model in which thyroid hormone control of contraction and the Ca2+-ATPase/phospholamban complex is studied in adult rat ventricular myocytes. Slack et al. 1997, J. Biol. Chem., 272, 18862-18868, describe studies in which the ectopic expression of phospholamban in mouse fast-twitch skeletal muscle cells alters sarcoplasmic reticulum Ca2+ transport and muscle relaxation. MacLennan et al., 1996, Soc. Gen. Physiol. Ser., 51, 89-103, in a review of regulatory interactions between calcium ATPases and phospholamban describe phospholamban/ Ca2+-ATPase interactions in protein expressed in heterologous cell culture experiments. Cornwell et al., 1991, Mol. Pharmacol., 40,923-931, describe the

regulation of sarcoplasmic reticulum protein phosphorylation by localized cyclic GMPdependent protein kinase in vascular smooth muscle cells.

Minamisawa et al., 1999, Cell, 99, 313-322, describe a phospholamban knockout mouse model which affords protection from induced dilated cardiomyopathy. Dillmann et al., 1999, Am. J. Cardiol., 83, 89H-91H, describe a transgenic rat model for the study of 5 altered expression of calcium regulatory proteins, including phospholamban, and their effect on myocyte contractile response. LekanneDeprez et al., 1998, J. Mol. Cell. Cardiol., 30, 1877-1888, describe a rat pressure-overload model to investigate alterations in gene expression of phospholamban, atrial natriuretic peptide (ANP), sarcoplasmic endoplasmic reticular calcium ATPase 2 (SERCA2), collagen IIIa1, and calsequestrin 10 (CSO). Jones et al., 1998, J. Clin. Invest., 101, 1385-1393, describe a mouse model for investigating the regulation of calcium signaling in transgenic mouse cardiac myocytes overexpressing calsequestrin. In this study, the upregulation and downregulation of calcium uptake and release proteins were determined, including phospholamban. Lorenz et al., 1997, Am J. Physiol., 273, 6, describe a mouse model for the study of regulatory 15 effects of phospholamban on cardiac function in intact mice. This study makes use of animal models with altered levels of phospholamban to permit in vivo evaluation of the physiological role of phospholamban. Arai et al., 1996, Saishin Igaku, 51, 1095-1104, presents a review article of gene targeted animal models expressing cardiovascular abnormalities. The study of phospholamban and other protein expression modification 20 effects in mice is presented. Wankerl et al., 1995, J. Mol. Med., 73, 487-496, presents a review article describing the study of calcium transport proteins in the nonfailing and failing heart. Animal models investigating the major calcium handling myocardial proteins, including phospholamban, are described. These models, as well as others, may be used to evaluate the effect of treatment with nucleic acid molecules of the instant 25 invention on cardiac function. Endpoints may be, but are not limited to, left ventricular pressure, left ventricular pressure as a function of time (LVdP/dt), and mean arterial blood pressure. Endpoints will be evaluated under basal and stimulated (cardiac load) conditions.

Particular degenerative and disease states that can be associated with phospholamban expression modulation include but are not limited to congestive heart failure, heart failure, dilated cardiomyopathy and pressure overload hypertrophy:

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Digoxin, Bendrofluazide, Dofetilide, and Carvedilol are non-limiting examples of pharmaceutical agents that can be combined with or used in conjunction with the nucleic acid molecules (e.g. ribozymes and antisense molecules) of the instant invention. Those skilled in the art will recognize that other drugs such as diurctic and antihypertensive compounds and therapies can be similarly be readily combined with the nucleic acid molecules of the instant invention (e.g. ribozymes and antisense molecules) are hence within the scope of the instant invention.

Identification of Potential Target Sites in Human phospholamban RNA

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The sequence of human phospholamban was screened for accessible sites using a computer folding algorithm. Regions of the RNA that did not form secondary folding structures and contained potential ribozyme and/or antisense binding/cleavage sites were identified. The sequences of these cleavage sites are shown in Tables 24-30.

Selection of Enzymatic Nucleic Acid Cleavage Sites in Human phospholamban RNA

Ribozyme target sites were chosen by analyzing sequences of Human phospholamban (Genbank sequence accession number: NM_002667) and prioritizing the sites on the basis of folding. Ribozymes were designed that could bind each target and were individually analyzed by computer folding (Christoffersen et al., 1994 J. Mol. Struc. Theochem, 311, 273, Jaeger et al., 1989, Proc. Natl. Acad. Sci. USA, 86, 7706) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable intramolecular interactions between the binding arms and the catalytic core were eliminated from consideration. As noted below, varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 bases on each arm are able to bind to, or otherwise interact with, the target RNA.

Chemical Synthesis and Purification of Ribozymes and Antisense for Efficient Cleavage and/or blocking of phospholamban RNA

Ribozymes and antisense constructs were designed to anneal to various sites in the RNA message. The binding arms of the ribozymes are complementary to the target site sequences described above, while the antisense constructs are fully complimentary to the target site sequences described above. The ribozymes and antisense constructs were

chemically synthesized. The method of synthesis used followed the procedure for normal RNA synthesis as described above and in Usman et al., (1987 J. Am. Chem. Soc., 109, 7845), Scaringe et al., (1990 Nucleic Acids Res., 18, 5433) and Wincott et al., *supra*, and made use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The average stepwise coupling yields were >98%

Ribozymes and antisense constructs were also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbeck, 1989, Methods Enzymol. 180, 51). Ribozymes and antisense constructs were purified by gel electrophoresis using general methods or were purified by high pressure liquid chromatography (HPLC; see Wincott et al., supra; the totality of which is hereby incorporated herein by reference) and were resuspended in water. The sequences of the chemically synthesized ribozymes and antisense constructs used in this study are shown below in Table 24-30.

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Ribozyme Cleavage of phospholamban RNA Target in vitro

Ribozymes targeted to the human phospholamban RNA are designed and synthesized as described above. These ribozymes can be tested for cleavage activity in vitro, for example using the following procedure. The target sequences and the nucleotide location within the phospholamban RNA are given in Tables 24-30.

Cleavage Reactions: Full-length or partially full-length, internally-labeled target

RNA for ribozyme cleavage assay is prepared by in vitro transcription in the presence of

[a-32p] CTP, passed over a G 50 Sephadex column by spin chromatography and used as

substrate RNA without further purification. Alternately, substrates are 5'-32p-end labeled

using T4 polynucleotide kinase enzyme. Assays are performed by pre-warming a 2X

concentration of purified ribozyme in ribozyme cleavage buffer (50 mM Tris-HCl, pH 7.5

at 37°C, 10 mM MgCl2) and the cleavage reaction was initiated by adding the 2X

ribozyme mix to an equal volume of substrate RNA (maximum of 1-5 nM) that was also

pre-warmed in cleavage buffer. As an initial screen, assays are carried out for 1 hour at

37°C using a final concentration of either 40 nM or 1 mM ribozyme, i.e., ribozyme excess.

The reaction is quenched by the addition of an equal volume of 95% formamide, 20 mM

EDTA, 0.05% bromophenol blue and 0.05% xylene cyanol after which the sample is heated to 95°C for 2 minutes, quick chilled and loaded onto a denaturing polyacrylamide gel. Substrate RNA and the specific RNA cleavage products generated by ribozyme cleavage are visualized on an autoradiograph of the gel. The percentage of cleavage is determined by Phosphor Imager® quantitation of bands representing the intact substrate and the cleavage products.

Tissue distribution of BrdU-labeled antisense in mice

CD1 mice were injected with a single bolus (30 mg/kg) of a BrdU-labeled antisense oligonucleotide or a similar molar amount of BrdU (as a control). At various time points (30 min, 2h and 6 h), mice were sacrificed and major tissues isolated and fixed. Distribution of antisense oligonucleotides was determined by probing with an anti-BrdU antibody and immunohistochemical staining. Tissue slices were probed with an anti-BrdU antibody followed by a reporter enzyme-conjugated second antibody and finally an enzyme substrate. Visualization of the colored product by microscopy indicated nuclear staining, demonstrating effective distribution of antisense oligonucleotide in cardiac tissue.

Tissue distribution of BrdU-labeled ribozymes in monkey

Rhesus monkeys were dosed with BrdU-labeled ribozyme by intravenous bolus injection at 0.1, 1.0, and 10 mg/kg once daily over five days. Saline injection was used in control animals. Animals were sacrificed and major tissues isolated and fixed. Tissue samples were probed with an anti-BrdU antibody followed by a reporter enzyme-conjugated second antibody and finally an enzyme substrate. Significant quantities of chemically modified ribozyme are detected in cardiac tissue following this dosing regimen.

Example 6: HBV

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Chronic hepatitis B is caused by an enveloped virus, commonly known as the hepatitis B virus or HBV. HBV is transmitted via infected blood or other body fluids, especially saliva and semen, during delivery, sexual activity, or sharing of needles contaminated by infected blood. Individuals may be "carriers" and transmit the infection to others without ever having experienced symptoms of the disease. Persons at highest

risk are those with multiple sex partners, those with a history of sexually transmitted diseases, parenteral drug users, infants born to infected mothers, "close" contacts or sexual partners of infected persons, and healthcare personnel or other service employees who have contact with blood. Transmission is also possible via tattooing, ear or body piercing, and acupuncture; the virus is also stable on razors, toothbrushes, baby bottles, eating utensils, and some hospital equipment such as respirators, scopes and instruments. There is no evidence that HBsAg positive food handlers pose a health risk in an occupational setting, nor should they be excluded from work. Hepatitis B has never been documented as being a food-borne disease. The average incubation period is 60 to 90 days, with a range of 45 to 180; the number of days appears to be related to the amount of virus to which the person was exposed. However, determining the length of incubation is difficult, since onset of symptoms is insidious. Approximately 50% of patients develop symptoms of acute hepatitis that last from 1 to 4 weeks. Two percent or less of these individuals develop fullminant hepatitis resulting in liver failure and death.

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The determinants of severity include: (1) The size of the dose to which the person was exposed; (2) the person's age with younger patients experiencing a milder form of the disease; (3) the status of the immune system with those who are immunosuppressed experiencing milder cases; and (4) the presence or absence of co-infection with the Delta virus (hepatitis D), with more severe cases resulting from co-infection. In symptomatic cases, clinical signs include loss of appetite, nausea, vomiting, abdominal pain in the right upper quadrant, arthralgia, and tiredness/loss of energy. Jaundice is not experienced in all cases, however, jaundice is more likely to occur if the infection is due to transfusion or percutaneous scrum transfer, and it is accompanied by mild pruritus in some patients. Bilirubin elevations are demonstrated in dark urine and clay-colored stools, and liver enlargement may occur accompanied by right upper-quadrant pain. The acute phase of the disease may be accompanied by severe depression, meningitis, Guillain-Barré syndrome, myelitis, encephalitis, agranulocytosis, and/or thrombocytopenia.

Hepatitis B is generally self-limiting and will resolve in approximately 6 months. Asymptomatic cases can be detected by serologic testing, since the presence of the virus leads to production of large amounts of HBsAg in the blood. This antigen is the first and most useful diagnostic marker for active infections. However, if HBsAg remains positive for 20 weeks or longer, the person is likely to remain positive indefinitely and is now a carrier. While only 10% of persons over age 6 who contract HBV become carriers, 90% of infants infected during the first year of life do so.

Hepatitis B virus (HBV) infects over 300 million people worldwide (Imperial, 1999, Gastroenterol. Hepatol., 14 (suppl), S1-5). In the United States approximately 1.25 million individuals are chronic carriers of HBV as evidenced by the fact that they have measurable hepatitis B virus surface antigen HBsAg in their blood. The risk of becoming a chronic HBsAg carrier is dependent upon the mode of acquisition of infection as well as the age of the individual at the time of infection. For those individuals with high levels of viral replication, chronic active hepatitis with progression to cirrhosis, liver failure and hepatocellular carcinoma (HCC) is common, and liver transplantation is the only treatment option for patients with end-stage liver disease from HBV.

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The natural progression of chronic HBV infection over a 10 to 20 year period leads to cirrhosis in 20-to-50% of patients and progression of HBV infection to hepatocellular carcinoma has been well documented. There have been no studies that have determined sub-populations that are most likely to progress to cirrhosis and/or hepatocellular carcinoma, thus all patients have equal risk of progression.

It is important to note that the survival for patients diagnosed with hepatocellular carcinoma is only 0.9 to 12.8 months from initial diagnosis (Takahashi et al., 1993, American Journal of Gastroenterology, 88, 240-243). Treatment of hepatocellular carcinoma with chemotherapeutic agents has not proven effective and only 10% of patients will benefit from surgery due to extensive tumor invasion of the liver (Trinchet et al., 1994, Presse Medicine, 23, 831-833). Given the aggressive nature of primary hepatocellular carcinoma, the only viable treatment alternative to surgery is liver transplantation (Pichlmayr et al., 1994, Hepatology, 20, 338-408).

Upon progression to cirrhosis, patients with chronic HCV infection present with clinical features, which are common to clinical cirrhosis regardless of the initial cause (D'Amico et al., 1986, Digestive Diseases and Sciences, 31, 468-475). These clinical features may include: bleeding esophageal varices, ascites, jaundice, and encephalopathy (Zakim D, Boyer TD. Hepatology a textbook of liver disease, Second Edition Volume 1. 1990 W.B. Saunders Company. Philadelphia). In the early stages of cirrhosis, patients are classified as compensated, meaning that although liver tissue damage has occurred, the patient's liver is still able to detoxify metabolites in the blood-stream. In addition, most

patients with compensated liver disease are asymptomatic and the minority with symptoms report only minor symptoms such as dyspepsia and weakness. In the later stages of cirrhosis, patients are classified as decompensated meaning that their ability to detoxify metabolites in the bloodstream is diminished and it is at this stage that the clinical features described above will present.

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In 1986, D'Amico et al. described the clinical manifestations and survival rates in 1155 patients with both alcoholic and viral associated cirrhosis (D'Amico supra). Of the 1155 patients, 435 (37%) had compensated disease although 70% were asymptomatic at the beginning of the study. The remaining 720 patients (63%) had decompensated liver disease with 78% presenting with a history of ascites, 31% with jaundice, 17% had bleeding and 16% had encephalopathy. Hepatocellular carcinoma was observed in six (0.5%) patients with compensated disease and in 30 (2.6%) patients with decompensated disease.

Over the course of six years, the patients with compensated cirrhosis developed clinical features of decompensated disease at a rate of 10% per year. In most cases, ascites was the first presentation of decompensation. In addition, hepatocellular carcinoma developed in 59 patients who initially presented with compensated disease by the end of the six-year study.

With respect to survival, the D'Amico study indicated that the five-year survival rate for all patients on the study was only 40%. The six-year survival rate for the patients who initially had compensated cirrhosis was 54% while the six-year survival rate for patients who initially presented with decompensated disease was only 21%. There were no significant differences in the survival rates between the patients who had alcoholic cirrhosis and the patients with viral related cirrhosis. The major causes of death for the patients in the D'Amico study were liver failure in 49%; hepatocellular carcinoma in 22%; and, bleeding in 13% (D'Amico supra).

Hepatitis B virus is a double-stranded circular DNA virus. It is a member of the Hepadnaviridae family. The virus consists of a central core that contains a core antigen (HBcAg) surrounded by an envelope containing a surface protein/surface antigen (HBsAg) and is 42 nm in diameter. It also contains an e antigen (HBeAg) which, along with HBcAg and HBsAg, is helpful in identifying this disease

In HBV virions, the genome is found in an incomplete double-stranded form. HBV uses a reverse transcriptase to transcribe a positive-sense full length RNA version of its genome back into DNA. This reverse transcriptase also contains DNA polymerase activity and thus begins replicating the newly synthesized minus-sense DNA strand. However, it appears that the core protein encapsidates the reverse-transcriptase/polymerase before it completes replication.

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From the free-floating form, the virus must first attach itself specifically to a host cell membrane. Viral attachment is one of the crucial steps which determines host and tissue specificity. However, currently there are no in vitro cell-lines that can be infected by HBV. There are some cells lines, such as HepG2, which can support viral replication only upon transient or stable transfection using HBV DNA.

After attachment, fusion of the viral envelope and host membrane must occur to allow the viral core proteins containing the genome and polymerase to enter the cell. Once inside, the genome is translocated to the nucleus where it is repaired and cyclized.

The complete closed circular DNA genome of HBV remains in the nucleus and gives rise to four transcripts. These transcripts initiate at unique sites but share the same 3'-ends. The 3.5-kb pregenomic RNA serves as a template for reverse transcription and also encodes the nucleocapsid protein and polymerase. A subclass of this transcript with a 5'-end extension codes for the precore protein that, after processing, is secreted as HBV e antigen. The 2.4-kb RNA encompasses the pre-S1 open reading frame (ORF) that encodes the large surface protein. The 2.1-kb RNA encompasses the pre-S2 and S ORFs that encode the middle and small surface proteins, respectively. The smallest transcript (~0.8-kb) codes for the X protein, a transcriptional activator.

Multiplication of the HBV genome begins within the nucleus of an infected cell. RNA polymerase II transcribes the circular HBV DNA into greater-than-full length mRNA. Since the mRNA is longer than the actual complete circular DNA, redundant ends are formed. Once produced, the pregenomic RNA exits the nucleus and enters the cytoplasm.

The packaging of pregenomic RNA into core particles is triggered by the binding of the HBV polymerase to the 5' epsilon stem-loop. RNA encapsidation is believed to occur as soon as binding occurs. The HBV polymerase also appears to require associated core protein in order to function. The HBV polymerase initiates reverse transcription from the

5' ensilon stem-loop three to four base pairs at which point the polymerase and attached nascent DNA are transferred to the 3' copy of the DR1 region. Once there, the (-)DNA is extended by the HBV polymerase while the RNA template is degraded by the HBV nolymerase RNAse H activity. When the HBV nolymerase reaches the 5' end, a small stretch of RNA is left undigested by the RNAse H activity. This segment of RNA is comprised of a small sequence just unstream and including the DR1 region. The RNA oligomer is then translocated and annealed to the DR2 region at the 5' end of the (-)DNA. It is used as a primer for the (+)DNA synthesis which is also generated by the HBV polymerase. It appears that the reverse transcription as well as plus strand synthesis may occur in the completed core particle.

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Since the pregenomic RNA is required as a template for DNA synthesis, this RNA is an excellent target for ribozyme cleavage. Nucleoside analogues that have been documented to inhibit HBV replication target the reverse transcriptase activity needed to convert the pregenomic RNA into DNA. Ribozyme cleavage of the pregenomic RNA template would be expected to result in a similar inhibition of HBV replication. Further, targeting the 3'-end of the pregenomic RNA that is common to all HBV transcripts could result in reduction of all HBV gene products and an additional level of inhibition of HBV replication.

As previously mentioned, HBV does not infect cells in culture. However, :0 transfection of HBV DNA (either as a head-to-tail dimer or as an "overlength" genome of >100%) into HuH7 or Hep G2 hepatocytes results in viral gene expression and production of HBV virions released into the media. Thus, HBV replication competent DNA would be co-transfected with ribozymes in cell culture. Such an approach has been used to report intracellular ribozyme activity against HBV (zu Putlitz, et al., 1999, J. Virol., 73, 5381-5387, and Kim et al., 1999, Biochem, Biophys, Res. Commun., 257, 759-765), In addition, stable hepatocyte cell lines have been generated that express HBV. In these cells only ribozyme would need to be delivered; however, a delivery screen would need to be performed. In addition, stable hepatocyte cell lines have been generated that express HBV.

Intracellular HBV gene expression can be assayed by a Taqman® assay for HBV RNA or by ELISA for HBV protein. Extracellular virus can be assayed by PCR for DNA or ELISA for protein. Antibodies are commercially available for HBV surface antigen and core protein. A secreted alkaline phosphatase expression plasmid can be used to

There are several small animal models to study HBV replication. One is the transplantation of HBV-infected liver tissue into irradiated mice. Viremia (as evidenced by measuring HBV DNA by PCR) is first detected 8 days after transplantation and peaks between 18 – 25 days (Ilan et al., 1999, Hepatology, 29, 553-562).

Transgenic mice that express HBV have also been used as a model to evaluate potential anti-virals. HBV DNA is detectable in both liver and serum (Morrey et al., 1999, Antiviral Res., 42, 97-108).

An additional model is to establish subcutaneous tumors in nude mice with Hep G2 cells transfected with HBV. Tumors develop in about 2 weeks after inoculation and express HBV surface and core antigens. HBV DNA and surface antigen is also detected in the circulation of tumor-bearing mice (Yao et al., 1996, J. Viral Hepat., 3, 19-22).

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Woodchuck hepatitis virus (WHV) is closely related to HBV in its virus structure, genetic organization, and mechanism of replication. As with HBV in humans, persistent WHV infection is common in natural woodchuck populations and is associated with chronic hepatitis and hepatocellular carcinoma (HCC). Experimental studies have established that WHV causes HCC in woodchucks and woodchucks chronically infected with WHV have been used as a model to test a number of anti-viral agents. For example, the nucleoside analogue 3T3 was observed to cause dose dependent reduction in virus (50% reduction after two daily treatments at the highest dose) (Hurwitz et al., 1998. Antimicrob. Agents Chemother., 42, 2804-2809).

Current therapeutic goals of treatment are three-fold: to eliminate infectivity and transmission of HBV to others, to arrest the progression of liver disease and improve the clinical prognosis, and to prevent the development of hepatocellular carcinoma (HCC).

Interferon alpha use is the most common therapy for HBV; however, recently Lamivudine (3TC) has been approved by the FDA. Interferon alpha (IFN-alpha) is one treatment for chronic hepatitis B. The standard duration of IFN-alpha therapy is 16 weeks, however, the optimal treatment length is still poorly defined. A complete response (HBV DNA negative HBeAg negative) occurs in approximately 25% of patients. Several factors have been identified that predict a favorable response to therapy including: High ALT, low HBV DNA, being female, and heterosexual orientation.

There is also a risk of reactivation of the hepatitis B virus even after a successful response, this occurs in around 5% of responders and normally occurs within 1 year.

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Side effects resulting from treatment with type 1 interferons can be divided into four general categories including: Influenza-like symptoms, neuropsychiatric, laboratory abnormalities, and other miscellaneous side effects. Examples of influenza-like symptoms include, fatigue, fever; myalgia, malaise, appetite loss, tachycardia, rigors, headache and arthralgias. The influenza-like symptoms are usually short-lived and tend to abate after the first four weeks of dosing (Dusheiko et al., 1994, Journal of Viral Hepatitis, 1, 3-5). Neuropsychiatric side effects include irritability, apathy, mood changes, insomnia, cognitive changes, and depression. Laboratory abnormalities include the reduction of myeloid cells, including granulocytes, platelets and to a lesser extent, red blood cells. These changes in blood cell counts rarely lead to any significant clinical sequellae. In addition, increases in triglyceride concentrations and elevations in serum alaine and aspartate aminotransferase concentration have been observed. Finally, thyroid abnormalities have been reported. These thyroid abnormalities are usually reversible after cessation of interferon therapy and can be controlled with appropriate medication while on therapy. Miscellaneous side effects include nausea, diarrhea, abdominal and back pain, pruritus, alopecia, and rhinorrhea. In general, most side effects will abate after 4 to 8 weeks of therapy (Dushieko et al., supra).

Lamivudine (3TC) is a nucleoside analogue, which is a very potent and specific inhibitor of HBV DNA synthesis. Lamivudine has recently been approved for the treatment of chronic Hepatitis B. Unlike treatment with interferon, treatment with 3TC does not eliminate the HBV from the patient. Rather, viral replication is controlled and chronic administration results in improvements in liver histology in over 50% of patients. Phase III studies with 3TC, showed that treatment for one year was associated with reduced liver inflammation and a delay in scarring of the liver. In addition, patients treated with Lamivudine (100mg per day) had a 98 percent reduction in hepatitis B DNA and a significantly higher rate of seroconversion, suggesting disease improvements after completion of therapy. However, stopping of therapy resulted in a reactivation of HBV replication in most patients. In addition recent reports have documented 3TC resistance in approximately 30% of patients.

Particular degenerative and disease states that can be associated with HBV expression modulation include but are not limited to, HBV infection, hepatitis, cancer, tumorigenesis, cirrhosis, liver failure and others.

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Lamivudine (3TC), L-FMAU, adefovir dipivoxil, type 1 Interferon, therapeutic vaccines, steriods, and 2'-5' Oligoadenylates are non-limiting examples of pharmaceutical agents that can be combined with or used in conjunction with the nucleic acid molecules (e.g. ribozymes and antisense molecules) of the instant invention. Those skilled in the art will recognize that other drugs such as diuretic and antihypertensive compounds or other therapies can similarly and readily be combined with the nucleic acid molecules of the instant invention (e.g. ribozymes and antisense molecules) and are, therefore, within the scope of the instant invention.

Current therapies for treating HBV infection, including interferon and nucleoside analogues, are only partially effective. In addition, drug resistance to nucleoside analogues is now emerging, making treatment of chronic Hepatitis B more difficult. Thus, a need exists for effective treatment of this disease which utilizes antiviral inhibitors which work by mechanisms other than those currently utilized in the treatment of both acute and chronic hepatitis B infections.

Draper, US patent No. 6,017,756, describes the use of ribozymes for the inhibition of Hepatitis B Virus.

Passman et al., 2000, Biochem. Biophys. Res. Commun., 268(3), 728-733.; Gan et al., 1998, J. Med. Coll. PLA, 13(3), 157-159.; Li et al., 1999, Jiefangjun Yixue Zazhi, 24(2), 99-101.; Putlitz et al., 1999, J. Virol., 73(7), 5381-5387.; Kim et al., 1999, Biochem. Biophys. Res. Commun., 257(3), 759-765.; Xu et al., 1998, Bingdu Xuebao, 14(4), 365-369.; Welch et al., 1997, Gene Ther., 4(7), 736-743.; Goldenberg et al., 1997, International PCT publication No. WO 97/08309, Wands et al., 1997, J. of Gastroenterology and Hepatology, 12(suppl.), S354-S369.; Ruiz et al., 1997, BioTechniques, 22(2), 338-345.; Gan et al., 1996, J. Med. Coll. PLA, 11(3), 171-175.; Beck and Nassal, 1995, Nucleic Acids Res., 23(24), 4954-62.; Goldenberg, 1995, International PCT publication No. WO 95/22600.; Xu et al., 1993, Bingdu Xuebao, 9(4), 331-6.; Wang et al., 1993, Bingdu Xuebao, 9(3), 278-80, all describe ribozymes that are targeted to cleave a specific HBV target site.

The enzymatic nucleic acid molecules of the instant invention exhibit a high degree of specificity for only the viral mRNA in infected cells. Nucleic acid molecules of the instant invention targeted to highly conserved sequence regions allow the treatment of many strains of human HBV with a single compound. No treatment presently exists which specifically attacks expression of the viral gene(s) that are responsible for transformation of hepatocytes by HBV.

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The methods of this invention can be used to treat human hepatitis B virus infections, which include productive virus infection, latent or persistent virus infection, and HBV-induced hepatocyte transformation. The utility can be extended to other species of HBV which infect non-human animals where such infections are of veterinary importance.

Preferred target sites are genes required for viral replication, a non-limiting example includes genes for protein synthesis, such as the 5' most 1500 nucleotides of the HBV pregenomic mRNAs. For sequence references, see Renbao et al., 1987, Sci. Sin., 30, 507. This region controls the translational expression of the core protein (C), X protein (X) and DNA polymerase (P) genes and plays a role in the replication of the viral DNA by serving as a template for reverse transcriptase. Disruption of this region in the RNA results in deficient protein synthesis as well as incomplete DNA synthesis (and inhibition of transcription from the defective genomes). Target sequences 5' of the encapsidation site can result in the inclusion of the disrupted 3' RNA within the core virion structure and targeting sequences 3' of the encapsidation site can result in the reduction in protein expression from both the 3' and 5' framements.

Alternative regions outside of the 5' most 1500 nucleotides of the pregenomic mRNA also make suitable targets of enzymatic nucleic acid mediated inhibition of HBV replication. Such targets include the mRNA regions that encode the viral S gene. Selection of particular target regions will depend upon the secondary structure of the pregenomic mRNA. Targets in the minor mRNAs can also be used, especially when folding or accessibility assays in these other RNAs reveal additional target sequences that are unavailable in the pregenomic mRNA species.

A desirable target in the pregenomic RNA is a proposed bipartite stem-loop structure in the 3'-end of the pregenomic RNA which is believed to be critical for viral replication (Kidd and Kidd-Ljunggren, 1996. Nuc. Acid Res. 24:3295-3302). The 5'end of the HBV

pregenomic RNA carries a cis-acting encapsidation signal, which has inverted repeat sequences that are thought to form a bipartite stem-loop structure. Due to a terminal redundancy in the pregenomic RNA, the putative stem-loop also occurs at the 3'-end. While it is the 5' copy which functions in polymerase binding and encapsidation, reverse transcription actually begins from the 3' stem-loop. To start reverse transcription, a 4 nt primer which is covalently attached to the polymerase is made, using a bulge in the 5' encapsidation signal as template. This primer is then shifted, by an unknown mechanism, to the DR1 primer binding site in the 3' stem-loop structure, and reverse transcription proceeds from that point. The 3' stem-loop, and especially the DR1 primer binding site, appear to be highly effective targets for ribozyme intervention.

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Sequences of the pregenomic RNA are shared by the mRNAs for surface, core, polymerase, and X proteins. Due to the overlapping nature of the HBV transcripts, all share a common 3'-end. Ribozyme targeting this common 3'-end will thus cleave the pregenomic RNA as well as all of the mRNAs for surface, core, polymerase and X proteins.

In preferred embodiments, the invention features a method for the analysis of HBV proteins. This method is useful in determining the efficacy of HBV inhibitors. Specifically, the instant invention features an assay for the analysis of HBsAg proteins and secreted alkaline phosphatase (SEAP) control proteins to determine the efficacy of agents used to modulate HBV expression.

The method consists of coating a micro-titer plate with an antibody such as anti-HBsAg Mab (for example, Biostride B88-95-31ad,ay) at 0.1 to 10 µg/ml in a buffer (for example, carbonate buffer, such as Na₂CO₃ 15 mM, NaHCO₃ 35 mM, pH 9.5) at 4°C overnight. The microtiter wells are then washed with PBST or the equivalent thereof, (for example, PBS, 0.05% Tween 20) and blocked for 0.1-24 hr at 37° C with PBST, 1% BSA or the equivalent thereof. Following washing as above, the wells are dried (for example, at 37° C for 30 min). Biotinylated goat anti-HBsAg or an equivalent antibody (for example, Accurate YVS1807) is diluted (for example at 1:1000) in PBST and incubated in the wells (for example, 1 hr. at 37° C). The wells are washed with PBST (for example, 4x). A conjugate, (for example, Streptavidin/Alkaline Phosphatase Conjugate, Pierce 21324) is diluted to 10-10,000 ng/ml in PBST, and incubated in the wells (for example, 1 hr. at 37° C). After washing as above, a substrate (for example, p-nitrophenyl phosphate substrate,

Pierce 37620) is added to the wells, which are then incubated (for example, 1 hr. at 37° C). The optical density is then determined (for example, at 405 nm). SEAP levels are then assayed, for example, using the Great EscAPe® Detection Kit (Clontech K2041-1), as per the manufacturers instructions. In the above example, incubation times and reagent concentrations may be varied to achieve optimum results, a non-limiting example is described in Example 6.

Comparison of this HBsAg ELISA method to a commercially available assay from World Diagnostics, Inc. 15271 NW 60th Ave, #201, Miami Lakes, FL 33014 (305) 827-3304 (Cat. No. EL10018) demonstrates an increase in sensitivity (signal:noise) of 3-20 fold.

Identification of Potential Target Sites in Human HBV RNA

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The sequence of human HBV was screened for accessible sites using a computerfolding algorithm. Regions of the RNA that did not form secondary folding structures and contained potential ribozyme and/or antisense binding/cleavage sites were identified. The sequences of these cleavage sites are shown in Tables 36-43.

Selection of Enzymatic Nucleic Acid Cleavage Sites in Human HBV RNA

Ribozyme target sites were chosen by analyzing sequences of Human HBV

(accession number: AF100308.1) and prioritizing the sites on the basis of folding.

Ribozymes were designed that could bind each target and were individually analyzed by computer folding (Christoffersen et al., 1994 J. Mol. Struc. Theochem, 311, 273; Jaeger et al., 1989, Proc. Natl. Acad. Sci. USA, 86, 7706) to assess whether the ribozyme sequences fold into the appropriate secondary structure. Those ribozymes with unfavorable intramolecular interactions between the binding arms and the catalytic core were eliminated from consideration. As noted herein, varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 bases on each arm are able to bind to, or otherwise interact with, the target RNA.

Chemical Synthesis and Purification of Ribozymes and Antisense for Efficient Cleavage and/or blocking of HBV RNA

Ribozymes and antisense constructs were designed to anneal to various sites in the RNA message. The binding arms of the ribozymes are complementary to the target site sequences described above, while the antisense constructs are fully complementary to the target site sequences described above. The ribozymes and antisense constructs were chemically synthesized. The method of synthesis used followed the procedure for normal RNA synthesis as described above and in Usman et al., (1987 J. Am. Chem. Soc., 109, 7845), Scaringe et al., (1990 Nucleic Acids Res., 18, 5433) and Wincott et al., supra, and made use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The average stepwise coupling yields were twoically >98%.

Ribozymes and antisense constructs were also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbeck, 1989, Methods Enzymol. 180, 51). Ribozymes and antisense constructs were purified by gel electrophoresis using general methods or were purified by high pressure liquid chromatography (HPLC; see Wincott et al., supra; the totality of which is hereby incorporated herein by reference) and were resuspended in water. The sequences of the chemically synthesized ribozymes used in this study are shown below in Table 43.

Ribozyme Cleavage of HBV RNA Target in vitro

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Ribozymes targeted to the human HBV RNA are designed and synthesized as described above. These ribozymes can be tested for cleavage activity in vitro, for example using the following procedure. The target sequences and the nucleotide location within the HBV RNA are given in Tables 36-43.

Cleavage Reactions: Full-length or partially full-length, internally-labeled target RNA for ribozyme cleavage assay is prepared by in vitro transcription in the presence of $[\alpha^{-32}\text{P}]$ CTP, passed over a G 50 Sephadex® column by spin chromatography and used as substrate RNA without further purification. Alternately, substrates are 5'-32P-end labeled using T4 polynucleotide kinase enzyme. Assays are performed by pre-warming a 2X concentration of purified ribozyme in ribozyme cleavage buffer (50 mM Tris-HCl, pH 7.5

at 37°C, 10 mM MgCl₂) and the cleavage reaction was initiated by adding the 2X ribozyme mix to an equal volume of substrate RNA (maximum of 1-5 nM) that was also pre-warmed in cleavage buffer. As an initial screen, assays are carried out for 1 hour at 37°C using a final concentration of either 40 nM or 1 mM ribozyme, i.e., ribozyme excess. The reaction is quenched by the addition of an equal volume of 95% formamide, 20 mM EDTA, 0.05% bromophenol blue and 0.05% xylene cyanol after which the sample is heated to 95°C for 2 minutes, quick chilled and loaded onto a denaturing polyacrylamide gel. Substrate RNA and the specific RNA cleavage products generated by ribozyme cleavage are visualized on an autoradiograph of the gel. The percentage of cleavage is determined by Phosphor Imagei. Quantitation of bands representing the intact substrate and the cleavage products.

Transfection of HepG2 Cells with psHBV-1 and Ribozymes

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The human hepatocellular carcinoma cell line Hep G2 was grown in Dulbecco's modified Eagle media supplemented with 10% fetal calf serum, 2 mM glutamine, 0.1 mM nonessential amino acids, 1 mM sodium pyruvate, 25 mM Hepes, 100 units penicillin, and 100 µg/ml streptomycin. To generate a replication competent cDNA, prior to transfection the HBV genomic sequences are excised from the bacterial plasmid sequence contained in the psHBV-1 vector (Those skilled in the art understand that other methods may be used to generate a replication competent cDNA). This was done with an EcoRI and Hind III restriction digest. Following completion of the digest, a ligation was performed under dilute conditions (20 µg/ml) to favor intermolecular ligation. The total ligation mixture was then concentrated using Qiagen spin columns.

Secreted alkaline phosphatase (SEAP) was used to normalize the HBsAg levels to control for transfection variability. The pSEAP2-TK control vector was constructed by ligating a Bgl II-Hind III fragment of the pRL-TK vector (Promega), containing the herpes simplex virus thymidine kinase promoter region, into Bgl II-Hind III digested pSEAP2-Basic (Clontech). Hep G2 cells were plated (3 x 10⁴ cells/well) in 96-well microtiter plates and incubated overnight. A lipid/DNA/ribozyme complex was formed containing (at final concentrations) cationic lipid (15 µg/ml), prepared psHBV-1 (4.5 µg/ml), pSEAP2-TK (0.5 µg/ml), and ribozyme (100 µM). Following a 15 min. incubation at 37° C, the

complexes were added to the plated Hep G2 cells. Media was removed from the cells 96 hr. post-transfection for HBsAg and SEAP analysis.

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Transfection of the human hepatocellular carcinoma cell line, Hep G2, with replication competent HBV DNA results in the expression of HBV proteins and the production of virions. To investigate the potential use of ribozymes for the treatment of chronic HBV infection, a series of ribozymes that target the 3' terminus of the HBV genome have been synthesized. Ribozymes targeting this region have the potential to cleave all four major HBV RNA transcripts as well as the potential to block the production of HBV DNA by cleavage of the pregenomic RNA. To test the efficacy of these HBV ribozymes, they were co-transfected with HBV genomic DNA into Hep G2 cells, and the subsequent levels of secreted HBV surface antigen (HBsAg) were analyzed by ELISA. To control for variability in transfection efficiency, a control vector which expresses secreted alkaline phosphatase (SEAP), was also co-transfected. The efficacy of the HBV ribozymes was determined by comparing the ratio of HBsAg:SEAP and/or HBeAg:SEAP to that of a scrambled attenuated control (SAC) ribozyme. Twenty-five ribozymes (RPI18341, RPI18356, RPI18363, RPI18364, RPI18365, RPI18366, RPI18367, RPI18368. RPI18369, RPI18370, RPI18371, RPI18372, RPI18373, RPI18374, RPI18303, RPI18405, RPI18406, RPI18407, RPI18408, RPI18409, RPI18410, RPI18411, RPI18418, RPI18419, and RPI18422) have been identified which cause a reduction in the levels of HBsAg and/or HBeAg as compared to the corresponding SAC ribozyme.

Example 6: Analysis of HBsAg and SEAP Levels Following Ribozyme Treatment

Immulon 4 (Dynax) microtiter wells were coated overnight at 4° C with anti-HBsAg Mab (Biostride B88-95-31ad,ay) at 1 µg/ml in Carbonate Buffer (Na₂CO₃ 15 mM, NaHCO₃ 35 mM, pH 9.5). The wells were then washed 4x with PBST (PBS, 0.05% Tween® 20) and blocked for 1 hr at 37° C with PBST, 1% BSA. Following washing as above, the wells were dried at 37° C for 30 min. Biotinylated goat anti-HBsAg (Accurate YVS1807) was diluted 1:1000 in PBST and incubated in the wells for 1 hr. at 37° C. The wells were washed 4x with PBST. Streptavidin/Alkaline Phosphatase Conjugate (Pierce 21324) was diluted to 250 ng/ml in PBST, and incubated in the wells for 1 hr. at 37° C. After washing as above, p-nitrophenyl phosphate substrate (Pierce 37620) was added to the wells, which were then incubated for 1 hr. at 37° C. The optical density at 405 mm was

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then determined. SEAP levels were assayed using the Great EscAPe® Detection Kit (Clontech K2041-1), as per the manufacturers instructions.

Example 7: X-gene Reporter Assay

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The effect of ribozyme treatment on the level of transactivation of a SV40 promoter driven firefly luciferase gene by the HBV X-protein was analyzed in transfected Hep G2 cells. As a control for variability in transfection efficiency, a Renilla luciferase reporter driven by the TK promoter, which is not transactivated by the X protein, was used. Hep G2 cells were plated (3 x 10^4 cells/well) in 96-well microtiter plates and incubated overnight. A lipid/DNA/ribozyme complex was formed containing (at final concentrations) cationic lipid (2.4 µg/ml), the X-gene vector pSBDR(2.5 µg/ml), the firefly reporter pSV40HCVluc (0.5 µg/ml), the Renilla luciferase control vector pRL-TK (0.5 µg/ml), and ribozyme (100 µM). Following a 15 min. incubation at 37° C, the complexes were added to the plated Hep G2 cells. Levels of firefly and Renilla luciferase were analyzed 48 hr. post transfection, using Promega's Dual-Luciferase Assay System.

The HBV X protein is a transactivator of a number of viral and cellular genes. Ribozymes which target the X region were tested for their ability to cause a reduction in X protein transactivation of a firefly luciferase gene driven by the SV40 promoter in transfected Hep G2 cells. As a control for transfection variability, a vector containing the Renilla luciferase gene driven by the TK promotor, which is not activated by the X protein, was included in the co-transfections. The efficacy of the HBV ribozymes was determined by comparing the ratio of firefly luciferase: Renilla luciferase to that of a scrambled attenuated control (SAC) ribozyme. Eleven ribozymes (RPI18365, RPI18367, RPI18372, RPI18373, RPI18405, RPI18406, RPI18411, RPI18418, RPI18423) were identified which cause a reduction in the level of transactivation of a reporter gene by the X protein, as compared to the corresponding SAC ribozyme.

Example 8: HBV transgenic mouse study

A transgenic mouse strain (founder strain 1.3.32 with a C57B1/6 background) that expresses HBV RNA and forms HBV viremia (Morrey et al., 1999, Antiviral Res., 42, 97-108; Guidotti et al., 1995, J. Virology, 69, 10, 6158-6169) was utilized to study the in vivo

activity of ribozymes of the instant invention. This model is predictive in screening for anti-HBV agents. Ribozyme or the equivalent volume of saline was administered via a continuous s.c. infusion using Alzet® mini-osmotic pumps for 14 days. Alzet® pumps were filled with test material(s) in a sterile fashion according to the manufacturer's instructions. Prior to in vivo implantation, pumps were incubated at 37°C overnight (> 18 hours) to prime the flow modulators. On the day of surgery, animals were lightly anesthetized with a ketamine/xylazine cocktail (94 mg/kg and 6 mg/kg, respectively; 0.3 ml. IP). Baseline blood samples (200 ul) were obtained from each animal via a retroorbital bleed. A 2 cm area near the base of the tail was shaved and cleansed with betadine surgical scrub and sequentially with 70% alcohol. A 1 cm incision in the skin was made with a #15 scalpel blade or a blunt pair of scissors near the base of the tail. Forceps were used to open a pocket rostrally (i.e., towards the head) by spreading apart the subcutaneous connective tissue. The pump was inserted with the delivery portal pointing away from the incision. Wounds were closed with sterile 9-mm stainless steel clips or with sterile 4-0 suture. Animals were then allowed to recover from anesthesia on a warm heating pad before being returned to their cage. Wounds were checked daily. Clips or sutures were replaced as needed. Incisions typically healed completely within 7 days post-op. Animals were then deeply anesthetized with the ketamine/xylazine cocktail (150 mg/kg and 10 mg/kg, respectively; 0.5 ml, IP) on day 14 post pump implantation. A midline thoracotomy/ laparatomy was performed to expose the abdominal cavity and the thoracic cavity. The left ventricle was cannulated at the base and animals exsanguinated using a 23G needle and 1 ml syringe. Serum was separated, frozen and analyzed for HBV DNA and antigen levels. Experimental groups were compared to the saline control group in respect to percent change from day 0 to day 14. HBV DNA was assayed by quantitative PCR

Results

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Table 44 is a summary of the group designation and dosage levels used in the HBV transgenic mouse study. Baseline blood samples were obtained via a retroorbital bleed and animals (N=10/group) received anti-HBV ribozymes (100 mg/kg/day) as a continuous SC infusion. After 14 days, animals treated with a ribozyme targeting site 273 (RPL18341) of

the HBV RNA showed a significant reduction in serum HBV DNA concentration, compared to the saline treated animals as measured by a quantitative PCR assay. More specifically, the saline treated animals had a 69% increase in serum HBV DNA concentrations over this 2-week period while treatment with the 273 ribozyme (RPI.18341) resulted in a 60% decrease in serum HBV DNA concentrations. Ribozymes directed against sites 1833 (RPI.18371), 1873 (RPI.18418), and 1874 (RPI.18372) decreased serum HBV DNA concentrations by 49%, 15% and 16%, respectively.

Example 7: Activity of NCH Ribozyme to inhibit HER2 gene expression

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HER2 (also known as neu, erbB2 and c-erbB2) is an oncogene that encodes a 185-kDa transmembrane tyrosine kinase receptor. HER2 is a member of the epidermal growth factor receptor (FEGFR) family and shares partial homology with other family members. In normal adult tissues HER2 expression is low. However, HER2 is overexpressed in at least 25-30% of breast (McGuire & Greene, 1989) and ovarian cancers (Berchuck, et al., 1990). Furthermore, overexpression of HER2 in malignant breast tumors has been correlated with increased metastasis, chemoresistance and poor survival rates (Slamon et al., 1987 Science 235: 177-182). Because HER2 expression is high in aggressive human breast and ovarian cancers, but low in normal adult tissues, it is an attractive target for ribozyme-mediated therapy (Thompson et al., supra).

The greatest HER2 specific effects have been observed in cancer cell lines that express high levels of HER2 protein (as measured by ELISA). Specifically, in one study that treated five human breast cancer cell lines with the HER2 antibody (anti-erbB2-sFv), the greatest inhibition of cell growth was seen in three cell lines (MDA-MB-361, SKBR-3 and BT-474) that express high levels of HER2 protein. No inhibition of cell growth was observed in two cell lines (MDA-MB-231 and MCF-7) that express low levels of HER2 protein (Wright et al., 1997). Another group successfully used SKBR-3 cells to show HER2 antisense oligonucleotide-mediated inhibition of HER2 protein expression and HER2 RNA knockdown (Vaughn et al., 1995). Other groups have also demonstrated a decrease in the levels of HER2 protein, HER2 mRNA and/or cell proliferation in cultured cells using anti-HER2 ribozymes or antisense molecules (Suzuki, T. et al., 1997; Weichen, et al., 1997; Czubayko, F. et al., 1997; Colomer, et al., 1994; Betram et al., 1994). Because cell lines that express higher levels of HER2 have been more sensitive to anti-

HER2 agents, we are pursuing several medium to high expressing cell lines, including SKBR-3 and T47D. for ribozyme screens in cell culture.

A variety of endpoints have been used in cell culture models to look at HER2-mediated effects after treatment with anti-HER2 agents. Phenotypic endpoints include inhibition of cell proliferation, apoptosis assays and reduction of HER2 protein expression. Because overexpression of HER2 is directly associated with increased proliferation of breast and ovarian tumor cells, a proliferation endpoint for cell culture assays will be our primary screen. There are several methods by which this endpoint can be measured. Following treatment of cells with ribozymes, cells are allowed to grow (typically 5 days) after which either the cell viability, the incorporation of [3H] thymidine into cellular DNA and/or the cell density can be measured. The assay of cell density is very straightforward and can be done in a 96-well format using commercially available fluorescent nucleic acid stains (such as Syto 13 or CyQuant). The assay using CyQuant is in place at RPI and is currently being employed to screen = 100 ribozymes targeting HER2 (details below).

As a secondary, confirmatory endpoint a ribozyme-mediated decrease in the level of HER2 protein expression can be evaluated using a HER2-specific ELISA.

Validation of Cell Lines and Ribozyme Treatment Conditions

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Two human breast cancer cell lines (T47D and SKBR-3) that are known to express medium to high levels of HER2 protein, respectively, were considered for ribozyme screening. In order to validate these cell lines for HER2-mediated sensitivity, both cell lines were treated with the HER2 specific antibody, Herceptin® (Genentech) and its effect on cell proliferation was determined. Herceptin was added to cells at concentrations ranging from 0-8 μM in medium containing either no serum (OptiMem), 0.1% or 0.5% FBS and efficacy was determined *via* cell proliferation. Maximal inhibition of proliferation (~50%) in both cell lines was observed after addition of Herceptin at 0.5 nM in medium containing 0.1% or no FBS. The fact that both cell lines are sensitive to an anti-HER2 agent (Herceptin) supports their use in experiments testing anti-HER2 ribozymes.

Prior to ribozyme screening, the choice of the optimal lipid(s) and conditions for ribozyme delivery was determined empirically for each cell line. Applicant has established a panel of proprietary lipids that can be used to deliver ribozymes to cultured cells and are very useful for cell proliferation assays that are typically 3-5 days in length. Initially, this panel of proprietary lipid delivery vehicles was screened in SKBR-3 and T47D cells using previously established control oligonucleotides. Specific lipids and conditions for optimal delivery were selected for each cell line based on these screens. These conditions were used to deliver HER2 specific ribozymes to cells for primary (inhibition of cell proliferation) and secondary (decrease in HER2 protein) efficacy endpoints.

Primary Screen: Inhibition of Cell Proliferation

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Although optimal ribozyme delivery conditions were determined for two cell lines, the SKBR-3 cell line were be used for the initial screen because it has the higher level of HER2 protein, and thus should be most susceptible to a HER2-specific ribozyme. Follow-up studies can be carried out in T47D cells to confirm leads as necessary.

Ribozyme screens were be performed using an automated, high throughput 96-well cell proliferation assay. Cell proliferation were measured over a 5-day treatment period using the nucleic acid stain CyQuant for determining cell density. The growth of cells treated with ribozyme/lipid complexes were compared to both untreated cells and to cells treated with Scrambled-arm Attenuated core Controls (SAC; or IA; Figure 8). SACs can no longer bind to the target site due to the scrambled arm sequence and have nucleotide changes in the core that greatly diminish ribozyme cleavage. These SACs are used to determine non-specific inhibition of cell growth caused by ribozyme chemistry (i.e. multiple 2' O-Me modified nucleotides, a single 2'C-allyl uridine, 4 phosphorothioates and a 3' inverted abasic). Lead ribozymes are chosen from the primary screen based on their ability to inhibit cell proliferation in a specific manner. Dose response assays are carried out on these leads and a subset was advanced into a secondary screen using the level of HER2 protein as an endooint.

Secondary Screen: Decrease in HER2 Protein

A secondary screen that measures the effect of anti-HER2 ribozymes on HER2 protein levels is used to support preliminary findings. A robust HER2 ELISA for both T47D and SKBR-3 cells has been established and is available for use as an additional endpoint.

Ribozyme Mechanism Assays

A Taqman assay for measuring the ribozyme-mediated decrease in HER2 RNA has also been established. This assay is based on PCR technology and can measure in real time the production of HER2 mRNA relative to a standard cellular mRNA such as GAPDH. This RNA assay is used to establish proof that lead ribozymes are working through an RNA cleavage mechanism and result in a decrease in the level of HER2 mRNA, thus leading to a decrease in cell surface HER2 protein receptors and a subsequent decrease in tumor cell proliferation.

0 Animal Models

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Evaluating the efficacy of anti-HER2 agents in animal models is an important prerequisite to human clinical trials. As in cell culture models, the most HER2 sensitive mouse tumor xenografts are those derived from human breast carcinoma cells that express high levels of HER2 protein. In a recent study, nude mice bearing BT-474 xenografts were sensitive to the anti-HER2 humanized monoclonal antibody Herceptin, resulting in an 80% inhibition of tumor growth at a 1 mg kg dose (ip, 2 X week for 4-5 weeks). Tumor eradication was observed in 3 of 8 mice treated in this manner (Baselga et al., 1998). This same study compared the efficacy of Herceptin alone or in combination with the commonly used chemotherapeutics, paclitaxel or doxorubicin. Although, all three anti-HER2 agents caused modest inhibition of tumor growth, the greatest antitumor activity was produced by the combination of Herceptin and paclitaxel (93% inhibition of tumor growth vs 35% with paclitaxel alone). The above studies provide proof that inhibition of HER2 expression by anti-HER2 agents causes inhibition of tumor growth in animals. Lead anti-HER2 ribozymes chosen from in vitro assays are further tested in mouse xenograft models. Ribozymes are first tested alone and then in combination with standard chemotherapies.

Animal Model Development

Three human breast tumor cell lines (T47D, SKBR-3 and BT-474) were characterized to establish their growth curves in mice. These three cell lines have been implanted into the mammary papillae of both nude and SCID mice and primary tumor volumes are measured 3 times per week. Growth characteristics of these tumor lines using

a Matrigel implantation format will also be established. In addition, the use of two other breast cell lines that have been engineered to express high levels of HER2 are also being used. The tumor cell line(s) and implantation method that supports the most consistent and reliable tumor growth is used in animal studies testing the lead HER2 ribozyme(s). Ribozyme are administered by daily subcutaneous injection or by continuous subcutaneous infusion from Alzet mini osmotic pumps beginning 3 days after tumor implantation and continuing for the duration of the study. Group sizes of at least 10 animals are employed. Efficacy is determined by statistical comparison of tumor volume of ribozyme-treated animals to a control group of animals treated with saline alone. Because the growth of these tumors is generally slow (45-60 days), an initial endpoint will be the time in days it takes to establish an easily measurable primary tumor (i.e. 50-100 mm²) in the presence or absence of ribozyme treatment.

Clinical Summary

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Breast cancer is a common cancer in women and also occurs in men to a lesser degree. The incidence of breast cancer in the United States is \sim 180,000 cases per year and \sim 46,000 die each year of the disease. In addition, 21,000 new cases of ovarian cancer per year lead to \sim 13,000 deaths (data from Hung et al., 1995 and the Surveillance, Epidemiology and End Results Program, NCI). Ovarian cancer is a potential secondary indication for anti-HER2 ribozyme therapy.

A full review of breast cancer is given in the NCI PDQ for Breast Cancer. A brief overview is given here. Breast cancer is evaluated or "staged" on the basis of tumor size, and whether it has spread to lymph nodes and/or other parts of the body. In Stage I breast cancer, the cancer is no larger than 2 centimeters and has not spread outside of the breast. In Stage II, the patient's tumor is 2-5 centimeters but cancer may have spread to the axillary lymph nodes. By Stage III, metastasis to the lymph nodes is typical, and tumors are 5 centimeters. Additional tissue involvement (skin, chest wall, ribs, muscles etc.) may also be noted. Once cancer has spread to additional organs of the body, it is classed as Stage IV.

Almost all breast cancers (>90%) are detected at Stage I or II, but 31% of these are already lymph node positive. The 5-year survival rate for node negative patients (with standard surgery/radiation/chemotherapy/hormone regimens) is 97%; however,

involvement of the lymph nodes reduces the 5-year survival to only 77%. Involvement of other organs (Stage III) drastically reduces the overall survival, to 22% at 5 years. Thus, chance of recovery from breast cancer is highly dependent on early detection. Because up to 10% of breast cancers are hereditary, those with a family history are considered to be at high risk for breast cancer and should be monitored very closely.

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Breast cancer is highly treatable and often curable when detected in the early stages. (For a complete review of breast cancer treatments, see the NCI PDQ for Breast Cancer.) Common therapies include surgery, radiation therapy, chemotherapy and hormonal therapy. Depending upon many factors, including the tumor size, lymph node involvement and location of the lesion, surgical removal varies from lumpectomy (removal of the tumor and some surrounding tissue) to mastectomy (removal of the breast, lymph nodes and some or all of the underlying chest muscle). Even with successful surgical resection, as many as 21% of the patients may ultimately relapse (10-20 years). Thus, once local disease is controlled by surgery, adjuvant radiation treatments, chemotherapies and/or hormonal therapies are typically used to reduce the rate of recurrence and improve survival. The therapy regimen employed depends not only on the stage of the cancer at its time of removal, but other variables such the type of cancer (ductal or lobular), whether lymph nodes were involved and removed, age and general health of the patient and if other organs are involved.

Common chemotherapies include various combinations cytotoxic drugs to kill the cancer cells. These drugs include paclitaxel (Taxol), docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil etc. Significant toxicities are associated with these cytotoxic therapies. Well-characterized toxicities include nausea and vomiting, myelosuppression, alopecia and mucosity. Serious cardiac problems are also associated with certain of the combinations. e.g. doxorubin and paclitaxel, but are less common.

Testing for estrogen and progesterone receptors helps to determine whether certain anti-hormone therapies might be helpful in inhibiting tumor growth. If either or both receptors are present, therapies to interfere with the action of the hormone ligands, can be given in combination with chemotherapy and are generally continued for several years. These adjuvant therapies are called SERMs, selective estrogen receptor modulators, and they can give beneficial estrogen-like effects on bone and lipid metabolism while antagonizing estrogen in reproductive tissues. Tamoxifen is one such compound. The

primary toxic effect associated with the use of tamoxifen is a 2 to 7-fold increase in the rate of endometrial cancer. Blood clots in the legs and lung and the possibility of stroke are additional side effects. However, tamoxifen has been determined to reduce breast cancer incidence by 49% in high-risk patients and an extensive, somewhat controversial, clinical study is underway to expand the prophylactic use of tamoxifen. Another SERM, raloxifene, was also shown to reduce the incidence of breast cancer in a large clinical trial where it was being used to treat osteoporosis. In additional studies, removal of the ovaries and/or drugs to keep the ovaries from working are being tested.

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Bone marrow transplantation is being studied in clinical trials for breast cancers that have become resistant to traditional chemotherapies or where >3 lymph nodes are involved. Marrow is removed from the patient prior to high-dose chemotherapy to protect it from being destroyed, and then replaced after the chemotherapy. Another type of "transplant" involves the exogenous treatment of peripheral blood stem cells with drugs to kill cancer cells prior to replacing the treated cells in the bloodstream.

One biological treatment, a humanized monoclonal anti-HER2 antibody, Herceptin (Genentech) has been approved by the FDA as an additional treatment for HER2 positive tumors. Herceptin binds with high affinity to the extracellular domain of HER2 and thus blocks its signaling action. Herceptin can be used alone or in combination with chemotherapeutics (i.e. paclitaxel, docetaxel, cisplatin, etc.) (Pegram, et al., 1998). In Phase III studies, Herceptin significantly improved the response rate to chemotherapy as well as improving the time to progression (Ross & Fletcher, 1998). The most common side effects attributed to Herceptin are fever and chills, pain, asthenia, nausea, vomiting, increased cough, diarrhea, headache, dyspnea, infection, rhinitis, and insomnia. Herceptin in combination with chemotherapy (paclitaxel) can lead to cardiotoxicity (Sparano, 1999), leukopenia, anemia, diarrhea, abdominal pain and infection.

HER2 Protein Levels for Patient Screening and as a Potential Endpoint

Because elevated HER2 levels can be detected in at least 30% of breast cancers, breast cancer patients can be pre-screened for elevated HER2 prior to admission to initial clinical trials testing an anti-HER2 ribozyme. Initial HER2 levels can be determined (by ELISA) from tumor biopsies or resected tumor samples.

During clinical trials, it may be possible to monitor circulating HER2 protein by ELISA (Ross and Fletcher, 1998). Evaluation of serial blood/serum samples over the course of the anti-HER2 ribozyme treatment period could be useful in determining early indications of efficacy. In fact, the clinical course of Stage IV breast cancer was correlated with shed HER2 protein fragment following a dose-intensified paclitaxel monotherapy. In all responders, the HER2 serum level decreased below the detection limit (Luftner et al.).

Two cancer-associated antigens, CA27.29 and CA15.3, can also be measured in the serum. Both of these glycoproteins have been used as diagnostic markers for breast cancer. CA27.29 levels are higher than CA15.3 in breast cancer patients; the reverse is true in healthy individuals. Of these two markers, CA27.29 was found to better discriminate primary cancer from healthy subjects. In addition, a statistically significant and direct relationship was shown between CA27.29 and large w small tumors and node postive w node negative disease (Gion, et al., 1999). Moreover, both cancer antigens were found to be suitable for the detection of possible metastases during follow-up (Rodriguez de Paterna et al., 1999). Thus, blocking breast tumor growth may be reflected in lower CA27.29 and/or CA15.3 levels compared to a control group. FDA submissions for the use of CA27.29 and CA15.3 for monitoring metastatic breast cancer patients have been filed (reviewed in Beveridge, 1999). Fully automated methods for measurement of either of these markers are commercially available.

References

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Baselga, J., Norton, L. Albanell, J., Kim, Y.M. and Mendelsohn, J. (1998)
Recombinant humanized anti-HER2 antibody (Herceptin) enhances the antitumor activity
of paclitaxel and doxorubicin against HER2/neu overexpressing human breast cancer
xenografis. Cancer Res. 15: 2825-2831.

Berchuck, A. Kamel, A., Whitaker, R. et al. (1990) Overexpression of her-2/neu is associated with poor survival in advanced epithelial ovarian cancer. Cancer Research 50: 4087-4091.

Bertram, J. Killian, M., Brysch, W., Schlingensiepen, K.-H., and Kneba, M. (1994) Reduction of erbB2 gene product in mamma carcinoma cell lines by erbB2 mRNAspecific and tyrosine kinase consensus phosphorothioate antisense oligonucleotides. *Biochem. BioPhys. Res. Comm.* 200: 661-667. Beveridge, R.A. (1999) Review of clinical studies of CA27.29 in breast cancer

management. Int. J. Biol. Markers 14: 36-39.

Colomer, R., Lupu, R., Bacus, S.S. and Gelmann, E.P. (1994) erbB-2 antisense oligonucloetides inhibit the proliferation of breast carcinoma cells with erbB-2 oncogene amplification, British J. Cancer 70: 819-825.

Czubayko, F., Downing, S.G., Hsieh, S.S., Goldstein, D.J., Lu P.Y., Trapnell, B.C. and Wellstein, A. (1997) Adenovirus-mediated transduction of ribozymes abrogates HER-2/neu and pleiotrophin expression and inhibits tumor cell proliferation. Gene Ther. 4: 943-949

0 Gion, M., Mione, R., Leon, A.E. and Dittadi, R. (1999) Comparison of the diagnostic accuracy of CA27.29 and CA15.3 in primary breast cancer. Clin. Chem. 45: 630-637.

Hung, M.-C., Matin, A., Zhang, Y., Xing, X., Sorgi, F., Huang, L. and Yu, D. (1995) HER-2/neu-targeting gene therapy - a review. Gene 159: 65-71.

5 Luftner, D., Schnabel, S. and Possinger, K. (1999) c-erbB-2 in serum of patients receiving fractionated paclitaxel chemotherapy. Int. J. Biol. Markers 14: 55-59.

McGuire, H.C. and Greene, M.I. (1989) The neu (c-erbB-2) oncogene, Semin. Oncol. 16: 148-155.

NCI PDO/Treatment/Health Professionals/Breast Cancer:

0 http://cancernet.nci.nih.gov/clinpdq/soa/Breast cancer Physician.html

NCI PDQ/Treatment/Patients/Breast Cancer:

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http://cancernet.nci.nih.gov/clinpdq/pif/Breast_cancer_Patient.html

Pegram, M.D., Lipton, A., Haves, D.F., Weber, B.L., Baselga, J.M., Tripathy, D., Baly, D., Baughman, S.A., Twaddell, T., Glaspy, J.A. and Slamon, D.J. (1998) Phase II

study of recentor-enhanced chemosensitivity using recombinant humanized anti-

n185HER2/neu monoclonal antibody plus cisplatin in patients with HER2/neuoverexpressing metastatic breast cancer refractory to chemotherapy treatment. J. Clin. Oncol. 16: 2659-2671.

Rodriguez de Paterna, L., Arnaiz, F., Estenoz, J. Ortuno, B. and Lanzos E. (1999) Study of serum tumor markers CEA, CA15.3, CA27.29 as diagnostic parameters in 0 patients with breast carcinoma. Int. J. Biol. Markers 10: 24-29.

Ross, J.S. and Fletcher, J.A. (1998) The HER-2/neu oncogene in breast cancer:

Prognostic factor, predictive factor and target for therapy. Oncologist 3: 1998.

Slamon, D.J., Clark, G.M., Wong, S.G., Levin, W.J., Ullrich, A. and McGuire, W.L. (1987) Human breast cancer: correlation of relapse and survival with amplification of the HER-2/neu oncogene. Science 235: 177-182.

Sparano, J.A. (1999) Doxorubicin/taxane combinations: Cardiac toxicity and pharmacokinetics. Semin. Oncol. 26: 14-19.

Surveillance, Epidemiology and End Results Program (SEER) Cancer Statistics Review: http://www.seer.ims.nci.nih.gov/Publications/CSR1973 1996/

0 Suzuki T., Curcio, L.D., Tsai, J. and Kashani-Sabet M. (1997) Anti-c-erb-B-2 Ribozyme for Breast Cancer. In Methods in Molecular Medicine, Vol. 11, Therapeutic Applications of Ribozmes, Human Press, Inc., Totowa, NJ.

aughn, J.P., Iglehart, J.D., Demirdji, S., Davis, P., Babiss, L.E., Caruthers, M.H., Marks, J.R. (1995) Antisense DNA downregulation of the ERBB2 oncogene measured by a flow cytometric assay. Proc Natl Acad Sci USA 92: 8338-8342.

Weichen, K., Zimmer, C. and Dietel, M. (1997) Selection of a high activity c-erbB-2 ribozyme using a fusion gene of c-erbB-2 and the enhanced green fluorescent protein. Cancer Gene Therapy 5: 45-51.

Wright, M., Grim, J., Deshane, J., Kim, M., Strong, T.V., Siegel, G.P., Curiel, D.T. (1997) An intracellular anti-erbB-2 single-chain antibody is specifically cytotoxic to human breast carcinoma cells overexpressing erbB-2. Gene Therapy 4: 317-322.

Applicant has designed, synthesized and tested several NCH ribozymes and HH ribozymes targeted against HER2 RNA (see for example Tables 31 and 34) in cell proliferation assays.

Proliferation assay:

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The model proliferation assay used in the study can require a cell plating density of 2000 cells/well in 96-well plates and at least 2 cell doublings over a 5-day treatment period. To calculate cell density for proliferation assays, the FIPS (fluoro-imaging processing system) method well in the art was used. This method allows for cell density measurements after nucleic acids are stained with CyQuant dye, and has the advantage of

accurately measuring cell densities over a very wide range 1,000-100,000 cells/well in 96well format.

Ribozymes (50-200 nM) were delivered in the presence of cationic lipid at 2.0 μg/mL and inhibition of proliferation was determined on day 5 post-treatment. Two full ribozyme screens were completed and 4 lead HH and 11 lead NCH ribozymes were chosen for further testing. Of the 15 lead Rzs chosen from primary screens, 4 NCH and 1 HH Rzs continued to inhibit cell proliferation in subsequent experiments. NCH Rzs against sites, 2001 (RPI No. 17236), 2783 (RPI No. 17249), 2939 (RPI No. 17251) or 3998 (RPI No. 17262) caused inhibition of proliferation ranging from 25-60% as compared to a scrambled control Rz (IA; RPI No. 17263). Of the five lead Rzs, the most efficacious is the NCH Rz (RPI No. 17251) against site 2939 of HER2 RNA. An example of results from cell culture assay is shown in Figure 8. Referring to Figure 8, NCH ribozymes and a HH ribozyme targeted against HER2 RNA, are shown to cause significant inhibition of proliferation of cells. This shows that ribozymes, for instance the NCH ribozymes are canable of inhibitine HER2 sene expression in mammalian cells.

Example 8: Activity of Class II (Zinzyme) nucleic acid catalysts to inhibit HER2 gene expression

Applicant has designed, synthesized and tested several class II (zinzyme) ribozymes targeted against HER2 RNA (see, for example, **Tables 58, 59, and 62**) in cell proliferation RNA reduction assays.

Proliferation assay:

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The model proliferation assay used in the study requires a cell-plating density of

2000-10000 cells/well in 96-well plates and at least 2 cell doublings over a 5-day treatment
period. Cells used in proliferation studies were either human breast or ovarian cancer cells
(SKBR-3 and SKOV-3 cells respectively). To calculate cell density for proliferation
assays, the FIPS (fluoro-imaging processing system) method well known in the art was
used. This method allows for cell density measurements after nucleic acids are stained

with CyQuant® dye, and has the advantage of accurately measuring cell densities over a
very wide range 1,000-100,000 cells/well in 96-well format.

Ribozymes (50-200 nM) were delivered in the presence of cationic lipid at 2.0-5.0 µg/mL and inhibition of proliferation was determined on day 5 post-treatment. Two full ribozyme screens were completed resulting in the selection of 14 ribozymes. Class II (zinzyme) ribozymes against sites, 314 (RPI No. 18653), 443 (RPI No. 18680), 597 (RPI No. 18697), 659 (RPI No. 18682), 878 (RPI No. 18683 and 18654), 881 (RPI No. 18684 and 18685) 934 (RPI No. 18651), 972 (RPI No. 18656, 19292, 19727, 19728, and 19293), 1292 (RPI No. 18726), 1541 (RPI No. 18687), 2116 (RPI No. 18729), 2932 (RPI No. 18678), 2540 (RPI No. 18715), and 3504 (RPI No. 18710) caused inhibition of proliferation ranging from 25-80% as compared to a scrambled control ribozyme. An example of results from a cell culture assay is shown in Figure 20. Referring to Figure 20, Class II ribozymes targeted against HER2 RNA are shown to cause significant inhibition of proliferation of cells. This shows that ribozymes, for instance the Class II (zinzyme) ribozymes are capable of inhibiting HER2 gene expression in mammalian cells.

5 RNA assay:

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RNA was harvested 24 hours post-treatment using the Qiagen RNeasy® 96 procedure. Real time RT-PCR (TaqMan® assay) was performed on purified RNA samples using separate primer/probe sets specific for either target HER2 RNA or control actin RNA (to normalize for differences due to cell plating or sample recovery). Results are shown as the average of triplicate determinations of HER2 to actin RNA levels post-treatment. Figure 30 shows class II ribozyme (zinzyme) mediated reduction in HER2 RNA targeting site 972 vs a scrambled attenuated control.

Dose response assays:

Active ribozyme was mixed with binding arm-attenuated control (BAC) ribozyme to a final oligonucleotide concentration of either 100, 200 or 400 nM and delivered to cells in the presence of cationic lipid at 5.0 µg/mL. Mixing active and BAC in this manner maintains the lipid to ribozyme charge ratio throughout the dose response curve. HER2 RNA reduction was measured 24 hours post-treatment and inhibition of proliferation was determined on day 5 post-treatment. The dose response antiproliferation results are summarized in Figure 31 and the dose-dependent reduction of HER2 RNA results are

summarized in Figure 32. Figure 33 shows a combined dose response plot of both antiproliferation and RNA reduction data for a class II ribozyme targeting site 972 of HER2 RNA (RPI 19293).

5 Example 9: Compositions having RNA cleaving activity

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Hammerhead ribozymes are an example of catalytic RNA molecules which are able to recognize and cleave a given specific RNA substrate (Hutchins et al., 1986, Nucleic Acids Res. 14:3627; Keese and Symons, in Viroids and viroid-like pathogens (J.J. Semanchik, publ., CRC-Press, Boca Raton, Florida, 1987, pages 1-47). The catalytic center of hammerhead ribozymes is flanked by three stems and can be formed by adjacent sequence regions of the RNA or also by regions, which are separated from one another by many nucleotides. Figure 6 shows a diagram of such a catalytically active hammerhead structure. The stems have been denoted I, II and III. The nucleotides are numbered according to the standard nomenclature for hammerhead ribozymes (Hertel et al., 1992, Nucleic Acids Res. 20:3252). In this nomenclature, bases are denoted by a number, which relates their position relative to the 5' side of the cleavage site. Furthermore, each base that is involved in a stem or loop region has an additional designation (which is denoted by a decimal point and then another number) that defines the position of that base within the stem or loop. A designation of A^{15.1} would indicate that this base is involved in a paired region and that it is the first nucleotide in that stem going away from the core region. This accepted convention for describing hammerhead-derived ribozymes allows for the nucleotides involved in the core of the enzyme to always have the same number relative to all of the other nucleotides. The size of the stems involved in substrate binding or core formation can be any size and of any sequence, and the position of A9, for example, will remain the same relative to all of the other core nucleotides. Nucleotides designated, for example, N¹² or N⁹ represent an inserted nucleotide where the position of the caret (^) relative to the number denotes whether the insertion is before or after the indicated nucleotide. Thus, N^12 represents a nucleotide inserted before nucleotide position 12, and Nº^ represents a nucleotide inserted after nucleotide position 9.

The consensus sequence of the catalytic core structure is described by Ruffiner and Uhlenbeck, 1990, *Nucleic Acids Res.* 18:6025-6029. Perriman et al., 1992, *Gene* 113:157-163, have meanwhile shown that this structure can also contain variations, for example,

naturally occurring nucleotide insertions such as N^{9} ^ and $N^{0,12}$. Thus, the positive strand of the satellite RNA of the tobacco ring-spot virus does not contain any of the two nucleotide insertions while the +RNA strand of the virusoid of the lucerne transient streak virus (vLTSV) contains a N^{9} ^ = U insertion which can be mutated to C or G without loss of activity (Sheldon and Symons, 1989, *Nucleic Acids Res.* 17:5679-5685). Furthermore, in this special case, N^7 = A and $R^{15.1}$ = A. On the other hand, the minus strand of the carnation stunt associated viroid (-CarSV) is quite unusual since it contains both nucleotide insertions, that is $N^{0,12}$ = A and $N^{19,0}$ = C (Hernandez *et al.*,1992, *Nucleic Acids Res.* 20:6323-6329). In this viroid N^7 = A and $R^{15.1}$ = A. In addition, this special hammerhead structure exhibits a very effective self-catalytic cleavage despite the more open central stem.

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Possible uses of hammerhead ribozymes include, for example, generation of RNA restriction enzymes and the specific inactivation of the expression of genes in, for example, animal, human or plant cells and prokaryotes, yeasts and plasmodia. A particular biomedical interest is based on the fact that many diseases, including many forms of tumors, are related to the overexpression of specific genes. Inactivating such genes by cleaving the associated mRNA represents a possible way to control and eventually treat such diseases. Moreover there is a great need to develop antiviral, antibacterial, and antifungal pharmaceutical agents. Ribozymes have potential as such anti-infective agents since RNA molecules vital to the survival of the organism can be selectively destroyed.

In addition to needing the correct hybridizing sequences for substrate binding, substrates for hammerhead ribozymes have been shown to strongly prefer the triplet N¹⁶²U^{16.1}H¹⁷ (NUH) where N can be any nucleotide, U is uridine, and H is either adenosine, cytidine, or uridine (Koizumi et al., 1988, FEBS Lett. 228, 228-230; Ruffner et al., 1990, Biochemistry 29, 10695-10702; Perriman et al., 1992, Gene 113, 157-163). NUH is sometimes designated as NUX. The fact that changes to this general rule for substrate specificity result in non-functional substrates implies that there are "non core compatible" structures which are formed when substrates are provided which deviate from the stated requirements. Evidence along these lines was recently reported by Uhlenbeck and co-workers (Uhlenbeck et al., 1997, Biochemistry 36:1108-1114) when they demonstrated that the substitution of a G at position 17 caused a functionally catastrophic base pair between G¹⁷ and C³ to form, both preventing the correct orientation of the

scissile bond for cleavage and the needed tertiary interactions of C³ (Murray et al., 1995, Biochem. J. 311:487-494). The strong preference for a U at position 16.1 may exist for similar reasons. Many experiments have been done in an attempt to isolate ribozymes which are able to efficiently relieve the requirement of a U at position 16.1, however, attempts to find hammerhead type ribozymes which can cleave substrates having a base other than a U at position 16.1 have proven impossible (Perriman et al., 1992, Gene 113, 157-163).

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Efficient catalytic molecules with reduced or altered requirements in the cleavage region are highly desirable because their isolation would greatly increase the number of available target sequences that molecules of this type could cleave. For example, it would be desirable to have a ribozyme variant that could efficiently cleave substrates containing triplets other than N^{16.2}U^{16.1}H¹⁷ since this would increase the number of potential target cleavage sites.

Chemically modified oligonucleotides which contain a block of deoxyribonucleotides in the middle region of the molecule have potential as pharmaceutical agents for the specific inactivation of the expression of genes (Giles et al., 1992, Nucleic Acids Res. 20:763-770). These oligonucleotides can form a hybrid DNA-RNA duplex in which the DNA bound RNA strand is degraded by RNase H. Such oligonucleotides are considered to promote cleavage of the RNA and so cannot be characterized as having an RNA-cleaving activity nor as cleaving an RNA molecule (the RNase H is cleaving). A significant disadvantage of these oligonucleotides for in vivo applications is their low specificity, since hybrid formation, and thus cleavage, can also take place at undesired positions on the RNA molecules.

Since, unmodified ribozymes are sensitive to degradation by RNases, chemically modified active substances have to be used in order to administer hammerhead ribozymes exogenously (discussed, for example, by Heidenreich et al., 1994, J. Biol. Chem. 269:2131-2138; Kiehntopf et al., 1994, EMBO J. 13:4645-4652; Paolella et al., 1992, EMBO J. 11:1913-1919; and Usman et al., 1994, Nucleic Acids Symp. Ser. 31:163-164).

Sproat et al., U.S. Pat. No. 5,334,711, describe such chemically modified active substances based on synthetic catalytic oligonucleotide structures with a length of 35 to 40 nucleotides which are suitable for cleaving a nucleic acid target sequence and contain modified nucleotides that contain an optionally substituted alkyl, alkenyl or alkynyl group

with 1 - 10 carbon atoms at the 2'-O atom of the ribose. These oligonucleotides contain modified nucleotide building blocks and form a structure resembling a hammerhead structure. These oligonucleotides are able to cleave specific RNA substrates.

Usman et al., U.S. Patent No. 5,891,684, describe enzymatic nucleic acid molecules with one or more nucleotide base modification(s) in a substrate binding arm.

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Thompson et al., US Patent No. 5,599,704 describe enzymatic RNA molecules targeted against ErbB2/neu/Her2 RNA.

Sullivan et al., US Patent No. 5,616,490 describe enzymatic RNA molecules targeted against protein kinase C (PKC) RNA.

O Sioud, International PCT publication No. WO 99/63066 describe hammerhead ribozymes targeted against specific sites within protein kinase C alpha (PKC alpha), VEGF, and TNF alpha RNA.

Jarvis et al., International PCT publication No. WO 98/505030, describe the synthesis of xylo-ribonucleosides and oligonucleotides comprising xylo modifications.

This invention relates to novel enzymatic nucleic acid molecules having an RNAcleavage activity, as well as their use for cleaving RNA substrates in vitro and in vivo. The
compositions contain an active center, the subunits of which are selected from nucleotides
and/or nucleotide analogues, as well as flanking regions contributing to the formation of a
specific hybridization with an RNA substrate. Preferred compositions form, in
combination with an RNA substrate, a structure resembling a hammerhead structure. The
active center of the disclosed compositions is characterized by the presence of I^{15,1} which
allows cleavage of RNA substrates having C^{16,1}. It is therefore an object of the present
invention to provide compositions that cleave RNA, and in particular to provide RNAcleaving oligomers which at the same time have a high stability, activity, and specificity.
This invention relates to novel nucleic acid molecules with catalytic activity, which are
particularly useful for cleavage of RNA or DNA or combination thereof. The nucleic acid
catalysts of the instant invention are distinct from other nucleic acid catalysts known in the
art. Specifically, nucleic acid catalysts of the instant invention are capable of catalyzing an
intermolecular or intramolecular endonuclease reaction.

It is another object of the present invention to provide compositions that cleave RNA substrates having a cleavage site triplet other than N¹⁶²U^{16.1}H¹⁷ (NUH; Figure 6), where N is a nucleotide, U is uridine and H is adenosine, uridine or cytidine. H is used

interchangably with X. Specifically, the enzymatic nucleic acid molecule of the instant invention has an endonuclease activity to cleave RNA substrates having a cleavage triplet $N^{16.2}C^{16.1}H^{17}$ (NCH; Figure 6), where N is a nucleotide, C is cytidine and H is adenosine, uridine or cytidine. H is used interchangeably with X. In another aspect the invention features an enzymatic nucleic acid molecule of the instant invention has an endonuclease activity to cleave RNA substrates having a cleavage triplet $N^{16.2}C^{16.1}N^{17}$ (NCN; Figure 6), where N is a nucleotide, C is cytidine.

In a preferred embodiment, the invention features an enzymatic nucleic acid molecule having formula 1:

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where N represents independently a nucleotide or a non-nucleotide linker, which may be same or different; D and E are independently oligonucleotides of length sufficient to stably interact (e.g., by forming hydrogen bonds with complementary nucleotides in the target) with a target nucleic acid molecule (the target can be an RNA, DNA or mixed polymers), preferably, the length of D and E are independently between 3-20 nucleotides long, specifically, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, and 20; o and n are integers independently greater than or equal to 1 and preferably less than about 100, specifically 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 50, wherein if (N)₀ and (N)_n are nucleotides, (N)₀ and (N)n are optionally able to interact by hydrogen bond interaction, in particular if n =1 and o=1 then (N)n is preferably a purine (e.g., G, and A) and (N)o is preferably a pyrimidine (e.g., C and U) and (N)n preferably forms; • indicates base-paired interaction; L is a linker which may be present or absent (i.e., the molecule may be assembled from two separate oligonucleotides), but when present, is a nucleotide and/or a non-nucleotide linker, which may be a single-stranded and/or double-stranded region; p is an integer 0 or 1. when p=1, (N)p is preferably A or U; and ______ represents a chemical linkage (e.g. a phosphate ester linkage, amide linkage, phosphorothioate linkage or others known in the art). A. U. I. C and G represent adenosine, uridine, inosine, cytidine and guanosine nucleotides, respectively. The N in 5'-CUGANGA-3' region of formula 1 is preferably U. The nucleotides in the formula 1 are unmodified or modified at the sugar, base, and/or phosphate as known in the art.

In a preferred embodiment, the invention features an enzymatic nucleic acid molecule having formula 2:

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where N represents independently a nucleotide or a non-nucleotide linker, which may be same or different; D and E are independently oligonucleotides of length sufficient to stably interact (e.g., by forming hydrogen bonds with complementary nucleotides in the target) with a target nucleic acid molecule (the target can be an RNA, DNA or mixed polymers), preferably, the length of D and E are independently between 3-20 nucleotides long, specifically, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, and 20; o and n are integers independently greater than or equal to 0 and preferably less than about 100, specifically 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 50, wherein if (N)o and (N)n are nucleotides, (N)o and (N)n are optionally able to interact by hydrogen bond interaction; • indicates basepaired interaction; L is a linker which may be present or absent (i.e., the molecule may be assembled from two separate oligonucleotides), but when present, is a nucleotide and/or a non-nucleotide linker, which may be a single-stranded and/or double-stranded region; p is an integer 0 or 1, when p=1, (N)p is preferably A, C or U; and represents a chemical linkage (e.g. a phosphate ester linkage, amide linkage, phosphorothioate linkage or others known in the art). A, U, I, C and G represent adenosine, uridine, inosine, cytidine and guanosine nucleotides, respectively. The N in 5'-CUGANGA-3' region of formula 2 is preferably U. The nucleotides in the formula 2 are unmodified or modified at the sugar, base, and/or phosphate as known in the art.

In a preferred embodiment, the I (inosine) in formula 1 and 2 is preferably a riboinosine or a xylo-inosine. In yet another embodiment, the nucleotide linker (L) is a nucleic acid aptamer, such as an ATP aptamer, HIV Rev aptamer (RRE), HIV Tat aptamer (TAR) and others (for a review see Gold et al., 1995, Annu. Rev. Biochem., 64, 763; and Szostak & Ellington, 1993, in The RNA World, ed. Gesteland and Atkins, pp 511, CSH Laboratory Press). A "nucleic acid aptamer" as used herein is meant to indicate nucleic acid sequence capable of interacting with a ligand. The ligand can be any natural or a synthetic molecule, including but not limited to a resin, metabolites, nucleosides, nucleotides, drugs, toxins, transition state analogs, peptides, lipids, proteins, amino acids, nucleic acid molecules, hormones, carbohydrates, receptors, cells, viruses, bacteria and others. In a preferred embodiment L has the sequence 5'-GAAA-3' or 5'-GIUIA-3'.

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In yet another embodiment, the non-nucleotide linker (L) is as defined herein. The term "non-nucleotide", as used herein, includes either abasic nucleotide, polyether, polyamine, polyamide, peptide, carbohydrate, lipid, or polyhydrocarbon compounds. Specific examples include those described by Seela and Kaiser, Nucleic Acids Res. 1990, 18:6353 and Nucleic Acids Res. 1987, 15:3113; Cload and Schepartz, J. Am. Chem. Soc. 1991, 113:6324; Richardson and Schepartz, J. Am. Chem. Soc. 1991. 113:5109; Ma et al., Nucleic Acids Res. 1993, 21:2585 and Biochemistry 1993, 32:1751; Durand et al., Nucleic Acids Res. 1990, 18:6353; McCurdy et al., Nucleosides & Nucleotides 1991, 10:287; Jschke et al., Tetrahedron Lett. 1993, 34:301; Ono et al., Biochemistry 1991, 30:9914; Arnold et al., International Publication No. WO 89/02439; Usman et al., International Publication No. WO 95/06731; Dudycz et al., International Publication No. WO 95/11910 and Ferentz and Verdine, J. Am. Chem. Soc. 1991, 113:4000, all hereby incorporated by reference herein. Non-nucleotide linkers can be any molecule, which is not an oligomeric sequence, that can be covalently coupled to an oligomeric sequence. Preferred non-nucleotide linkers are oligomeric molecules formed of non-nucleotide subunits. Examples of such non-nucleotide linkers are described by Letsinger and Wu, (J. Am. Chem. Soc. 117:7323-7328 (1995)), Benseler et al., (J. Am. Chem. Soc. 115:8483-8484 (1993)) and Fu et al., (J. Am. Chem. Soc. 116:4591-4598 (1994)). Preferred non-nucleotide linkers, or subunits for non-nucleotide linkers, include substituted or unsubstituted C1-C10 straight chain or branched alkyl, substituted or unsubstituted C2-C10 straight chain or branched alkenyl, substituted or unsubstituted C2-C10 straight chain or branched alkynyl, substituted or unsubstituted C1-C10 straight chain or

branched alkoxy, substituted or unsubstituted C₂-C₁₀ straight chain or branched alkenyloxy, and substituted or unsubstituted C₂-C₁₀ straight chain or branched alkynyloxy. The substituents for these preferred non-nucleotide linkers (or subunits) can be halogen, cyano, amino, carboxy, ester, ether, carboxamide, hydroxy, or mercapto. Thus, in a preferred embodiment, the invention features an enzymatic nucleic acid molecule having one or more non-nucleotide moieties, and having enzymatic activity to cleave an RNA or DNA molecule. By the term "non-nucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine. The terms "abasic" or "abasic nucleotide" as used herein encompass sugar moieties lacking a base or having other chemical groups in place of nucleotide base at the 1' position.

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In a preferred embodiment, the invention features modified ribozymes with phosphate backbone modifications comprising one or more phosphorothioate, phosphorodithioate, methylphosphonate, morpholino, amidate carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and/or alkylsilyl, substitutions. For a review of oligonucleotide backbone modifications ee Hunziker and Leumann, 1995, Nucleic Acid Analogues: Synthesis and Properties, in Modern Synthetic Methods, VCH, 331-417, and Mesmaeker et al., 1994, Novel Backbone Replacements for Oligonucleotides, in Carbohydrate Modifications in Antisense Research, ACS, 24-39.

In a further preferred embodiment of the instant invention, an inverted deoxy abasic moiety is utilized at the 3' end of the enzymatic nucleic acid molecule.

By "pyrimidines" is meant nucleotides comprising modified or unmodified derivatives of a six membered pyrimidine ring. An example of a pyrimidine is modified or unmodified uridine.

In a preferred embodiment, the nucleosides of the instant invention include, 2'-O-methyl-2,6-diaminopurine riboside; 2'-deoxy-2'amino-2,6-diaminopurine riboside; 2'-(N-alanyl) amino-2'-deoxy-uridine; 2'-(N-phenylalanyl)amino-2'-deoxy-uridine; 2'-deoxy-2'-(N-beta-alanyl) amino; 2'-deoxy-2'-(lysiyl) amino uridine; 2'-C-allyl uridine; 2'-O-amino-

uridine; 2'-O-methylthiomethyl adenosine; 2'-O-methylthiomethyl cytidine; 2'-O-methylthiomethyl guanosine; 2'-O-methylthiomethyl-uridine; 2'-Deoxy-2'-(N-histidyl) amino uridine; 2'-deoxy-2'-amino-5-methyl cytidine; 2'-(N-β-carboxamidine-beta-alanyl)amino-2'-deoxy-uridine; 2'-deoxy-2'-(N-beta-alanyl)-guanosine; 2'-O-amino-adenosine; 2'-(N-lysyl)amino-2'-deoxy-cytidine; 2'-Deoxy-2'-(L-histidine) amino Cytidine; and 5-Imidazoleacetic acid 2'-deoxy-5'-triphosphate uridine.

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By "oligonucleotide" as used herein is meant a molecule having two or more nucleotides. The polynucleotide can be single, double or multiple stranded and may have modified or unmodified nucleotides or non-nucleotides or various mixtures and combinations thereof.

In a preferred embodiment, the enzymatic nucleic acid molecule of formula 1 or 2 include at least three ribonucleotide residues, preferably 4, 5, 6, 7, 8, 9, and 10 ribonucleotide residues.

In preferred embodiments, the enzymatic nucleic acid of the instant invention includes one or more stretches of RNA, which provide the enzymatic activity of the molecule, linked to the non-nucleotide moiety. The necessary RNA components are known in the art (see for e.g., Usman et al., supra).

Thus, in one preferred embodiment, the invention features enzymatic nucleic acid molecules that inhibit gene expression and/or cell proliferation in vitro or in vivo (e.g. in patients). These chemically or enzymatically synthesized nucleic acid molecules contain substrate binding domains that bind to accessible regions of specific target nucleic acid molecules. The nucleic acid molecules also contain domains that catalyze the cleavage of target. Upon binding, the enzymatic nucleic acid molecules cleave the target molecules, preventing for example, translation and protein accumulation. In the absence of the expression of the target gene, cell proliferation, for example, is inhibited.

In another preferred embodiment, catalytic activity of the molecules described in the instant invention can be optimized as described by Draper et al., supra. The details will not be repeated here, but include altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications (base, sugar and/or phosphate) that prevent their degradation by serum ribonucleases and/or enhance their enzymatic activity (see e.g., Eckstein et al., International Publication No. WO 92/07065; Perrault et al., 1990 Nature 344, 565; Picken et al., 1991 Science 253, 314; Usman and Cedergren, 1992

Trends in Biochem. Sci. 17, 334; Usman et al., International Publication No. WO 93/15187; and Rossi et al., International Publication No. WO 91/03162; Sproat, US Patent No. 5,334,711; and Burgin et al., supra; all of these describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of enzymatic RNA molecules). Modifications which enhance their efficacy in cells, and removal of bases from stem loop structures to shorten RNA synthesis times and reduce chemical requirements are desired. (All these publications are hereby incorporated by reference herein.).

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By "nucleic acid catalyst" as used herein is meant a nucleic acid molecule (e.g., the 10 molecule of formulae 1 and 2) capable of catalyzing (altering the velocity and/or rate of) a variety of reactions including the ability to repeatedly cleave other separate nucleic acid molecules (endonuclease activity) in a nucleotide base sequence-specific manner. Such a molecule with endonuclease activity may have complementarity in a substrate binding region to a specified gene target, and also has an enzymatic activity that specifically cleaves RNA or DNA in that target. That is, the nucleic acid molecule with endonuclease 15 activity is able to intramolecularly or intermolecularly cleave RNA or DNA and thereby inactivate a target RNA or DNA molecule. This complementarity functions to allow sufficient hybridization of the enzymatic RNA molecule to the target RNA or DNA to allow the cleavage to occur. 100% complementarity is preferred, but complementarity as 20 low as 50-75% may also be useful in this invention. The nucleic acids may be modified at the base, sugar, and/or phosphate groups. The term enzymatic nucleic acid as used herein is used interchangeably with phrases such as ribozymes, catalytic RNA, enzymatic RNA, catalytic oligonucleotides, nucleozyme, RNA enzyme, endoribonuclease, endonuclease, minizyme, oligozyme, finderon or nucleic acid catalyst. All of these terminologies 25 describe nucleic acid molecules of the instant invention with enzymatic activity. The specific examples of enzymatic nucleic acid molecules described in the instant application are not limiting in the invention and those skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target nucleic acid regions, and that it have nucleotide sequences within or surrounding that substrate binding 30 site which impart a nucleic acid cleaving activity to the molecule (Cech et al., U.S. Patent No. 4,987,071; Cech et al., 1988, 260 JAMA 3030).

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The enzymatic nucleic acid molecule of Formula 1 or 2 may independently comprise a cap structure which may independently be present or absent.

By "chimeric nucleic acid molecule" or "mixed polymer" is meant that, the molecule may be comprised of both modified or unmodified nucleotides.

5 In yet another preferred embodiment, the 3'-cap is selected from a group comprising, 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate, 3aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; 10 modified base nucleotide; phosphorodithioate; threo-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide: 3,4-dihydroxybutyl nucleotide: 3,5-dihydroxypentyl nucleotide, 5'-5'inverted nucleotide moiety: 5'-5'-inverted abasic moiety: 5'-phosphoramidate: 5'phosphorothioate; 1.4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging 15 methylphosphonate and 5'-mercapto mojeties (for more details, see Beaucage and Iver. 1993, Tetrahedron 49, 1925; incorporated by reference herein). By the term "nonnucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The 20 group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine. The terms "abasic" or "abasic nucleotide" as used herein encompass sugar moieties lacking a base or having other chemical groups in place of a base at the 1' position.

In a preferred embodiment, the invention features 1-(beta-D-xylofuranosyl)xypoxanthine phosphoramidite and a process for the synthesis thereof and incorporation into oligonucleotides, such as enzymatic nucleic acid molecule.

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In yet another preferred embodiment, the invention features enzymatic nucleic acid molecules targeted against HER2 RNA, specifically, ribozymes in the hammerhead and NCH motifs.

In a preferred embodiment, the invention features enzymatic nucleic acid molecules targeted against PKC alpha RNA, specifically, ribozymes in the hammerhead and NCH motifs.

Targets, for example PKC alpha RNA, for useful ribozymes and antisense nucleic acids can be determined, for example, as described in Draper et al., WO 95/04818; McSwiggen et al., U.S. Patent Nos. 5,525,468 and 5,646,042, all are hereby incorporated by reference herein in their totality. Other examples include the following PCT applications, which concern inactivation of expression of disease-related genes: WO 95/23225, WO 95/13380, WO 94/02595, all incorporated by reference herein.

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The specific enzymatic nucleic acid molecules described in the instant application are not limiting in the invention and those skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site (e.g., D and E of Formula 1 above) which is complementary to one or more of the target nucleic acid regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart a nucleic acid cleaving activity to the molecule.

All naturally occurring hammerhead ribozymes have an A^{15.1}-U^{16.1} base pair. In addition, it is known that substrates for ribozymes based on the consensus hammerhead sequence strongly prefer a substrate that contains an N^{16.2}U^{16.1}H¹⁷ triplet in which H¹⁷ is not a guanosine (Koizumi et al., FEBS Lett. 228, 228-230 (1988); Ruffner et al., Biochemistry 29, 10695-10702 (1990); Perriman et al., Gene 113, 157-163 (1992)). Many experiments have been done in an attempt to isolate ribozymes which are able to efficiently relieve the requirement of a U at position 16.1, however, attempts to find ribozymes which can cleave substrates having a base other than a U at position 16.1 have proven largely unsuccessful (Perriman et al., Gene 113, 157-163 1992, Singh et al., Antisense and Nucleic Acid Drug Development 6:165-168 (1996)).

However, examination of the recently published X-ray crystal structures (Pley et al., Nature 372:68-74 (1994), Scott et al., Cell 81:991-1002 (1995), and Scott et al., Science 274:2065-2069 (1996)) led to the realization that the A^{15.1}-U^{16.1} interaction is a non-standard base pair with a single hydrogen bond between the exocyclic amine (N6) of the adenosine and the 4-oxo group of the uridine. Modeling studies (based on the crystal structure) then led to the discovery that the interaction of the wild-type A^{15.1}-U^{16.1} base pair 0 can be spatially mimicked by replacement with an I^{15.1}-C^{16.1} base pair that adopts an isostructural orientation and which preserves the required contact of the 2-keto group of C^{16.1} with A⁶ of the uridine turn. In the model, the polarity of the stabilizing hydrogen

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bond between positions 15.1 and 16.1 is reversed in the I^{15.1}-C^{16.1} interaction, but the correct orientation of the bases around this bond is maintained.

It has been discovered that hammerhead ribozyme analogues containing an inosine at position 15.1 readily cleave RNA substrates containing an $N^{162}C^{16.1}H^{17}$ triplet. Based on this, disclosed are compositions, preferably synthetic oligomers, which cleave a nucleic acid target sequence containing the triplet $N^{16.2}C^{16.1}H^{17}$. It is preferred that H^{17} is not guanosine, however, under certain circumstances, NCG triplet containing RNA can be cleaved by the ribozymes of the instant invention. The ability to cleave substrates having $N^{16.2}C^{16.1}X^{17}$ triplets effectively doubles the number of targets available for cleavage by compositions of the type disclosed.

Example 10: Synthesis of 1-(beta-D-xylofuranosyl)-xypoxanthine phosphoramidite

Referring to Figure 9, Inosine (1) was 5'-O-monomethoxytritylated and 2'-O-silylated under standard conditions to afford 2 (Charubala, R; Pfleiderer, W. Heterocycles 1990, 30, 1141). Oxidation/reduction procedure afforded 3 in moderate yield (Matulic-Adamic, J.; Daniher, A.T.; Gonzalez, C.; Beigelman, L. Bioorg. Med. Chem. Lett.. 1999, 9, 157): ¹H NMR (CDCl₃) δ 12.80 (br s, 1H, NH), 8.11 (s, 1H, H-8), 8.08 (s, 1H, H-2), 7.45-6.80 (m, 14H, trityl), 5.85 (d, J_{1',2'}=1.6, 1H, H-1'), 4.83 (d, J_{2',3'}=7.2, 1H, H-2'), 4.46 (br s, 1H, 3'-OH), 4.34 (m, 1H, H-4'), 4.06 (m, 1H, H-3'), 3.77 (s, 6H, 2 x OMe), 3.60 (app d, 2H, H-5', H-5"), 0.89 (s, 9H, ι-Bu), 0.07 (s, 3H, Me), 0.06 (s, 3H, Me). Standard phosphitylation of 3 afforded the desired phosphoramidite 4.

More acid stable 5'-O-MMT group is used in this particular case because applicant found that 5'-O-DMT protection is more labile in xylo nucleoside series than in ribo nucleoside series.

The xylo-inosine was incorporated into oligonucleotides using the standard procedures known in the art and as described herein.

Example 11: Activity of the xylo-Inosine-modified NCH Ribozyme

Several NCH ribozymes with xylo-inosine at position 15.1 were designed (Figure 7) to cleave RNA containing GCA, ACA, UCA or the CCA triplet. These ribozymes were

synthesized and purified as described herein and tested using standard RNA cleavage reaction conditions (see Table 31, for example, and see below).

The ribozymes were chemically synthesized. The method of synthesis used followed the procedure for normal RNA synthesis as described above and in Usman et al., (1987 J. Am. Chem. Soc., 109, 7845), Scaringe et al., (1990 Nucleic Acids Res., 18, 5433) and Wincott et al., supra, and made use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The average stepwise coupling yields were >98%.

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Ribozymes were purified by gel electrophoresis using general methods or were purified by high pressure liquid chromatography (HPLC; See Wincott et al., supra; the totality of which is hereby incorporated herein by reference) and were resuspended in water. The sequences of the chemically synthesized ribozymes used in this study are shown below in Table 33.

Cleavage Reactions: Full-length or partially full-length, internally-labeled target RNA for ribozyme cleavage assay is prepared by in vitro transcription in the presence of [alpha-32p] CTP, passed over a G 50 Sephadex column by spin chromatography and used as substrate RNA without further purification. Alternately, substrates were 5'-32P-end labeled using T4 polynucleotide kinase enzyme. Assays are performed by pre-warming a 2X concentration of purified ribozyme in ribozyme cleavage buffer (50 mM Tris-HCl, pH 7.5 at 37°C, 10 mM MgCl₂) and the cleavage reaction was initiated by adding the 2X ribozyme mix to an equal volume of substrate RNA (maximum of 1-5 nM) that was also pre-warmed in cleavage buffer. As an initial screen, assays are carried out for 1 hour at 37°C using a final concentration of 40 nM or 1 mM ribozyme, i.e., ribozyme excess. The reaction is quenched by the addition of an equal volume of 95% formamide, 20 mM EDTA, 0.05% bromophenol blue and 0.05% xylene cyanol after which the sample is heated to 95°C for 2 minutes, quick chilled and loaded onto a denaturing polyacrylamide gel. Substrate RNA and the specific RNA cleavage products generated by ribozyme cleavage are visualized on an autoradiograph of the gel. The percentage of cleavage is determined by Phosphor Imager® quantitation of bands representing the intact substrate and the cleavage products.

The results of the experiments are summarized in **Table 32**, which shows that NCHxvlo ribozymes are catalytically active to cleave target RNA.

Example 12: Activity of NCH Ribozyme variants

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The nucleic acid molecules of the instant invention allow for the ability to cleave a new set of 12 NCH triplets. Determination of single turnover rate constants at pH 6 of these ribozymes in the all ribo form show that with NCA type triplets, the cleavage rate is higher than at NUA sites. NCC and NUC site rates are similar, and NCU sites are slightly lower than NUU sites. Additional measurements of multiple turnover parameters of the all ribo ribozymes performed under non-saturating conditions using 5nM ribozyme and changing the substrate concentration from 50 to 500 nM at pH 7.4 with 10 mM Mg ⁺⁺ at 37 °C gave Km = 100 nM and kcat =6.5 min ⁻¹ for GCA vs Km =30 nM and kcat =2.0 min ⁻¹ for GUA cleaving all ribo ribozymes. These data verify that the ribozymes with an I-C base pair are efficient catalysts in multiple turnover reactions and the relative order of activity between NCH and NUH cleavers established at pH 6 (Ludwig et al., 1998, Nucleic Acids Res., 26, 2279-2285) remains unchanged.

To gain more insight into the structural requirements of the 15.1-16.1 base pair of the ribozymes of the instant invention, applicant synthesized several variants of the active I-15.1-C-16.1 structure and tested these ribozyme analogues with their corresponding substrates. The influence of several core stabilization strategies on the activity of the NCH cleaving ribozymes was also investigated.

Various nucleoside analogs were incorporated at position 15.1 of the ribozyme.

Cleavage activity was tested with the complementary FI* labeled substrates at pH 7.4 in the presence of 10 mM Mg ++ under conditions of ribozyme excess (i.e. single turnover conditions). The modified oligonucleotides were synthesized by standard oligonucleotide synthesis procedures. Xanthosine was protected using O-2,O-4 pivaloyloxymethyl groups; N,N-dimethylguanosine with 6-O-(2-nitrophenyl-)ethyl and 6-thio-inosine with S-cyanoethyl protecting groups. The cleavage activity of the ribozymes containing the 15.1 analogs is summarized in Figure 36. For comparison Figure 37 summarizes reported functional group modification studies performed at the A 15.1 residue in the A-15.1 *U-16.1 context of NUH cleaving ribozymes.

Modifications at the purine 15.1 N1 and/or C6 positions (Figure 36 A, B, C)

In the 6-thio-inosine (A) (sf) 15.1 substituted ribozyme, the original (I-15.1) position 6 O•H-N (C-16.1) bonds are replaced by weaker (sI-15.1) position 6 S•H-N (C-16.1) hydrogen bonds while all other functional groups remain unchanged. Ribozymes with an adenosine (B) at position 15.1 (A-15.1) are inactive with C-16.1 substrates since the ribozyme geometry requires the [A-15.1] position 6 amino group and the [C-16.1] position 4 amino group hydrogen-bond donor functional groups to be in close proximity. Similarly, low activity is observed with I-15.1 ribozymes and U-16.1 substrates, where the [I-15.1] position 6 keto and [C-16.1] position 4 keto hydrogen-bond acceptor groups are opposed (Figure 37, B). Although inosine can form stable mismatch pairs with uridine in RNA duplexes or in tRNA anticodon-mRNA interactions, these results suggest that the geometry in the I-U mismatches differ from that of the A-U (or I-C) base pair in the active NUH ribozyme. Substitution of NI-Methyl-inosine (C) in place of inosine at position 15.1 leads to complete loss of cleavage activity.

Modifications at the purine 15.1 C2 and/or N3 position (Figure 36 D. E. F)

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The extremely low activity observed with the G-15.1 (**D**) substituted analog may be explained by the formation of a G-C Watson-Crick base pair. The replacement of the I·C pair with a G-C pair can significantly distort the geometry at the 15.1-16.1 position. G-15.1 N2-alkylation (**E**) gives only minimal recovery of catalytic activity compared to G-15.1, suggesting that the steric problems introduced by the bulky N-methyl groups may interfere with stacking interactions. The activity of this construct is significantly less than that of iso-G-15.1 (**Figure 37**, **E**) containing ribozymes in the standard A-U context. Xanthosine 15.1 (**F**) contains the same functional groups as inosine at the N1 and C6 sites but contains an additional hydrogen-bond donor site at position N3 along with a C2 carbonyl group. The complete lack of activity seen with this construct reinforces the importance of the purine N3 acceptor functionality in transition state formation. Similarly, 3-deaza-adenosine (**Figure 37**, **F**) containing ribozymes were also inactive. The C2 carbonyl of the 15.1 purine shows no significant negative interference in iso-guanosine containing 15.1 ribozymes.

Activity of modified core variants

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To complete the characterization of the I²C pair containing ribozymes, the acceptance of various core substitution patterns was tested. Short substrates containing GCH and GUH (H= non G) triplets were compared using 3 different modified ribozymes. The acceptance of the U-42'-O-alkyl substituent is the greatest with GCA triplets while U-4=2'-deoxy-2'-amino uridine and U-4= ribo uridine substituted ribozymes show a similar level of activity with NCH and NUH triplets. The results of this comparison are summarized in Table 64. In addition, a ribozyme construct in which ribo inosine replaces adenosine at positions 14 and 15.1 was tested which demonstrated cleavage activity.

Apart from the A-15.1 •U-16.1 to I-15.1 •C-16.1 change that reverses the polarity of an important H-bond in the ribozyme structure, no other functional group changes at the 15.1 purine residue seem to be compatible with the requirements of efficient catalysis. The I-15.1 and A-15.1 ribozymes are equally suitable for practical applications because there are only minor differences in the acceptance of stabilizing residues.

Example 13: Activity of NCH Ribozyme to inhibit HER2 gene expression

Applicant has designed, synthesized and tested several NCH ribozymes and HH ribozymes targeted against HER2 RNA (see, for example, **Tables 31 and 34**) in cell proliferation assays.

Proliferation assay: The model proliferation assay used in the study can require a cell plating density of 2000 cells/well in 96-well plates and at least 2 cell doublings over a 5-day treatment period. To calculate cell density for proliferation assays, the FIPS (fluoro-imaging processing system) method well in the art was used. This method allows for cell density measurements after nucleic acids are stained with CyQuant® dye, and has the advantage of accurately measuring cell densities over a very wide range 1,000-100,000 cells/well in 96-well format.

Ribozymes (50-200 nM) were delivered in the presence of cationic lipid at 2.0 µg/mL and inhibition of proliferation was determined on day 5 post-treatment. Two full ribozyme screens were completed and 4 lead HH and 11 lead NCH ribozymes were chosen for further testing. Of the 15 lead Rzs chosen from primary screens, 4 NCH and 1 HH Rzs continued to inhibit cell proliferation in subsequent experiments. NCH Rzs against sites, 2001 (RPI No. 17236), 2783 (RPI No. 17249), 2939 (RPI No. 17251) or 3998 (RPI No. 17262) caused inhibition of proliferation ranging from 25-60% as compared to a scrambled control Rz (IA; RPI No. 17263). Of the five lead Rzs, the most efficacious is the NCH Rz (RPI No. 17251) against site 2939 of HER2 RNA. An example of results from cell culture assay is shown in Figure 3. Referring to Figure 3, NCH ribozymes and a HH ribozyme targeted against HER2 RNA are shown to cause significant inhibition of proliferation of cells. This shows that ribozymes, for instance, the NCH ribozymes are capable of inhibiting HER2 gene expression in mammalian cells.

Example 14: Activity of NCH Ribozyme to inhibit PKC alpha gene expression

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The Protein Kinase C family contains twelve currently known isozymes divided into three classes: the classic, Ca⁺⁺ dependent (PKCα, βI, βII, γ), the novel, non-Ca⁺⁺ dependent (PKCδ, ε, μ, η, θ) and the atypical (PKC ξ, i/λ); all of which are serine/threonine kinases. These isozymes show distinct and overlapping tissue. cellular. and subcellular distribution. They aid in the regulation of cell growth and differentiation through their response to second messenger products of lipid metabolism (Blobe, et al., 1996, Cancer Surveys, 27, 213-248). These second messengers include diacylglyceral (DAG), inositol-triphosphate (IP3), lysophospholipids, free fatty acids, and phosphatidate which act directly or in addition to changes in the Ca++ concentration. A simple model for $PKC\alpha$ activation follows a two step mechanism. First, membrane association of $PKC\alpha$ is through Ca⁺⁺ and phospholipid interactions and second, the kinase is activated by interaction with DAG. An example of a signal cascade subsequent to PKC activation is PKC's phosphorylation of c-Raf, which phosphorylates MEK, which phosphorylates MAP, which phosphorylates transcription factors such as Jun and thereby activates a mitogenic program in the nucleus. There are numerous substrates for the various PKC's, one which for PKCa ultimately stimulates transcription factors that activate Pglycoprotein (P-gp) causing the multi-drug resistant phenotype (MDR) (Blobe, et al., 1994. Cancer and Metastasis Reviews, 13, 411-431).

Cell Culture Review

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PKC's have been implicated in tumor promotion since the discovery that these molecules can serve as receptors for tumor-promoting phorbol esters. An increase in PKC overexpression in numerous tumor cell lines and tumor tissues has also been demonstrated. PKC overexpression has been shown to be associated with increased invasion and metastasis in mouse Lewis lung carcinoma, mouse B16 melanoma (Lee et al., 1997, Molecular Carcinogenesis, 18, 44-53), mouse mammary adenocarcinoma, mouse fibrosarcoma, human lung carcinoma (Wang and Liu, 1998, Acta Pharmacologica Sinica, 19, 265-268), human bladder carcinoma, human pancreatic cancer (Denham et al., 1998, Surgery, 124, 218-223), and human gastric cancer (Dean et al., 1996, Cancer Research, 56, 3499-3507). Mounting evidence suggests PKCa can stimulate adhesion molecule expression and can directly act on these membrane bound species as substrates, thereby modulating cellular adhesion to the extracellular matrix and increasing metastic potential. Furthermore, human surgical specimens have demonstrated elevated PKC in breast tumors, thyroid carcinomas and melanomas (Becker et al., 1990, Oncogene, 5, 1133-1139).

Utz et al., 1994, Int. J. Cancer, 57, 104-110, describe a cell proliferation assay in which small molecule inhibitors of PKC demonstrate anti-proliferative activity in CCRF-VCR 1000 and KB-8511 cells with the multidrug resistant (MDR) phenotype. PKC α is overexpressed in tumor tissues that express the MDR phenotype. This phenotype is associated with the expression of a 170 kDa broad specificity drug efflux pump, P-gp. PKC α phosphorylation of P-gp has been shown in vitro. In addition, PKC expression correlates with resistance to doxorubicin and high P-gp levels in human renal carcinoma and non-small cell lung carcinoma. Inhibitors of PKC partially reverse the MDR phenotype and decrease phosphorylation of P-gp (Caponigro et al., 1997, Anti-Cancer Drugs, 8, 26-33).

Dean et al., 1994, Journal of Biological Chemistry, 269, 16416-24, describe cell culture studies in which antisense targeting of PKC α resulted in the potent inhibition of mRNA and protein expression in human lung carcinoma (A549) cells. In this study, PKC α inhibition resulted in the reduced induction of intercellular adhesion molecule 1 (ICAM-1) mRNA by phorbol esters.

Yano et al., 1999, Endocrinology, 140, 4622-4632, describe a cell proliferation study in which down regulation of different PKC isoforms, including PKCα, results in the inhibition of insulin like growth factor I induced vascular smooth muscle cell proliferation, migration, and gene expression.

Wang et al., 1999, Experimental Cell Research, 250, 253-263, describe cell culture studies in which antisense inhibition of PKC α results in the reversal of the transformed phenotype in human lung carcinoma (LTEPa-2) cells. In this study, the amounts of PKC α protein and total PKC activity were decreased when compared to control cells.

Sioud and Sorensen, 1998, Nature Biotechnology, 16, 556-561, describe hammerhead ribozyme inhibition of PKC α in rat glioma cell lines (BT4C and BT4Cn). This study demonstrated inhibition of malignant glioma cell proliferation along with the inhibition of regulatory Bcl-x_L protein expression. Bcl-x_L is overexpressed in glioma cells and is an apoptosis inhibitor. The ribozyme mediated inhibition of cell proliferation presumably results from apoptosis induction of transformed glioma cells through suppression of PKC α and Bcl-x_L (Leirdal and Sioud, 1999, British J. of Cancer, 80, 1558-1564).

Animal Models

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Evaluating the efficacy of anti-PKCα agents in animal models is an important prerequisite to human clinical trials. A variety of mouse xenograft models using human tumor cell lines have been developed using cell lines which express high levels of PKCα protein. McGraw et al. 1997, Anti-Cancer Drug Design, 12, 315-326, describe mouse xenograft models using human breast (MDA MB-321), prostate (Du-145), colon (Colo 205, WiDr), lung (NCI H69, H209, J460, H520, A549), bladder (T-24), and melanoma (SK-mel 1) carcinoma cells. Antisense oligonucleotides targeting PKCα administered intravenously following s.c. transplanted tumor cells resulted in dose dependant decreases in tumor size when compared to controls in most cases. Similar studies using T-24 bladder carcinoma, non-small cell lung carcinoma (A549), and Colo 205 colon carcinoma mouse xenografts are described in Dean et al, 1996, Biochemical Society Transactions, 24, 623. Sioud and Sorensen, 1998, Nature Biotechnology, 16, 556-561, describe a rat model in which inbred syngeneic BDIX rats were inoculated subcutaneously with BT4Cn glioma cells. After approximately three weeks, rats were treated with a single injection of

ribozyme targeting PKC α resulting in inhibition of tumor growth as determined by tumor size and/or weight when compared to controls. The above studies provide proof that inhibition of PKC α expression by anti-PKC α agents causes inhibition of tumor growth in animals. Lead anti-PKC α ribozymes chosen from in vitro assays can be further tested in mouse xenograft models. Ribozymes can be first tested alone and then in combination with standard chemotherapies.

Animal Model Development

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Human lung (A549, NCI H520) tumor and breast (MDA-MB 231) cell lines can be characterized to establish their growth curves in mice. These cell lines are been implanted into both nude and SCID mice and primary tumor volumes are measured 3 times per week. Growth characteristics of these tumor lines using a Matrigel implantation format can also be established. In addition, the use of other cell lines that have been engineered to express high levels of PKCα can also be used. The tumor cell line(s) and implantation method that supports the most consistent and reliable tumor growth can be used in animal studies to test promising PKCa ribozyme(s). Ribozymes can be administered by daily subcutaneous injection or by continuous subcutaneous infusion from Alzet mini osmotic pumps beginning 3 days after tumor implantation and continuing for the duration of the study. Group sizes of at least 10 animals are employed. Efficacy is determined by statistical comparison of tumor volume of ribozyme-treated animals to a control group of animals treated with saline alone. Because the growth of these tumors is generally slow (45-60 days), an initial endpoint will be the time in days it takes to establish an easily measurable primary tumor (i.e. 50-100 mm³) in the presence or absence of ribozyme treatment.

Clinical Summary

25 Overview

Ribozymes targeting PKCα have strong potential to develop into useful therapeutics directed towards numerous cancer types. Lung cancer is the leading cause of cancer deaths for both men and women in the USA. The incidence of lung cancer in the United States is ~172,000 cases per year, accounting for 14% of cancer diagnoses. Approximately 158,000 die each year of lung cancer, accounting for 28% of all cancer deaths. Numerous other

indications exist including cancers of the bladder, colon, breast, prostate, and ovary in addition to melanoma and glioblastoma.

McGraw et al., 1997, Anti-Cancer Drug Design, 12, 315-326, describe a Phase I trial for ISIS 3521/CGP 64128A, a PKC alpha antisense construct. In this trial, ISIS 3521/CGP 64128A was administered as either a two-hour i.v. infusion three times per week for three consecutive weeks, or as a continuous i.v. infusion for twenty-one consecutive days. The authors report that patients demonstrated excellent tolerance to the antisense compound when administered at doses of up to 2.5 mg/kg by the two-hour i.v. infusion and at 1.5 mg/kg/day by continuous i.v. infusion. In patients receiving the two-hour i.v. infusion schedule, the post-infusion plasma concentration of the compound increased proportional to the dose, and metabolites were determined to have been cleared rapidly from plasma with a half-life of thirty to forty-five minutes. These metabolites were composed of chain-shortened oligonucleotides, consistent with exonuclease-mediated degradation. No evidence of accumulation, induction, or inhibition of metabolism was found after the administration of repetitive doses.

Therapy

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Treatment options for lung cancer are determined by the type and stage of the cancer and include surgery, radiation therapy, and chemotherapy. For many localized cancers, surgery is usually the treatment of choice. Because the disease has usually spread by the time it is discovered, radiation therapy and chemotherapy are often needed in combination with surgery. Chemotherapy alone or combined with radiation has replaced surgery as the treatment of choice for small cell lung cancer; on this regimen, a large percentage of patients experience remission, which in some cases is long-lasting. The 1-year relative survival rates for lung cancer have increased from 32% in 1973 to 41% in 1994, largely due to improvements in surgical techniques. The 5-year relative survival rate for all stages combined is only 14%. The survival rate is 50% for cases detected when the disease is still localized, but only 15% of lung cancers are discovered that early.

Common chemotherapies include various combinations of cytotoxic drugs to kill the cancer cells. These drugs include paclitaxel (Taxol), docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil etc. Significant toxicities are associated with these cytotoxic therapies. Well-characterized toxicities include nausea and vomiting, myelosuppression, alopecia and mucosity. Serious cardiac problems are also associated with certain of the combinations, e.g. doxorubin and paclitaxel, but are less common.

Applicant has designed several NCH ribozymes targeted against PKCα RNA (Genebank accession No NM_002737) (see, for example, Table 63). These ribozymes are used first in a proliferation assay that is used to select ribozyme leads.

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Proliferation assay: The model proliferation assay useful in the study can require a cell plating density of 2000 cells/well in 96-well plates and at least 2 cell doublings over a 5-day treatment period. To calculate cell density for proliferation assays, the FIPS (fluoro-imaging processing system) method well known in the art can be used. This method allows for cell density measurements after nucleic acids are stained with CyQuant® dye, and has the advantage of accurately measuring cell densities over a very wide range 1,000-100,000 cells/well in 96-well format.

Ribozymes (50-200 nM) are delivered in the presence of cationic lipid at 2.0 μ g/mL and inhibition of proliferation is determined on day 5 post-treatment. Two full ribozyme screens are usually completed and lead ribozymes are chosen for further testing. Of the lead ribozymes chosen from primary screens, ribozymes which continue to inhibit cell proliferation in subsequent experiments are selected for PKC α RNA and protein inhibition studies.

Example 15: Nucleoside Triphosphates and their incorporation into oligonucleotides

The synthesis of nucleotide triphosphates and their incorporation into nucleic acids using polymerase enzymes has greatly assisted in the advancement of nucleic acid research. The polymerase enzyme utilizes nucleotide triphosphates as precursor molecules to assemble oligonucleotides. Each nucleotide is attached by a phosphodiester bond formed through nucleophilic attack by the 3' hydroxyl group of the oligonucleotide's last nucleotide onto the 5' triphosphate of the next nucleotide. Nucleotides are incorporated one at a time into the oligonucleotide in a 5' to 3' direction. This process allows RNA to be produced and amplified from virtually any DNA or RNA templates.

Most natural polymerase enzymes incorporate standard nucleotide triphosphates into nucleic acid. For example, a DNA polymerase incorporates dATP, dTTP, dCTP, and dGTP into DNA and an RNA polymerase generally incorporates ATP, CTP, UTP, and

GTP into RNA. There are however, certain polymerases that are capable of incorporating non-standard nucleotide triphosphates into nucleic acids (Joyce, 1997, PNAS 94, 1619-1622, Huang et al., Biochemistry 36, 8231-8242).

Before nucleosides can be incorporated into RNA transcripts using polymerase enzymes they must first be converted into nucleotide triphosphates which can be recognized by these enzymes. Phosphorylation of unblocked nucleosides by treatment with POCl₃ and trialkyl phosphates was shown to yield nucleoside 5'-phosphorodichloridates (Yoshikawa et al., 1969, Bull. Chem. Soc.(Japan) 42, 3505). Adenosine or 2'-deoxyadenosine 5'-triphosphate was synthesized by adding an additional step consisting of treatment with excess tri-n-butylammonium pyrophosphate in DMF followed by hydrolysis (Ludwig, 1981, Acta Biochim. et Biophys. Acad. Sci. Hung. 16, 131-133).

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Non-standard nucleotide triphosphates are not readily incorporated into RNA transcripts by traditional RNA polymerases. Mutations have been introduced into RNA polymerase to facilitate incorporation of deoxyribonucleotides into RNA (Sousa & Padilla, 1995, EMBO J. 14,4609-4621, Bonner et al., 1992, EMBO J. 11, 3767-3775, Bonner et al., 1994, J. Biol. Chem. 42, 25120-25128, Aurup et al., 1992, Biochemistry 31, 9636-9641).

McGee et al., International PCT Publication No. WO 95/35102, describes the incorporation of 2'-NH₂-NTP's, 2'-F-NTP's, and 2'-deoxy-2'-benzyloxyamino UTP into RNA using bacteriophage T7 polymerase.

Wieczorek et al., 1994, Bioorganic & Medicinal Chemistry Letters 4, 987-994, describes the incorporation of 7-deaza-adenosine triphosphate into an RNA transcript using bacteriophage T7 RNA polymerase.

Lin et al., 1994, Nucleic Acids Research 22, 5229-5234, reports the incorporation of 2'-NH₂-CTP and 2'-NH₂-UTP into RNA using bacteriophage T7 RNA polymerase and polyethylene glycol containing buffer. The article describes the use of the polymerase synthesized RNA for in vitro selection of aptamers to human neutrophil elastase (HNE).

This invention relates to novel nucleotide triphosphate (NTP) molecules, and their incorporation into nucleic acid molecules, including nucleic acid catalysts. The NTPs of the instant invention are distinct from other NTPs known in the art. The invention further relates to incorporation of these nucleotide triphosphates into oligonucleotides using an RNA polymerase; the invention further relates to novel transcription conditions for the

incorporation of modified (non-standard) and unmodified NTP's, into nucleic acid molecules. Further, the invention relates to methods for synthesis of novel NTP's

In a first aspect, the invention features NTP's having the formula triphosphate-OR, for example the following formula 3:

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2-fluoro cytidine.

where R is any nucleoside; specifically the nucleosides 2'-O-methyl-2,6diaminopurine riboside; 2'-deoxy-2'amino-2,6-diaminopurine riboside; 2'-(N-alanyl) amino-2'-deoxy-uridine: 2'-(N-phenylalanyl)amino-2'-deoxy-uridine: 2'-deoxy -2'-(N-βalanyl) amino : 2'-deoxy-2'-(lysiyl) amino uridine: 2'-C-allyl uridine: 2'-O-amino-uridine: 2'-O-methylthiomethyl adenosine: 2'-O-methylthiomethyl cytidine: 2'-Omethylthiomethyl guanosine; 2'-Q-methylthiomethyl-uridine; 2'-deoxy-2'-(N-histidyl) amino uridine; 2'-deoxy-2'-amino-5-methyl cytidine; 2'-(N-β-carboxamidine-βalanyl)amino-2'-deoxy-uridine: 2'-deoxy-2'-(N-B-alanyl)-guanosine: 2'-O-aminoadenosine: 2'-(N-lysyl)amino-2'-deoxy-cytidine: 2'-Deoxy -2'-(L-histidine) amino Cytidine: 5-Imidazoleacetic acid 2'-deoxy uridine, 5-I3-(N-4imidazoleacetyl)aminopropynyl]-2'-O-methyl uridine, 5-(3-aminopropynyl)-2'-O-methyl uridine, 5-(3-aminopropyl)-2'-O-methyl uridine, 5-[3-(N-4-imidazoleacetyl)aminopropyl]-2'-O-methyl uridine, 5-(3-aminopropyl)-2'-deoxy-2-fluoro uridine, 2'-Deoxy-2'-(β-alanyl-L-histidyl)amino uridine, 2'-deoxy-2'-β-alaninamido-uridine, 3-(2'-deoxy-2'-fluoro-β-Dribofuranosyl)piperazino[2,3-D]pyrimidine-2-one, 5-[3-(N-4imidazoleacety])aminopropy[]-2'-deoxy-2'-fluoro uridine, 5-[3-(N-4-

In a second aspect, the invention features inorganic and organic salts of the nucleoside triphosphates of the instant invention.

imidazoleacetyl)aminopropynyl]-2'-deoxy-2'-fluoro uridine, 5-E-(2-carbox yvinyl-2'-deoxy-2'-fluoro uridine, 5-[3-(N-4-aspartyl)aminopropynyl-2'-fluoro uridine, 5-(3-aminopropyl)-2'-deoxy-2-fluoro cytidine, and 5-[3-(N-4-succynyl)aminopropyl-2'-deoxy-

In a third aspect, the invention features a process for the synthesis of pyrimidine nucleotide triphosphate (such as UTP, 2'-O-MTM-UTP, dUTP and the like) including the steps of monophosphorylation where the pyrimidine nucleoside is contacted with a mixture having a phosphorylating agent (such as phosphorus oxychloride, phospho-tristriazolides, phospho-tristrimidazolides and the like), trialkyl phosphate (such as triethylphosphate or trimethylphosphate or the like) and a hindered base (such as dimethylaminopyridine, DMAP and the like) under conditions suitable for the formation of pyrimidine monophosphate; and pyrophosphorylation where the pyrimidine monophosphate is contacted with a pyrophosphorylating reagent (such as tributylammonium pyrophosphate) under conditions suitable for the formation of pyrimidine triphosphates.

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By "nucleotide triphosphate" or "NTP" is meant a nucleoside bound to three inorganic phosphate groups at the 5' hydroxyl group of the modified or unmodified ribose or deoxyribose sugar where the 1' position of the sugar may comprise a nucleic acid base or hydrogen. The triphosphate portion may be modified to include chemical moieties which do not destroy the functionality of the group (i.e., allow incorporation into an RNA molecule).

In another preferred embodiment, nucleotide triphosphates (NTPs) of the instant invention are incorporated into an oligonucleotide using an RNA polymerase enzyme. RNA polymerases include but are not limited to mutated and wild type versions of bacteriophage T7, SP6, or T3 RNA polymerases. Applicant has also found that the NTPs of the present invention can be incorporated into oligonucleotides using certain DNA polymerases, such as Taq polymerase.

In yet another preferred embodiment, the invention features a process for incorporating modified NTP's into an oligonucleotide including the step of incubating a mixture having a DNA template, RNA polymerase, NTP, and an enhancer of modified NTP incorporation under conditions suitable for the incorporation of the modified NTP into the oligonucleotide.

By "enhancer of modified NTP incorporation" is meant a reagent which facilitates the incorporation of modified nucleotides into a nucleic acid transcript by an RNA polymerase. Such reagents include, but are not limited to, methanol, LiCl, polyethylene glycol (PEG), diethyl ether, propanol, methyl amine, ethanol, and the like.

In another preferred embodiment, the modified nucleotide triphosphates can be incorporated by transcription into a nucleic acid molecules including enzymatic nucleic acid, antisense, 2-5A antisense chimera, oligonucleotides, triplex forming oligonucleotide (TFO), aptamers and the like (Stull et al., 1995 Pharmaceutical Res. 12, 465).

By "triplex forming oligonucleotides (TFO)" it is meant an oligonucleotide that can bind to a double-stranded DNA in a sequence-specific manner to form a triple-strand helix. Formation of such triple helix structure has been shown to inhibit transcription of the targeted gene (Duval-Valentin et al., 1992 Proc. Natl. Acad. Sci. USA 89, 504).

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In yet another preferred embodiment, the modified nucleotide triphosphates of the instant invention can be used for combinatorial chemistry or *in vitro* selection of nucleic acid molecules with novel function. Modified oligonucleotides can be enzymatically synthesized to generate libraries for screening.

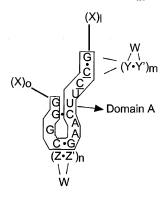
In another preferred embodiment, the invention features nucleic acid based techniques (e.g., enzymatic nucleic acid molecules), antisense nucleic acids, 2-5A antisense chimeras, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups) isolated using the methods described in this invention and methods for their use to diagnose, down regulate or inhibit gene expression.

In yet another preferred embodiment, the invention features enzymatic nucleic acid molecules targeted against HER2 RNA, specifically including ribozymes in the class II (zinzyme) motif.

Targets, for example HER2 RNA, for useful ribozymes and antisense nucleic acids can be determined, for example, as described in Draper et al., WO 93/23569; Sullivan et al., WO 93/23057; Thompson et al., WO 94/02595; Draper et al., WO 95/04818; McSwiggen et al., US Patent Nos. 5,525,468 and 5,646,042, all are hereby incorporated by reference herein in their totalities. Other examples include the following PCT applications, which concern inactivation of expression of disease-related genes: WO 95/23225, and WO 95/13380; all of which are incorporated by reference herein.

In yet another preferred embodiment, the invention features a process for incorporating a plurality of compounds of formula 3.

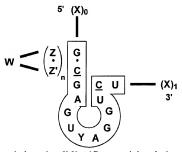
In yet another embodiment, the invention features a nucleic acid molecule with catalytic activity having formula 4:



In the formula shown above X, Y, and Z represent independently a nucleotide or a non-nucleotide linker, which may be same or different; • indicates hydrogen bond formation between two adjacent nucleotides which may or may not be present; Y' is a 5 nucleotide complementary to Y; Z' is a nucleotide complementary to Z; 1 is an integer greater than or equal to 3 and preferably less than 20, more specifically 4, 5, 6, 7, 8, 9, 10, 11, 12, or 15; m is an integer greater than 1 and preferably less than 10, more specifically 2, 3, 4, 5, 6, or 7; n is an integer greater than 1 and preferably less than 10, more 10 specifically 3, 4, 5, 6, or 7; o is an integer greater than or equal to 3 and preferably less than 20, more specifically 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 15; I and o may be the same length (1 = 0) or different lengths $(1 \neq 0)$; each X(1) and X(0) are oligonucleotides which are of sufficient length to stably interact independently with a target nucleic acid sequence (the target can be an RNA. DNA or RNA/DNA mixed polymers); W is a linker of ≥ 2 nucleotides in length or may be a non-nucleotide linker; A. U. C. and G represent the 15 nucleotides: G is a nucleotide, preferably 2'-O-methyl or ribo; A is a nucleotide, preferably 2'-O-methyl or ribo; U is a nucleotide, preferably 2'-amino (e.g., 2'-NH2 or 2'-O-NH2), 2'-O-methyl or ribo; C represents a nucleotide, preferably 2'-amino (e.g., 2'-NH2 or 2'-O-

NH₂), and ______ represents a chemical linkage (e.g. a phosphate ester linkage, amide linkage, phosphorothioate, phosphorodithioate or others known in the art).

In yet another embodiment, the invention features a nucleic acid molecule with catalytic activity having formula 5:



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In the formula shown above X, Y, and Z represent independently a nucleotide or a non-nucleotide linker, which may be same or different; \bullet indicates hydrogen bond formation between two adjacent nucleotides which may or may not be present; Z? is a nucleotide complementary to Z; 1 is an integer greater than or equal to 3 and preferably less than 20, more specifically 4, 5, 6, 7, 8, 9, 10, 11, 12, or 15; n is an integer greater than 1 and preferably less than 10, more specifically 3, 4, 5, 6, or 7; o is an integer greater than or equal to 3 and preferably less than 20, more specifically 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 15; l and o may be the same length (l = o) or different lengths (l \neq o); each $X_{(1)}$ and $X_{(o)}$ are oligonucleotides which are of sufficient length to stably interact independently with a target nucleic acid sequence (the target can be an RNA, DNA or RNA/DNA mixed polymers); $X_{(o)}$ preferably has a G at the 3'-end, $X_{(1)}$ preferably has a G at the 5'-end; W is a linker of \geq 2 nucleotides in length or may be a non-nucleotide linker; Y is a linker of \geq 1 nucleotides in length, preferably G, 5'-CA-3', or 5'-CAA-3', or may be a non-nucleotide linker; A, U, C, and G represent nucleotides; G is a nucleotide, preferably 2'-O-methyl, 2'-deozy-2'-fluoro, or 2'-OH; A is a nucleotide, preferably 2'-O-methyl, 2'-deozy-2'-

fluoro, or 2'-OH; U is a nucleotide, preferably 2'-O-methyl, 2'-deozy-2'-fluoro, or 2'-OH;

C represents a nucleotide, preferably 2'-amino (e.g., 2'-NH₂ or 2'-O- NH₂, and ______

represents a chemical linkage (e.g. a phosphate ester linkage, amide linkage, phosphorothioate, phosphorodithioate or others known in the art).

The enzymatic nucleic acid molecules of Formula 4 and Formula 5 may independently comprise a cap structure which may independently be present or absent.

In yet another preferred embodiment, the 3'-cap is selected from a group comprising, 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide; carbocyclic nucleotide: 5'-amino-alkyl phosphate: 1.3-diamino-2-propyl phosphate: 3-

caroocyetic nucleotide; 3-amino-ankyl pnospnate; 1,3-anamino-2-propyl pnospnate; 3aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; threo-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide; 5'-5'inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'phosphorothioate; 1,4-butanediol phosphate 5'-amino; bridging and/or non-bridging 5'phosphoramidate, phosphorothioate and/or hosphorodithioate; bridging or non bridging

1993, Tetrahedron 49, 1925; incorporated by reference herein).
In another aspect, the invention provides mammalian cells containing one or more nucleic acid molecules and/or expression vectors of this invention. The one or more nucleic acid molecules may independently be targeted to the same or different sites.

methylphosphonate and 5'-mercapto moieties (for more details, see Beaucage and Iyer,

Nucleotide Synthesis

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Addition of dimethylaminopyridine (DMAP) to the phosphorylation protocols known in the art can greatly increase the yield of nucleotide monophosphates while decreasing the reaction time. Synthesis of the nucleosides of the invention have been described in several publications and Applicants previous applications (Beigelman et al., International PCT publication No. WO 96/18736; Dudzcy et al., Int. PCT Pub. No. WO 95/11910; Usman et al., Int. PCT Pub. No. WO 95/13378; Matulic-Adamic et al., 1997, Tetrahedron Lett. 38, 203; Matulic-Adamic et al., 1997, Tetrahedron Lett. 38, 1669; all of which are incorporated herein by reference). These nucleosides are dissolved in triethyl phosphate and chilled in an ice bath. Phosphorus oxychloride (POCl₃) is then added

followed by the introduction of DMAP. The reaction is then warmed to room temperature and allowed to proceed for 5 hours. This reaction allows the formation of nucleotide monophosphates which can then be used in the formation of nucleotide triphosphates. Tributylamine is added followed by the addition of anhydrous acetonitrile and tributylammonium pyrophosphate. The reaction is then quenched with TEAB and stirred overnight at room temperature (about 20°C). The triphosphate is purified using Sephadex® column purification or equivalent and/or HPLC and the chemical structure is confirmed using NMR analysis. Those skilled in the art will recognize that the reagents, temperatures of the reaction, and purification methods can easily be alternated with substitutes and equivalents and still obtain the desired product.

Nucleotide Triphosphates

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The invention provides nucleotide triphosphates which can be used for a number of different functions. The nucleotide triphosphates formed from nucleosides found in Table 45 are unique and distinct from other nucleotide triphosphates known in the art. Incorporation of modified nucleotides into DNA or RNA oligonucleotides can alter the properties of the molecule. For example, modified nucleotides can hinder binding of nucleases, thus increasing the chemical half-life of the molecule. This is especially important if the molecule is to be used for cell culture or in vivo. It is known in the art that the introduction of modified nucleotides into these molecules can greatly increase the stability and thereby the effectiveness of the molecules (Burgin et al., 1996, Biochemistry 35, 14090-14097; Usman et al., 1996, Curr. Opin. Struct. Biol. 6, 527-533).

Modified nucleotides are incorporated using either wild type or mutant polymerases. For example, mutant T7 polymerase is used in the presence of modified nucleotide triphosphate(s), DNA template and suitable buffers. Those skilled in the art will recognize that other polymerases and their respective mutant versions can also be utilized for the incorporation of NTP's of the invention. Nucleic acid transcripts were detected by incorporating radiolabelled nucleotides (a-32P NTP). The radiolabeled NTP contained the same base as the modified triphosphate being tested. The effects of methanol, PEG and LiCl were tested by adding these compounds independently or in combination. Detection and quantitation of the nucleic acid transcripts was performed using a Molecular Dynamics

PhosphorImager. Efficiency of transcription was assessed by comparing modified nucleotide triphosphate incorporation with all-ribonucleotide incorporation control. Wild-type polymerase was used to incorporate NTP's using the manufacturer's buffers and instructions (Boehringer Mannheim).

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Transcription Conditions

Incorporation rates of modified nucleotide triphosphates into oligonucleotides can be increased by adding to traditional buffer conditions, several different enhancers of modified NTP incorporation. Applicant has utilized methanol and LiCl in an attempt to increase incorporation rates of dNTP using RNA polymerase. These enhancers of modified NTP incorporation can be used in different combinations and ratios to optimize transcription. Optimal reaction conditions differ between nucleotide triphosphates and can readily be determined by standard experimentation. Overall, however, Applicant has found that inclusion of enhancers of modified NTP incorporation such as methanol or inorganic compound such as lithium chloride increase the mean transcription rates.

Applicant synthesized pyrimidine nucleotide triphosphates using DMAP in the reaction. For purines, applicant utilized standard protocols previously described in the art (Yoshikawa et al supra; Ludwig, supra). Described below is one example of a pyrimdine nucleotide triphosphate and one purine nucleotide triphosphate synthesis.

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Synthesis of purine nucleotide triphosphates: 2'-O-methyl-guanosine-5'-triphosphate

2'-O-methyl guanosine nucleoside (0.25 grams, 0.84 mmol) was dissolved in triethyl
phosphate (5.0) ml by heating to 100°C for 5 minutes. The resulting clear, colorless
solution was cooled to 0°C using an ice bath under an argon atmosphere. Phosphorous
oxychloride (1.8 eq., 0.141 ml) was then added to the reaction mixture with vigorous
stirring. The reaction was monitored by HPLC, using a sodium perchlorate gradient.
After 5 hours at 0°C, tributylamine (0.65 ml) was added followed by the addition of
anhydrous acetonitrile (10.0 ml), and after 5 minutes (reequilibration to 0°C)
tributylammonium pyrophosphate (4.0 eq., 1.53 g) was added. The reaction mixture was
quenched with 20 ml of 2M TEAB after 15 minutes at 0°C (HPLC analysis with above
conditions showed consumption of monophosphate at 10 minutes) then stirred overnight at
room temperature, the mixture was evanorated in vacuo with methanol co-evaporation

(4x) then diluted in 50 ml 0.05M TEAB. DEAE sephadex purification was used with a gradient of 0.05 to 0.6 M TEAB to obtain pure triphosphate (0.52 g, 66.0% yield) (elutes around 0.3M TEAB); the purity was confirmed by HPLC and NMR analysis.

5 Synthesis of Pyrimidine nucleotide triphosphates: 2'-O-methylthiomethyl-uridine-5'triphosphate

2°-O-methylthiomethyl uridine nucleoside (0.27 grams, 1.0 mmol) was dissolved in triethyl phosphate (5.0 ml). The resulting clear, colorless solution was cooled to 0°C with an ice bath under an argon atmosphere. Phosphorus oxychloride (2.0 eq., 0.190 ml) was then added to the reaction mixture with vigorous stirring. Dimethylaminopyridine (DMAP, 0.2eq., 25 mg) was added, the solution warmed to room temperature and the reaction was monitored by HPLC, using a sodium perchlorate gradient. After 5 hours at 20°C, tributylamine (1.0 ml) was added followed by anhydrous acetonitrile (10.0 ml), and after 5 minutes tributylammonium pyrophosphate (4.0 eq., 1.8 g) was added. The reaction mixture was quenched with 20 ml of 2M TEAB after 15 minutes at 20°C (HPLC analysis with above conditions showed consumption of monophosphate at 10 minutes) then stirred overnight at room temperature. The mixture was evaporated *in vacuo* with methanol co-evaporation (4x) then diluted in 50 ml 0.05M TEAB. DEAE fast flow Sepharose purification with a gradient of 0.05 to 1.0 M TEAB was used to obtain pure triphosphate (0.40 g, 44% yield) (elutes around 0.3M TEAB) as determined by HPLC and NMR analysis.

Utilization of DMAP in Uridine 5'-Triphosphate Synthesis

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The reactions were performed on 20 mg aliquots of nucleoside dissolved in 1 ml of triethyl phosphate and 19 ul of phosphorus oxychloride. The reactions were monitored at 40 minute intervals automatically by HPLC to generate yield-of-product curves at times up to 18 hours. A reverse phase column and ammonium acetate/sodium acetate buffer system (50mM & 100mM respectively at pH 4.2) was used to separate the 5', 3', 2' monophosphates (the monophosphates elute in that order) from the 5'-triphosphate and the starting nucleoside. The data is shown in Table 46. These conditions doubled the product yield and resulted in a 10-fold improvement in the reaction time to maximum yield (1200 minutes down to 120 minutes for a 90% yield). Selectivity for 5'-monophosphorylation

was observed for all reactions. Subsequent triphosphorylation occurred in nearly quantitative yield.

Materials Used in Bacteriophage T7 RNA Polymerase Reactions

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Buffer 1: Reagents are mixed together to form a 10X stock solution of buffer 1

(400 mM Tris-Cl [pH 8.1], 200 mM MgCl₂, 100 mM DTT, 50 mM spermidine, and 0.1% triton® X-100). Prior to initiation of the polymerase reaction methanol, LiCl is added and the buffer is diluted such that the final reaction conditions for condition 1 consisted of:

40mM tris (pH 8.1), 20mM MgCl₂, 10 mM DTT, 5 mM spermidine, 0.01% triton® X-100, 10% methanol, and 1 mM LiCl.

BUFFER 2: Reagents are mixed together to form a 10X stock solution of buffer 2 (400 mM Tris-Cl [pH 8.1], 200 mM MgCl₂, 100 mM DTT, 50 mM spermidine, and 0.1% triton® X-100). Prior to initiation of the polymerase reaction PEG, LiCl is added and the buffer is diluted such that the final reaction conditions for buffer 2 consisted of: 40mM tris (pH 8.1), 20mM MgCl₂, 10 mM DTT, 5 mM spermidine, 0.01% triton® X-100, 4% PEG, and 1 mM LiCl.

BUFFER 3: Reagents are mixed together to form a 10X stock solution of buffer 3 (400 mM Tris-Cl [pH 8.0], 120 mM MgCl₂, 50 mM DTT, 10 mM spermidine and 0.02% triton® X-100). Prior to initiation of the polymerase reaction PEG is added and the buffer is diluted such that the final reaction conditions for buffer 3 consisted of: 40mM tris (pH 8.0), 12 mM MgCl₂, 5 mM DTT, 1 mM spermidine, 0.002% triton® X-100, and 4% PEG.

BUFFER 4: Reagents are mixed together to form a 10X stock solution of buffer 4 (400 mM Tris-Cl [pH 8.0], 120 mM MgCl₂, 50 mM DTT, 10 mM spermidine and 0.02% triton® X-100). Prior to initiation of the polymerase reaction PEG, methanol is added and the buffer is diluted such that the final reaction conditions for buffer 4 consisted of: 40mM tris (pH 8.0), 12 mM MgCl₂, 5 mM DTT, 1 mM spermidine, 0.002% triton® X-100, 10% methanol, and 4% PEG.

BUFFER 5: Reagents are mixed together to form a 10X stock solution of buffer 5 (400 mM Tris-CI [pH 8.0], 120 mM MgCl₂, 50 mM DTT, 10 mM spermidine and 0.02% triton® X-100). Prior to initiation of the polymerase reaction PEG, LiCl is added and the buffer is diluted such that the final reaction conditions for buffer 5 consisted of: 40mM

tris (pH 8.0), 12 mM MgCl₂, 5 mM DTT, 1 mM spermidine, 0.002% triton® X-100, 1 mM LiCl and 4% PEG.

BUFFER 6: Reagents are mixed together to form a 10X stock solution of buffer 6 (400 mM Tris-Cl [pH 8.0], 120 mM MgCl₂, 50 mM DTT, 10 mM spermidine and 0.02% triton® X-100). Prior to initiation of the polymerase reaction PEG, methanol is added and the buffer is diluted such that the final reaction conditions for buffer 6 consisted of: 40mM tris (pH 8.0), 12 mM MgCl₂, 5 mM DTT, 1 mM spermidine, 0.002% triton® X-100, 10% methanol, and 4% PEG.

BUFFER 7: Reagents are mixed together to form a 10X stock solution of buffer 6 (400 mM Tris-Cl [pH 8.0], 120 mM MgCl₂, 50 mM DTT, 10 mM spermidine and 0.02% triton® X-100). Prior to initiation of the polymerase reaction PEG, methanol and LiCl is added and the buffer is diluted such that the final reaction conditions for buffer 6 consisted of: 40mM tris (pH 8.0), 12 mM MgCl₂, 5 mM DTT, 1 mM spermidine, 0.002% triton® X-100, 10% methanol, 4% PEG, and 1 mM LiCl.

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Screening of Modified nucleotide triphosphates with Mutant T7 RNA Polymerase

Modified nucleotide triphosphates were tested in buffers 1 through 6 at two different temperatures (25 and 37°C). Buffers 1-6 tested at 25°C were designated conditions 1-6 and buffers 1-6 tested at 37°C were designated conditions 7-12 (Table 47). In each condition, Y639F mutant T7 polymerase (Sousa and Padilla, *supra*) (0.3-2 mg/20 ml reaction), NTP's (2 mM each), DNA template (10 pmol), inorganic pyrophosphatase (5U/ml) and α-³²P NTP (0.8 mCi/pmol template) were combined and heated at the designated temperatures for 1-2 hours. The radiolabeled NTP used was different from the modified triphosphate being testing. The samples were resolved by polyacrylamide gel electrophoresis. Using a PhosphorImager (Molecular Dynamics, Sunnyvale, CA), the amount of full-length transcript was quantified and compared with an all-RNA control reaction. The data is presented in Table 48; results in each reaction are expressed as a percent compared to the all-ribonucleotide triphosphate (rNTP) control. The control was run with the mutant T7 polymerase using commercially available polymerase buffer (Boehringer Mannheim, Indianapolis, IN).

Incorporation of Modified NTP's using Wild-type T7 RNA polymerase

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Bacteriophage T7 RNA polymerase was purchased from Boehringer Mannheim at $0.4~U/\mu L$ concentration. Applicant used the commercial buffer supplied with the enzyme and $0.2~\mu Ci$ alpha. ^{32}P NTP in a 50 μL reaction with nucleotides triphosphates at 2 mM each. The template was a double-stranded PCR fragment, which was used in previous screens. Reactions were carried out at 37°C for 1 hour. Ten μL of the sample was run on a 7.5% analytical PAGE and bands were quantitated using a PhosphorImager. Results are calculated as a comparison to an "all ribo" control (non-modified nucleotide triphosphates) and the results are in Table 49.

10 Incorporation of Multiple Modified nucleotide triphosphates Into Oligonucleotides

Combinations of modified nucleotide triphosphates were tested with the transcription protocol described above, to determine the rates of incorporation of two or more of these triphosphates. Incorporation of 2'-Deoxy-2'-(L-histidine) amino uridine (2'-his-NH₂-UTP) was tested with unmodified cytidine nucleotide triphosphates, rATP and rGTP in reaction condition number 9. The data is presented as a percentage of incorporation of modified NTP's compared to the all rNTP control and is shown in Table 50a.

Two modified cytidines (2'-NH₂-CTP or 2'dCTP) were incorporated along with 2'-his-NH₂-UTP with identical efficiencies. 2'-his-NH₂-UTP and 2'-NH₂-CTP were then tested with various unmodified and modified adenosine triphosphates in the same buffer (Table 50b). The best modified adenosine triphosphate for incorporation with both 2'-his-NH₂-UTP and 2'-NH₂-CTP was 2'-NH₂-DAPTP.

Optimization of Reaction conditions for Incorporation of Modified Nucleotide Triphosphate

The combination of 2'-his-NH₂-UTP, 2'-NH₂-CTP, 2'-NH₂-DAP, and rGTP was tested in several reaction conditions (Table 51) using the incorporation protocol described above. The results demonstrate that of the buffer conditions tested, incorporation of these modified nucleotide triphosphates occur in the presence of both methanol and LiCl.

Selection of Novel Enzymatic nucleic acid molecule Motifs using 2'-deoxy-2'amino Modified GTP and CTP

For selection of new enzymatic nucleic acid molecule motifs, pools of enzymatic nucleic acid molecules were designed to have two substrate binding arms (5 and 16 nucleotides long) and a random region in the middle. The substrate has a biotin on the 5' end, 5 nucleotides complementary to the short binding arm of the pool, an unpaired G (the desired cleavage site), and 16 nucleotides complementary to the long binding arm of the pool. The substrate was bound to column resin through an avidin-biotin complex. The general process for selection is shown in Figure 11. The protocols described below represent one possible method that may be utilized for selection of enzymatic nucleic acid molecules and are given as a non-limiting example of enzymatic nucleic acid molecules and are given as a non-limiting example of enzymatic nucleic acid molecule selection with combinatorial libraries.

Construction of Libraries:

The oligonucleotides listed below were synthesized by Operon Technologies (Alameda, CA). Templates were gel purified and then run through a Sep-Pak™ cartridge (Waters, Millford, MA) using the manufacturers protocol. Primers (MST3, MST7c, MST3del) were used without purification.

Primers:

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MST3 (30 mer): 5'-CAC TTA GCA TTA ACC CTC ACT AAA GGC CGT-3'
MST7c (33 mer): 5'-TAA TAC GAC TCA CTA TAG GAA AGG TGT GCA ACC-3'
MST3del (18 mer): 5'-ACC CTC ACT AAA GGC CGT-3'

Templates:

MSN60c (93 mer): 5'-ACC CTC ACT AAA GGC CGT (N) $_{60}$ GGT TGC ACA CCT TTG-3'

MSN40c (73 mer): 5'-ACC CTC ACT AAA GGC CGT (N)₄₀ GGT TGC ACA CCT TTG-3'

MSN20c (53 mer): 5'-ACC CTC ACT AAA GGC CGT (N)₂₀ GGT TGC ACA CCT TTG-3'

N60 library was constructed using MSN60c as a template and MST3/MST7c as primers. N40 and N20 libraries were constructed using MSN40c (or MSN20c) as template and MST3del/MST7c as primers. Single-stranded templates were converted into double-stranded DNA by the following protocol: 5 nmol template, 10 nmol each primer, in 10 ml reaction volume using standard PCR buffer, dNTP's, and taq DNA polymerase (all reagents from Boerhinger Mannheim). Synthesis cycle conditions were 94°C, 4 minutes; (94°C, 1 minute; 42°C, 1 minute; 72°C, 2 minutes) x 4; 72°C, 10 minutes. Products were checked on agarose gel to confirm the length of each fragment (N60=123 bp, N40=91 bp, N20=71 bp) and then were phenol/chloroform extracted and ethanol precipitated. The concentration of the double-stranded product was 25 μM.

Transcription of the initial pools was performed in a 1 ml volume comprising: 500 pmol double-stranded template (3 x 10¹⁴ molecules), 40 mM tris-HCl (pH 8.0), 12 mM MgCl₂, 1 mM spermidine, 5 mM DTT, 0.002% triton X-100, 1 mM LiCl, 4% PEG 8000, 10% methanol, 2 mM ATP (Pharmacia), 2 mM GTP (Pharmacia), 2 mM 2'-deoxy-2'-amino-CTP (USB), 2 mM 2'-deoxy-2'-amino-CTP (USB), 5 U/µl T7 RNA polymerase (USB; Y639F mutant was used in some cases at 0.1 mg/ml (Sousa and Padilla, supra)), 37°C, 2 hours. Transcribed libraries were purified by denaturing PAGE (N60=106 ntds, N40=74, N20=54) and the resulting product was desalted using Sep-PakTM columns and then ethanol precipitated.

Initial column-Selection:

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The following biotinylated substrate was synthesized using standard protocols (Usman et al., 1987 J. Am. Chem. Soc., 109, 7845; Scaringe et al., 1990 Nucleic Acids Res., 18, 5433; and Wincott et al., 1995 Nucleic Acids Res. 23, 2677-2684):

5'-biotin-C18 spacer-GCC GUG GGU UGC ACA CCU UUC C-C18 spacer-thiolmodifier C6 S-S-inverted abasic-3'

Substrate was purified by denaturing PAGE and ethanol precipitated. 10 nmol of substrate was linked to a NeutrAvidin™ column using the following protocol: 400 µl UltraLink Immobilized NeutrAvidin™ slurry (200 µl beads, Pierce, Rockford, IL) were loaded into a polystyrene column (Pierce). The column was washed twice with 1 ml of binding buffer (20 mM NaPO4 (pH 7.5), 150 mM NaCl) and then capped off (i.e., a cap was put on the bottom of the column to stop the flow). 200 µl of the substrate suspended in binding buffer was applied and allowed to incubate at room temperature for 30 minutes

with occasional vortexing to ensure even linking and distribution of the solution to the resin. After the incubation, the cap was removed and the column was washed with 1 ml binding buffer followed by 1 ml column buffer (50 mM tris-HCL (pH 8.5), 100 mM NaCl, 50 mM KCl). The column was then ready for use and capped off. 1 nmol of the initial pool RNA was loaded on the column in a volume of 200 µl column buffer. It was allowed to bind the substrate by incubating for 30 minutes at room temperature with occasional vortexing. After the incubation, the cap was removed and the column was washed twice with 1 ml column buffer and capped off. 200 µl of elution buffer (50 mM tris-HCl (pH 8.5), 100 mM NaCl, 50 mM KCl, 25 mM MgCl₂) was applied to the column followed by 30 minute incubation at room temperature with occasional vortexing. The cap was removed and four 200 µl if fractions were collected using elution buffer.

Second column (counter selection):

A diagram for events in the second column is generally shown in Figure 12 and substrate oligonucleotide used is shown below:

5'-GGU UGC ACA CCU UUC C-C18 spacer-biotin-inverted abasic-3'

This column substrate was linked to UltraLink NeutrAvidin™ resin as previously described (40 pmol) which was washed twice with elution buffer. The eluent from the first column purification was then run on the second column. The use of this column allowed for binding of RNA that non-specifically diluted from the first column, while RNA that performed a catalytic event and had product bound to it, flowed through the second column. The fractions were ethanol precipitated using glycogen as carrier and rehydrated in sterile water for amplification.

25 Amplification:

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RNA and primer MST3 (10-100 pmol) were denatured at 90°C for 3 minutes in water and then snap-cooled on ice for one minute. The following reagents were added to the tube (final concentrations given): 1X PCR buffer (Boerhinger Mannheim), 1 mM dNTP's (for PCR, Boerhinger Mannheim), 2 U/µl RNase-Inhibitor (Boerhinger Mannheim), 10 U/µl SuperscriptTM II Reverse Transcriptase (BRL). The reaction was incubated for 1 hour at 42°C, then at 95°C for 5 minutes in order to destroy the

SuperscriptTM. The following reagents were then added to the tube to increase the volume five-fold for the PCR step (final concentrations/amounts given): MST7c primer (10-100 pmol, same amount as in RT step), 1X PCR buffer, taq DNA polymerase (0.025-0.05 U/µl, Boerhinger Mannheim). The reaction was cycled as follows: 94°C, 4minutes; (94°C, 30s; 42-54°C, 30s; 72°C, 1minute) x 4-30 cycles; 72°C, 5minutes; 30°C, 30 minutes. Cycle number and annealing temperature were decided on a round by round basis. In cases where heteroduplex was observed, the reaction was diluted five-fold with fresh reagents and allowed to progress through 2 more amplification cycles. Resulting products were analyzed for size on an agarose gel (N60-123 bp, N40-103 bp, N20-83 bp)

Transcriptions:

and then ethanol precipitated.

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Transcription of amplified products was done using the conditions described above with the following modifications: 10-20% of the amplification reaction was used as template, reaction volume was 100-500 µl, and the products sizes varied slightly (N60=106 ntds, N40=86, N20=66). A small amount of ³²P-GTP was added to the reactions for quantitation purposes.

Subsequent rounds:

Subsequent rounds of selection used 20 pmols of input RNA and 40 pmol of the 22 nucleotide substrate on the column.

Activity of pools:

Pools were assayed for activity under single turnover conditions every three to four rounds. Activity assay conditions were as follows: 50 mM tris-HCl (pH 8.5), 25 mM MgCl₂, 100 mM NaCl, 50 mM KCl, trace 32 P-labeled substrate, 10 nM RNA pool. 2X pool in buffer and, separately, 2X substrate in buffer were incubated at 90°C for 3 minutes, then at 37°C for 3 minutes. Equal volume 2X substrate was then added the 2X pool tube (t=0). Initial assay time points were taken at 4 and 24 hours: 5 μ 1 was removed and quenched in 8 μ 1 cold Stop buffer (96% formamide, 20 mM EDTA, 0.05% bromphenyl blue/xylene cyanol). Samples were heated 90°C, 3 minutes, and loaded on a 20%

sequencing gel. Quantitation was performed using a Molecular Dynamics Phosphorimager and ImageOuaNITM software. The data is shown in Table 52.

Samples from the pools of oligonucleotide were cloned into vectors and sequenced using standard protocols (Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press). The enzymatic nucleic acid molecules were transcribed from a representative number of these clones using methods described in this application. Individuals from each pool were tested for RNA cleavage from N60 and N40 by incubating the enzymatic nucleic acid molecules from the clones with 5/16 substrate in 2mM MgCl2, pH 7.5, 10mM KCl at 37°C. The data in Table 54 shows that the enzymatic nucleic acid molecules isolated from the pool are individually active.

Kinetic Activity:

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Kinetic activity of the enzymatic nucleic acid molecule shown in **Table 54**, was determined by incubating enzymatic nucleic acid molecule (10 nM) with substrate in a cleavage buffer (pH 8.5, 25 mM MgCl₂, 100 mM NaCl, 50 mM KCl) at 37°C.

Magnesium Dependence:

Magnesium dependence of round 15 of N20 was tested by varying MgCl₂ while other conditions were held constant (50 mM tris [pH 8.0], 100 mM NaCl, 50 mM KCl, single turnover, 10 nM pool). The data is shown in Table 55, which demonstrates increased activity with increased magnesium concentrations.

Selection of Novel Enzymatic nucleic acid molecule Motifs using 2'-Deoxy-2'-(N-histidyl) amino UTP, 2'-Fluoro-ATP, and 2'-deoxy-2'-amino CTP and GTP

The method used for selection of novel enzymatic nucleic acid molecule motifs using 2'-deoxy-2'amino modified GTP and CTP was repeated using 2'-Deoxy-2'-{N-histidyl) amino UTP, 2'-Fluoro-ATP, and 2'-deoxy-2'-amino CTP and GTP. However, rather than causing cleavage on the initial column with MgCl₂, the initial random modified-RNA pool was loaded onto substrate-resin in the following buffer; 5 mM NaOAc pH 5.2, 1 M NaCl at 4° C. After ample washing, the resin was moved to 22 ° C and the buffer switch 20 mM HEPES pH 7.4, 140 mM KCl, 10 mM NaCl, 1 mM CaCl₂, 1 mM MgCl₂. In one selection of N60 oligonucleotides, no divalent cations (MgCl₂,

CaCl₂) was used. The resin was incubated for 10 minutes to allow reaction and the eluant collected.

The enzymatic nucleic acid molecule pools were capable of cleaving 1-3% of the present substrate even in the absence of divalent cations, the background (in the absence of modified pools) was 0.2 - 0.4 %.

Synthesis of 5-substituted 2'-modified nucleosides

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When designing monomeric nucleoside triphosphates for selection of therapeutic catalytic RNAs, one has to take into account nuclease stability of such molecules in 10 biological sera. A common approach to increase RNA stability is to replace the sugar 2'-OH group with other groups like 2'-fluoro, 2'-O-methyl or 2'-amino. Fortunately such 2'modified pyrimidine 5'triphosphates are shown to be substrates for RNA polymerases. (Aurup, H.; Williams, D.M.; Eckstein, F. Biochemistry 1992, 31, 9637; and Padilla, R.; Sousa, R. Nucleic Acids Res. 1999, 27, 1561.) On the other hand it was shown that 15 variety of substituents at pyrimidine 5-position is well tolerated by T7 RNA polymerase (Tarasow, T.M.: Eaton, B.E. Biopolymers 1998, 48, 29), most likely because the natural hydrogen-bonding pattern of these nucleotides is preserved. We have chosen 2'-fluoro and 2'-O-methyl pyrimidine nucleosides as starting materials for attachment of different functionalities to the 5-position of the base. Both rigid (alkynyl) and flexible (alkyl) spacers are used. The choice of imidazole, amino and carboxylate pendant groups is based on their ability to act as general acids, general bases, nucleophiles and metal ligands, all of which can improve the catalytic effectiveness of selected nucleic acids. Figures 21 - 24 relate to the synthesis of these compounds.

2'-O-methyluridine was 3'.5'-bis-acetylated using acetic anhydride in pyridine and then converted to its 5-iodo derivative 1a using I₂/ceric ammonium nitrate reagent (Asakura, J.; Robins, M.J. J. Org. Chem. 1990, 55, 4928) (Scheme 1). Both reactions proceeded in a quantitative yield and no chromatographic purifications were needed. Coupling between 1 and N-trifluoroacetyl propargylamine using copper(I) iodide and tetrakis(triphenylphosphine)palladium(0) catalyst as described by Hobbs (Hobbs, F.W., Jr. J. Org. Chem. 1989, 54, 3420) yielded 2a in 89% yield. Selective O-deacylation with aqueous NaOH afforded 3a which was phosphorylated with POCl₂/triethylphosphate

(TEP) in the presence of 1,8-bis(dimethylamino)naphthalene (Proton-Sponge) (Method A) (Kovácz, T; Ötvös, L. Tetrahedron Lett. 1988, 29, 4525). The intermediate nucleoside phosphorodichloridate was condensed in situ with tri-n-butylammonium pyrophosphate. At the end, the N-TFA group was removed with concentrated ammonia. 5'- Triphosphate was purified on Sephadex® DEAE A-25 ion exchange column using a linear gradient of 0.1-0.8M triethylammonium bicarbonate (TEAB) for elution. Traces of contaminating inorganic pyrophosphate are removed using C-18 RP HPLC to afford analytically pure material. Conversion into Na-salt was achieved by passing the aqueous solution of triphosphate through Dowex 50WX8 ion exchange resin in Na+ form to afford 4a in 45% yield. When Proton-Sponge was omitted in the first phosphorylation step, yields were reduced to 10-20%. Catalytic hydrogenation of 3a yielded 5-aminopropyl derivative 5a which was phosphorylated under conditions identical to those described for propynyl derivative 3a to afford triphosphate 6a in 50% yield.

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For the preparation of imidazole derivatized triphosphates 9a and 11a, we developed an efficient synthesis of N-diphenylcarbamoyl 4-imidazoleacetic acid (ImAADPC): Transient protection of carboxyl group as TMS-ester using TMS-Cl/pyridine followed by DPC-Cl allowed for a clean and quantitative conversion of 4-imidazoleacetic acid (ImAA) to its N-DPC protected derivative.

Complete deacylation of 2a afforded 5-(3-aminopropynyl) derivative 8a which was condensed with 4-imidazoleacetic acid in the presence of 1-(3-dimethylaminopropyl)-3-ethylcarbodiimide (EDC) to afford 9a in 68% yield. Catalytic hydrogenation of 8a yielded 5-(3-aminopropyl) derivative 10a which was condensed with ImAADPC to yield conjugate 11a in 32% yield. Yields in these couplings were greatly improved when 5'-OH was protected with DMT group (not shown) thus efficiently preventing undesired 5'-O-esterification. Both 9a and 11a failed to yield triphosphate products in reaction with POCl₃/TEP/Proton-Sponge.

On the contrary, phosphorylation of 3'-O-acetylated derivatives 12a and 13a using 2-chloro-4H-1,3,2-benzodioxaphosphorin-4-one followed by pyrophosphate addition and oxidation (Method B, Scheme 2; Ludwig, J., Eckstein, F., J. Org. Chem. 1989, 54, 631) afforded the desired triphosphates 14a and 15a in 57% yield, respectively.

2'-Deoxy-2'-fluoro nucleoside 5'-triphosphates containing amino- (4b, 6b) and imidazole- (14b, 15b) linked groups were synthesized in a manner analogous to that described for the preparation of 2'-O-methyl nucleoside 5'-triphosphates (Schemes 1 and 2). Again, only Ludwig-Eckstein's phosphorylation worked for the preparation of 4-imidazoleacetyl derivatized triphosphates.

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It is worth noting that when "one-pot-two-steps" phosphorylation reaction (Kovácz, T; Ötvös, L. Tetrahedron Lett. 1988, 29, 4525) of 5b was quenched with 40% aqueous methylamine instead of TEAB or $\rm H_2O$, the γ -amidate 7b was generated as the only detectable product. Similar reaction was reported recently for the preparation of the γ -amidate of pppA2'p5'A2'p5'A. 12

Carboxylate group was introduced into 5-position of uridine both on the nucleoside level and post-synthetically (Method C) (Scheme 3). 5-lodo-2'-deoxy-2'-fluorouridine (16) was coupled with methyl acrylate using modified Heck reaction 13 to yield 17 in 85% yield. 5'-O-Dimethoxytritylation, followed by in situ 3'-O-acetylation and subsequent detriylation afforded 3'-protected derivative 18. Phosphorylation using 2-chloro-4H-1,3,2-benzodioxa-phosphorin-4-one followed by pyrophosphate addition and oxidation (Ludwig, J.; Eckstein, F. J. Org. Chem. 1989, 54, 631) afforded the desired triphosphate in 54% yield. On the other hand, 5-(3-aminopropyl)uridine 5'-triphosphate 6b was coupled with N-hydroxysuccinimide ester of Fmoc-Asp-OFm to afford, after removal of Fmoc and Fm groups with diethylamine, the desired aminoacyl conjugate 20 in 50% yield.

Cytidine derivatives comprising 3-aminopropyl and 3(N-succinyl)aminopropyl groups were synthesized according to Scheme 4. Peracylated 5-(3-aminopropynyl)uracil derivative 2b is reduced using catalytic hydrogenation and then converted in seven steps and 5% overall yield into 3'-acetylated cytidine derivative 25. This synthesis was plagued by poor solubility of intermediates and formation of the N⁴-cyclized byproduct during ammonia treatment of the 4-triazolyl intermediate. Phosphorylation of 25 as described in reference 11 yielded triphosphate 26 and N⁴-cyclized product 27 in 1:1 ratio. They were easily separated on Sephadex DEAE A-25 ion exchange column using 0.1-0.8M TEAB gradient. It appears that under basic conditions the free primary amine can displace any remaining intact 4-NHBz group leading to the cyclized product. This is similar to displacement of 4-triazolyl group by primary amine as mentioned above.

We reasoned that utilization of N^4 -unprotected cytidine will solve this problem. This lead to an improved synthesis of 26: Iodination of 2^3 -deoxy- 2^3 -fluorocytidine (28) provided the 5-iodo derivative 29 in 58% yield. This compound was then smoothly converted into 5-(3-aminopropynyl) derivative 30. Hydrogenation afforded 5-(3-aminopropyl) derivative 31 which was phosphorylated directly with $POCl_3/PPi$ to afford 26 in 37% yield. Coupling of the 5^3 -triphosphate 26 with succinic anhydride yielded succinylated derivative 32 in 36% yield.

Synthesis of 5-Imidazoleacetic acid 2'-deoxy-5'-triphosphate uridine

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5-dintrophenylimidazoleacetic acid 2'-deoxy uridine nucleoside (80 mg) was dissolved in 5 ml of triethylphosphate while stirring under argon, and the reaction mixture was cooled to 0°C. Phosphorous oxychloride (1.8 eq. 22 ml) was added to the reaction mixture at 0°C, three more aliquots were added over the course of 48 hours at room temperature. The reaction mixture was then diluted with anhydrous MeCN (5 ml) and cooled to 0°C, followed by the addition of tributylamine (0.65 ml) and tributylammonium pyrophosphate (4.0 eq. 0.24 g). After 45 minutes, the reaction was quenched with 10 ml aq. methyl amine for four hours. After co-evaporation with MeOH (3x), purified material on DEAE Sephadex followed by RP chromatography to afford 15 mg of triphosphate. Synthesis of 2"(N-lysyl)-amino-2'-deoxy-cytidine Triphosphate

2'-(N-lysyl)-amino-2'-deoxy cytidine (0.180 g. 0.22 mmol) was dissolved in triethyl 20 phosphate (2.00 ml) under Ar. The solution was cooled to 0 °C in an ice bath. Phosphorus oxychloride (99.999%, 3 eq., 0.0672 mL) was added to the solution and the reaction was stirred for two hours at 0 °C. Tributylammonium pyrophosphate (4 eq., 0.400 g) was dissolved in 3.42 mL of acetonitrile and tribuytylamine (0.165 mL). Acetonitrile (1 mL) was added to the monophosphate solution followed by the pyrophosphate solution 25 which was added dropwise. The resulting solution was clear. The reaction was allowed to warm up to room temperature. After stirring for 45 minutes, methylamine (5 mL) was added and the reaction and stirred at room temperature for 2 hours. A biphasic mixture appeared (little beads at the bottom of the flask). TLC (7:1:2 iPrOH:NH4OH:H2O) showed the appearance of triphosphate material. The solution was concentrated, dissolved 30 in water and loaded on a newly prepared DEAE Sephadex A-25 column. The column was washed with a gradient up to 0.6 M TEAB buffer and the product eluted off in fractions

90-95. The fractions were analyzed by ion exchange HPLC. Each fraction showed one triphosphate peak that cluted at ~4.000 minutes. The fractions were combined and pumped down from methanol to remove buffer salt to yield 15.7 mg of product.

Synthesis of 2'-deoxy-2'-(L-histidine)amino Cytidine Triphosphate

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2'-[N-Fmoc, Nimid -dinitrophenyl-histidyl]amino-2'-cytidine (0.310 g, 4.04 mmol) was dissolved in triethyl phosphate (3 ml) under Ar. The solution was cooled to 0 °C. Phosphorus oxychloride (1.8 eq., 0.068 mL) was added to the solution and stored overnight in the freezer. The next morning TLC (10% MeOH in CH2Cl2) showed significant starting material, one more equivalent of POCl3 was added. After two hours, TLC still showed starting material. Tributylamine (0.303 mL) and Tributylammonium pyrophosphate (4 eq., 0.734 g) dissolved in 6.3 mL of acetonitrile (added dropwise) were added to the monophosphate solution. The reaction was allowed to warm up to room temperature. After stirring for 15 min, methylamine (10 mL) was added at room temperature and stirring continued for 2 hours, TLC (7:1:2 iPrOH:NH4OH:H2O) showed the appearance of triphosphate material. The solution was concentrated, dissolved in water and loaded on a DEAE Sephadex A-25 column. The column was washed with a gradient up to 0.6 M TEAB buffer and the product eluted off in fractions 170-179. The fractions were analyzed by ion exchange HPLC. Each fraction showed one triphosphate peak that eluted at ~6.77 minutes. The fractions were combined and pumped down from methanol to remove buffer salt to afford 17 mg of product.

Screening for Novel Enzymatic nucleic acid molecule Motifs Using Modified NTPs (Class I Motif)

Our initial pool contained 3 x 10¹⁴ individual sequences of 2'-amino-dCTP/2'-amino-dUTP RNA. We optimized transcription conditions in order to increase the amount of RNA product by inclusion of methanol and lithium chloride. 2'-amino-2'-deoxynucleotides do not interfere with the reverse transcription and amplification steps of selection and confer nuclease resistance. We designed the pool to have two binding arms complementary to the substrate, separated by the random 40 nucleotide region. The 16-mer substrate had two domains, 5 and 10 nucleotides long, that bind the pool, separated by an unpaired guanosine. On the 5' end of the substrate was a biotin attached by a C18 linker. This enabled us to link the substrate to a NeutrAvidinTM resin in a column format.

The desired reaction would be cleavage at the unpaired G upon addition of magnesium cofactor followed by dissociation from the column due to instability of the 5 base pair helix. A detailed protocol follows:

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Enzymatic nucleic acid molecule Pool Prep: The initial pool DNA was prepared by converting the following template oligonucleotides into double-stranded DNA by filling in with taq polymerase. (template=5'-ACC CTC ACT AAA GGC CGT (N)40 GGT TGC ACA CCT TTC-3'; primer 1=5'-CAC TTA GCA TTA ACC CTC ACT AAA GGC CGT-3'; primer 2=5'-TAA TAC GAC TCA CTA TAG GAA AGG TGT GCA ACC-3'.) All DNA oligonucleotides were synthesized by Operon technologies. Template oligos were purified by denaturing PAGE and Sep-pak chromatography columns (Waters). RNA substrate oligos were using standard solid phase chemistry and purified by denaturing PAGE followed by ethanol precipitation. Substrates for *in vitro* cleavage assays were 5'-end labeled with gamma-³²P-ATP and T4 polynucleotide kinase followed by denaturing

PAGE purification and ethanol precipitation.

5 nmole of template, 10 nmole of each primer and 250 U tag polymerase were incubated in a 10 ml volume with 1X PCR buffer (10 mM tris-HCl (pH 8.3), 1.5 mM MgCl₂, 50 mM KCl) and 0.2 mM each dNTP as follows: 94°C, 4 minutes; (94°C, 1 min; 42°C, 1 min; 72°C, 2 min) through four cycles; and then 72°C, for 10 minutes. The product was analyzed on 2% Separide™ agarose gel for size and then was extracted twice with buffered phenol, then chloroform-isoamyl alcohol, and ethanol precipitated. The initial RNA pool was made by transcription of 500 pmole (3 x 10¹⁴ molecules) of this DNA as follows. Template DNA was added to 40 mM tris-HCl (pH 8.0), 12 mM MgCl₂, 5 mM dithiothreitol (DTT), 1 mM spermidine, 0.002% triton X-100, 1 mM LiCl, 4% PEG-8000, 10% methanol, 2 mM ATP, 2 mM GTP, 2 mM 2'-amino-dCTP, 2 mM 2'amino-dUTP, 5 U/ml inorganic pyrophosphatase, and 5 U/ul T7 RNA polymerase at room temperature for a total volume of 1 ml. A separate reaction contained a trace amount of alpha-32P-GTP for detection. Transcriptions were incubated at 37°C for 2 hours followed by addition of equal volume STOP buffer (94% formamide, 20 mM EDTA, 0.05% bromophenol blue). The resulting RNA was purified by 6% denaturing PAGE gel, SeppakTM chromatography, and ethanol precipitated.

INITIAL SELECTION: 2 nmole of 16 mer 5'-biotinylated substrate (5'-biotin-C18 linker-GCC GUG GGU UGC ACA C-3') was linked to 200 µl UltraLink Immobilized

NeutrAvidin™ resin (400 µl slurry, Pierce) in binding buffer (20 mM NaPO₄ (pH 7.5), 150 mM NaCl) for 30 minutes at room temperature. The resulting substrate column was washed with 2 ml binding buffer followed by 2 ml column buffer (50 mM tris-HCl (pH 8.5), 100 mM NaCl, 50 mM KCl). The flow was capped off and 1000 pmole of initial 5 pool RNA in 200 ul column buffer was added to the column and incubated 30 minutes at room temperature. The column was uncapped and washed with 2 ml column buffer, then capped off. 200 µl elution buffer (=column buffer + 25 mM MgCl₂) was added to the column and allowed to incubate 30 minutes at room temperature. The column was uncapped and eluent collected followed by three 200 ul elution buffer washes. The 10 eluent/washes were ethanol precipitated using glycogen as carrier and rehydrated in 50 µl sterile H2O. The eluted RNA was amplified by standard reverse transcription/PCR amplification techniques. 5-31 ul RNA was incubated with 20 pmol of primer 1 in 14 ul volume 90° for 3 min then placed on ice for 1 minute. The following reagent were added (final concentrations noted): 1X PCR buffer, 1 mM each dNTP, 2 U/ul RNase Inhibitor, 15 10 U/µl SuperScript™ II reverse transcriptase. The reaction was incubated 42° for 1 hour followed by 95° for 5 min in order to inactivate the reverse transcriptase. The volume was then increased to 100 µl by adding water and reagents for PCR: 1X PCR buffer, 20 pmol primer 2, and 2.5 U tag DNA polymerase. The reaction was cycled in a Hybaid thermocycler: 94°, 4 min: (94°C, 30 sec; 54°C, 30 sec; 72°C, 1 min) X 25; 72°C, 5 min. 20 Products were analyzed on agarose gel for size and ethanol precipitated. One-third to onefifth of the PCR DNA was used to transcribe the next generation, in 100 µl volume, as described above. Subsequent rounds used 20 pmol RNA for the column with 40 pmol substrate.

TWO COLUMN SELECTION: At generation 8 (G8), the column selection was

changed to the two column format. 200 pmoles of 22 mer 5'-biotinylated substrate (5'biotin-C18 linker-GCC GUG GGU UGC ACA CCU UUC C-C18 linker-thiol modifier C6
S-S-inverted abasic-3') was used in the selection column as described above. Elution was
in 200 µl elution buffer followed by a 1 ml elution buffer wash. The 1200 µl eluent was
passed through a product trap column by gravity. The product trap column was prepared

as follows: 200 pmol 16 mer 5'-biotinylated "product" (5'-GGU UGC ACA CCU UUC
C-C18 linker-biotin-3') was linked to the column as described above and the column was
equilibrated in elution buffer. Eluent from the product column was precipitated as

previously described. The products were amplified as above only with 2.5-fold more volume and 100 pmol each primer. 100 µl of the PCR reaction was used to do a cycle course; the remaining fraction was amplified the minimal number of cycles needed for product. After 3 rounds (G11), there was visible activity in a single turnover cleavage assay. By generation 13, 45% of the substrate was cleaved at 4 hours; kobs of the pool was 0.037 min⁻¹ in 25 mM MgCl₂. We subcloned and sequenced generation 13; the pool was still very diverse. Since our goal was a enzymatic nucleic acid molecule that would work in a physiological environment, we decided to change selection pressure rather than exhaustively catalog G13.

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Reselection of the N40 pool was started from G12 DNA. Part of the G12 DNA was subjected to hypermutagenic PCR (Vartanian et al., 1996, Nucleic Acids Research 24, 2627-2631) to introduce a 10% per position mutation frequency and was designated N40H. At round 19, part of the DNA was hypermutagenized again, giving N40M and N40HM (a total of 4 parallel pools). The column substrates remained the same; buffers were changed and temperature of binding and elution was raised to 37°C. Column buffer was replaced by physiological buffer (50 mM tris-HCl (pH 7.5), 140 mM KCl, 10 mM NaCl) and elution buffer was replaced by 1 mM Mg buffer (physiological buffer + 1 mM MgCl₂). Amount of time allowed for the pool to bind the column was eventually reduced to 10 min and elution time was gradually reduced from 30 min to 20 sec. Between rounds 18 and 23, k_{obs} for the N40 pool stayed relatively constant at 0.035-0.04 min ¹. Generation 22 from each of the 4 pools was cloned and sequenced.

CLONING AND SEQUENCING: Generations 13 and 22 were cloned using Novagen's Perfectly Blunt™ Cloning kit (pT7Blue-3 vector) following the kit protocol. Clones were screened for insert by PCR amplification using vector-specific primers.

Positive clones were sequenced using ABI Prism 7700 sequence detection system and vector-specific primer. Sequences were aligned using MacVector software; two-dimensional folding was performed using Mulfold software (Zuker., 1989, Science 244, 48-52; Jaeger et al., 1989, Biochemistry 86, 7706-7710; Jaeger et al., 1989, R. F. Doolittle ed., Methods in Enzymology, 183, 281-306). Individual clone transcription units were constructed by PCR amplification with 50 pmol each primer 1 and primer 2 in 1X PCR buffer, 0.2 mM each dNTP, and 2.5 U of taq polymerase in 100 µl volume cycled as follows: 94°C, 4 min; (94°C, 30 sec; 54°C, 30 sec; 72°C, 1 min) X 20; 72°C, 5 min.

Transcription units were ethanol precipitated, rehydrated in 30 μ l H2O, and 10 μ l was

transcribed in 100 µl volume and purified as previously described. Thirty-six clones from each pool were sequenced and were found to be variations of the same consensus motif. Unique clones were assayed for activity in 1 mM MgCl2 and physiological conditions; nine clones represented the consensus sequence and were used in subsequent experiments. There were no mutations that significantly increased activity; most of the mutations were in regions believed to be duplex, based on the proposed secondary structure. In order to make the motif shorter, we deleted the 3'-terminal 25 nucleotides necessary to bind the primer for amplification. The measured rates of the full length and truncated molecules were both 0.04 min-1; thus we were able reduce the size of the motif from 86 to 61 nucleotides. The molecule was shortened even further by truncating base pairs in the stem loop structures as well as the substrate recognition arms to yield a 48 nucleotide molecule. In addition, many of the ribonucleotides were replaced with 2-O-methyl modified nucleotides to stabilize the molecule. An example of the new motif is given in Figure 13. Those of ordinary skill in the art will recognize that the molecule is not limited to the chemical modifications shown in the figure and that it represents only one possible chemically modified molecule.

Kinetic Analysis:

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Single turnover kinetics were performed with trace amounts of 5'-²⁹P-labeled substrate and 10-1000 nM pool of enzymatic nucleic acid molecule. 2X substrate in 1X buffer and 2X pool/enzymatic nucleic acid molecule in 1X buffer were incubated separately 90° for 3 min followed by equilibration to 37° for 3 min. Equal volume of 2X substrate was added to pool/enzymatic nucleic acid molecule at t₀ and the reaction was incubated at 37°C. Time points were quenched in 1.2 vol STOP buffer on ice. Samples were heated to 90°C for 3 min prior to separation on 15% sequencing gels. Gels were imaged using a PhosphorImager and quantitated using ImageQuant™ software (Molecular Dynamics). Curves were fit to double-exponential decay in most cases, although some of the curves required linear fits.

STABILITY: Serum stability assays were performed as previously described (Beigelman et al., 1995, J. Biol. Chem. 270, 25702-25708). 1 µg of 5'-32P-labeled

synthetic enzymatic nucleic acid molecule was added to 13 µl cold and assayed for decay in human serum. Gels and quantitation were as described in kinetics section.

SUBSTRATE REQUIREMENTS: Table 60 outlines the substrate requirements for Class I motif. Substrates maintained Watson-Crick or wobble base pairing with mutant Class I constructs. Activity in single turnover kinetic assay is shown relative to wild type Class I and 22 mer substrate (50 mM Tris-HCL (pH 7.5), 140 mM KCl, 10 mM NaCl, 1 mM MgCl₂, 100 nM ribozyme, 5 nM substrate, 37°C).

RANDOM REGION MUTATION ALIGNMENT: Table 61 outlines the random region alignment of 134 clones from generation 22 (1.x = N40, 2.x = N40M, 3.x = N40H, 4.x = N40HM). The number of copies of each mutant is in parenthesis in the table, deviations from consensus are shown. Mutations that maintain base pair U19:A34 are shown in italic. Activity in single turnover kinetic assay is shown relative to the G22 pool rate (50 mM Tris-HCL pH 7.5, 140 mM KCl, 10 mM NaCl, 1 mM MgCl₂, 100 nM ribozyme, trace substrate, 37° C).

STEM TRUNCATION AND LOOP REPLACEMENT ANALYSIS: Figure 25 shows a representation of Class I ribozyme stem truncation and loop replacement analysis. The $K_{\rm rel}$ is compared to a 61 mer Class I ribozyme measured as described above. Figure 26 shows examples of Class I ribozymes with truncated stem(s) and/or non-nucleotide linker replaced loop structures.

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Inhibition of HCV Using Class I (Amberzyme) Motif

During HCV infection, viral RNA is present as a potential target for enzymatic nucleic acid molecule cleavage at several processes: uncoating, translation, RNA replication and packaging. Target RNA may be more or less accessible to enzymatic nucleic acid molecule cleavage at any one of these steps. Although the association between the HCV initial ribosome entry site (IRES) and the translation apparatus is mimicked in the HCV 5'UTR/luciferase reporter system, these other viral processes are not represented in the OST7 system. The resulting RNA/protein complexes associated with the target viral RNA are also absent. Moreover, these processes may be coupled in an HCV-infected cell which could further impact target RNA accessibility. Therefore, we

tested whether enzymatic nucleic acid molecules designed to cleave the HCV 5'UTR could effect a replicating viral system.

Recently, Lu and Wimmer characterized an HCV-poliovirus chimera in which the poliovirus IRES was replaced by the IRES from HCV (Lu & Wimmer, 1996, *Proc. Natl. Acad. Sci. USA.* 93, 1412-1417). Poliovirus (PV) is a positive strand RNA virus like HCV, but unlike HCV is non-enveloped and replicates efficiently in cell culture. The HCV-PV chimera expresses a stable, small plaque phenotype relative to wild type PV.

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The capability of the new enzymatic nucleic acid molecule motifs to inhibit HCV RNA intracellularly was tested using a dual reporter system that utilizes both firefly and Renilla luciferase (Figure 14). A number of enzymatic nucleic acid molecules having the new class I motif (Amberzyme) were designed and tested (Table 56). The Amberzyme ribozymes were targeted to the 5° HCV UTR region, which when cleaved, would prevent the translation of the transcript into luciferase. OST-7 cells were plated at 12,500 cells per well in black walled 96-well plates (Packard) in medium DMEM containing 10% fetal bovine serum, 1% pen/strep, and 1% L-glutamine and incubated at 37°C overnight. A plasmid containing T7 promoter expressing 5° HCV UTR and firefly luciferase (T7C1-341 (Wang et al., 1993, J. of Virol. 67, 3338-3344)) was mixed with a pRLSV40 Renilla control plasmid (Promega Corporation) followed by enzymatic nucleic acid molecule, and cationic lipid to make a 5X concentration of the reagents (T7C1-341 (4 μg/ml), pRLSV40 renilla luciferase control (6 μg/ml), enzymatic nucleic acid molecule (250 nM), transfection reagent (28.5 μg/ml).

The complex mixture was incubated at 37° C for 20 minutes. The media was removed from the cells and $120 \,\mu$ l of Opti-mem media was added to the well followed by $30 \,\mu$ l of the 5X complex mixture. $150 \,\mu$ l of Opti-mem was added to the wells holding the untreated cells. The complex mixture was incubated on OST-7 cells for 4 hours, lysed with passive lysis buffer (Promega Corporation) and luminescent signals were quantified using the Dual Luciferase Assay Kit using the manufacturer's protocol (Promega Corporation). The data shown in Figure 15 is a dose curve of enzymatic nucleic acid molecule targeting site 146 of the HCV RNA and is presented as a ratio between the firefly and Renilla luciferase fluorescence. The enzymatic nucleic acid molecule was able to reduce the quantity of HCV RNA at all enzymatic nucleic acid molecule concentrations

yielding an IC₅₀ of approximately 5 nM. Other sites were also efficacious (Figure 16), in particular enzymatic nucleic acid molecules targeting sites 133, 209, and 273 were also able to reduce HCV RNA compared to the irrelevant (IRR) controls.

5 Cleavage of Substrates Using Completely Modified class I (Amberzyme) enzymatic nucleic acid molecule

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The ability of an enzymatic nucleic acid, which is modified at every 2' position to cleave a target RNA was tested to determine if any ribonucleotide positions are necessary in the Amberzyme motif. Enzymatic nucleic acid molecules were constructed with 2'-O-methyl, and 2'-amino (NH₂) nucleotides and included no ribonucleotides (**Table 56**; gene name: no ribo) and kinetic analysis was performed as described in example 13. 100 nM enzymatic nucleic acid was mixed with trace amounts of substrate in the presence of 1 mM MgCl₂ at physiological conditions (37°C). The Amberzyme with no ribonucleotide present in it has a K_{rel} of 0.13 compared to the enzymatic nucleic acid with a few ribonucleotides present in the molecule shown in **Table 56** (ribo). This shows that Amberzyme enzymatic nucleic acid molecule may not require the presence of 2'-OH groups within the molecule for activity.

Substrate Recognition Rules for Class II (zinzyme) enzymatic nucleic acid molecules

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Class II (zinzyme) ribozymes were tested for their ability to cleave base-paired substrates with all sixteen possible combinations of bases immediately 5' and 3' proximal to the bulged cleavage site G. Ribozymes were identical in all remaining positions of their 7 base pair binding arms. Activity was assessed at two and twenty-four hour time points under standard reaction conditions [20 mM HEPES pH 7.4, 140 mM KCl, 10 mM NaCl, 1 mM MgCl₂, 1 mM CaCl₂ – 37° Cl. Figure 19 shows the results of this study. Base paired substrate UGG (not shown in the figure) cleaved as poorly as CGG shown in the figure. The figure shows the cleavage site substrate triplet in the 5'-3' direction and 2 and 24 hour time points are shown top to bottom respectively. The results indicate the cleavage site triplet is most active with a 5'-Y-G-H-3' (where Y is C or U and H is A, C or U with cleavage between G and H); however, activity is detected particularly with the 24 hour time point for most paired substrates. All positions outside of the cleavage triplet were found to tolerate any base pairings (data not shown).

All possible mispairs immediately 5' and 3' proximal to the bulged cleavage site G were tested to a class II ribozyme designed to cleave a 5'-C-G-C -3'. It was observed the 5' and 3' proximal sites are as active with G:U wobble pairs, in addition, the 5' proximal site will tolerate a mismatch with only a slight reduction in activity [data not shown].

Screening for Novel Enzymatic nucleic acid molecule Motifs (Class II Motifs)

The selections were initiated with pools of > 10¹⁴ modified RNA's of the following sequence: 5'-GGGAGGAGGGAGUGCCU(N)₁₅ UGCCGCGCUCGCUCCCAGUCC-3'. The RNA was enzymatically generated using the mutant T7 Y639F RNA polymerase prepared by Rui Souza. The following modified NTP's were incorporated: 2'-deoxy-2'-fluoro-adenine triphosphate, 2'-deoxy-2'-fluoro-uridine triphosphate or 2'-deoxy-2'-fluoro-5-[(N-imidazole-4acetyl)propyl amine] uridine triphosphate, and 2'-deoxy-2'-amino-cytidine triphosphate; natural guanidine triphosphate was used in all selections so that alpha -3²P-GTP could be used to label pool RNA's. RNA pools were purified by denaturing gel electrophoresus 8% polyacrilamide 7 M Urea.

The following target RNA (resin A) was synthesized and coupled to Iodoacetyl

Ultralink™ resin (Pierce) by the supplier's proceedure:5' -b-L
GGACUGGGAGCGAGCGCGGCAGGCACU GAAG-L-S-B-3'; where b is biotin (Glenn

Research cat# 10-1953-nn), L is polyethylene glycol spacer (Glenn Research cat# 10-1918nn), S is thiol-modifier C6 S-S (Glenn Research cat# 10-1936-nn), B is a standard inverted deoxy abasic.

RNA pools were added to 100 µl of 5 µM Resin A in the buffer A (20 mM HEPES pH 7.4, 140 mM KCL, 10 mM NaCl) and incubated at 22°C for 5 minutes. The 5 temperature was then raised to 37°C for 10 minutes. The resin was washed with 5 ml buffer A. Reaction was triggered by the addition of buffer B(20 mM HEPES pH 7.4, 140 mM KCL, 10 mM NaCl, 1 mM MgCl₂, 1 mM CaCl₂). Incubation proceeded for 20 minutes in the first generation and was reduced progressively to 1 minute in the final generations; with 13 total generations. The reaction eluent was collected in 5 M NaCl to 10 give a final concentration of 2 M NaCl. To this was added 100 µl of 50% slurry Ultralink NeutraAvidin™ (Pierce). Binding of cleaved biotin product to the avidin resin was allowed by 20 minute incubation at 220 C. The resin was subsequently washed with 5 ml of 20 mM HEPES pH 7.4. 2 M NaCl. Desired RNA's were removed by a 1.2 ml denaturing wash 1M NaCl, 10 M Urea at 94° C over 10 minutes. RNA's were double 15 precipitated in 0.3 M sodium acetate to remove Cl' ions inhibitory to reverse transcription. Standard protocols of reverse transcription and PCR amplification were performed. RNA's were again transcribed with the modified NTP's described above. After 13 generations cloning and sequencing provided 14 sequences which were able to cleave the target substrate. Six sequences were characterized to determine secondary structure and 20 kinetic cleavage rates. The structures and kinetic data are given in Figure 17. The sequences of eight other enzymatic nucleic acid molecule sequences are given in Table 57. The size, sequence, and chemical compositions of these molecules can be modified as described below or using other techniques well known in the art.

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Nucleic Acid Catalyst Engineering

Sequence, chemical and structural variants of Class I and Class II enzymatic nucleic acid molecule can be engineered and re-engineered using the techniques shown in this application and known in the art. For example, the size of class I and class II enzymatic nucleic acid molecules can, be reduced or increased using the techniques known in the art (Zaug et al., 1986, Nature, 324, 429; Ruffner et al., 1990, Biochem., 29, 10695; Beaudry et

al., 1990, Biochem., 29, 6534; McCall et al., 1992, Proc. Natl. Acad. Sci., USA., 89, 5710; Long et al., 1994, supra; Hendry et al., 1994, BBA 1219, 405; Benseler et al., 1993, JACS, 115, 8483; Thompson et al., 1996, Nucl. Acids Res., 24, 4401; Michels et al., 1995, Biochem., 34, 2965; Been et al., 1992, Biochem., 31, 11843; Guo et al., 1995, EMBO. J., 14, 368; Pan et al., 1994, Biochem., 33, 9561; Cech, 1992, Curr. Op. Struc. Bio., 2, 605; Sugiyama et al., 1996, FEBS Lett., 392, 215; Beigelman et al., 1994, Biocrg. Med. Chem., 4, 1715; Santoro et al., 1997, PNAS 94, 4262; all are incorporated in their totality by reference herein), to the extent that the overall catalytic activity of the ribozyme is not significantly decreased.

Further rounds of *in vitro* selection strategies described herein and variations thereof can be readily used by a person skilled in the art to evolve additional nucleic acid catalysts and such new catalysts are within the scope of the instant invention.

Example 16: Activity of Class II (zinzyme) nucleic acid catalysts to inhibit HER2 gene expression

Applicant has designed, synthesized and tested several class Π (zinzyme) ribozymes targeted against HER2 RNA (see, for example, Tables 58, 59, and 62) in cell proliferation RNA reduction assays.

Proliferation assay:

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The model proliferation assay used in the study can require a cell-plating density of 2000-10000 cells/well in 96-well plates and at least 2 cell doublings over a 5-day treatment period. Cells used in proliferation studies were either human breast or ovarian cancer cells (SKBR-3 and SKOV-3 cells respectively). To calculate cell density for proliferation assays, the FIPS (fluoro-imaging processing system) method well known in the art was used. This method allows for cell density measurements after nucleic acids are stained with CyQuant® dye, and has the advantage of accurately measuring cell densities over a very wide range 1.000-100.000 cells/well in 96-well format.

Ribozymes (50-200 nM) were delivered in the presence of cationic lipid at 2.0-5.0 µg/mL and inhibition of proliferation was determined on day 5 post-treatment. Two full ribozyme screens were completed resulting in the selection of 14 ribozymes. Class II (zinzyme) ribozymes against sites, 314 (RPI No. 18653), 443 (RPI No. 18680), 597 (RPI

No. 18697), 659 (RPI No. 18682), 878 (RPI Nos. 18683 and 18654), 881 (RPI Nos. 18684 and 18685) 934 (RPI No. 18651), 972 (RPI No. 18656, 19292, 19727, 19728, and 19293), 1292 (RPI No. 18726), 1541 (RPI No. 18687), 2116 (RPI No. 18729), 2932 (RPI No. 18678), 2540 (RPI No. 18715), and 3504 (RPI No. 18710) caused inhibition of proliferation ranging from 25-80% as compared to a scrambled control ribozyme. An example of results from a cell culture assay is shown in Figure 20. Referring to Figure 20, Class II ribozymes targeted against HER2 RNA are shown to cause significant inhibition of proliferation of cells. This shows that ribozymes, for instance the Class II (zinzyme) ribozymes are capable of inhibiting HER2 gene expression in mammalian cells.

RNA assay:

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RNA was harvested 24 hours post-treatment using the Qiagen RNeasy® 96 procedure. Real time RT-PCR (TaqMan® assay) was performed on purified RNA samples using separate primer/probe sets specific for either target HER2 RNA or control actin RNA (to normalize for differences due to cell plating or sample recovery). Results are shown as the average of triplicate determinations of HER2 to actin RNA levels post-treatment. Figure 30 shows class II ribozyme (zinzyme) mediated reduction in HER2 RNA targeting site 972 vs a scrambled attenuated control.

20 Dose response assays:

Active ribozyme was mixed with binding arm-attenuated control (BAC) ribozyme to a final oligonucleotide concentration of either 100, 200 or 400 nM and delivered to cells in the presence of cationic lipid at 5.0 μg/mL. Mixing active and BAC in this manner maintains the lipid to ribozyme charge ratio throughout the dose response curve. HER2 RNA reduction was measured 24 hours post-treatment and inhibition of proliferation was determined on day 5 post-treatment. The dose response antiproliferation results are summarized in Figure 31 and the dose-dependent reduction of HER2 RNA results are summarized in Figure 32. Figure 33 shows a combined dose response plot of both antiproliferation and RNA reduction data for a class II ribozyme targeting site 972 of HER2 RNA (RPI 19293).

Example 17: Reduction of ribose residues in Class II (zinzyme) nucleic acid catalysts

Class II (zinzyme) nucleic acid catalysts were tested for their activity as a function ribonucleotide content. A Zinzyme having no ribonucleotide residue (ie., no 2'-OH group at the 2' position of the nucleotide sugar) against the K-Ras site 521 was designed. This molecules were tested utilizing the chemistry shown in Figure 27a. The in vitro catalytic activity zinzyme construct was not significantly effected (the cleavage rate reduced only 10 fold).

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The Kras zinzyme shown in Figure 27a was tested in physiological buffer with the divalent concentrations as indicated in the legend (high NaCl is an altered monovalent condition shown) of Figure 28. The 1 mM Ca⁺⁺ condition yielded a rate of 0.005 min⁻¹ while the 1 mM Mg⁺⁺ condition yielded a rate of 0.002 min⁻¹. The ribose containing wild type yields a rate of 0.05 min⁻¹ while substrate in the absence of zinzyme demonstrates less than 2% degradation at the longest time point under reaction conditions shown. This illustrates a well-behaved cleavage reaction done by a non-ribose containing catalyst with only a 10-fold reduced cleavage as compared to ribonucleotide-containing zinzyme and vastly above non-catalyzed degradation.

A more detailed investigation into the role of ribose positions in the Class II (zinzyme) motif was carried out in the context of the HER2 site 972 (Applicant has further designed a fully modified Zinzyme as shown in Figure 27b targeting the HER2 RNA site 972). Figure 29 is a diagram of the alternate formats tested and their relative rates of catalysis. The effect of substitution of ribose G for the 2'-O-methyl C-2'-O-methyl A in the loop of Zinzyme (see Figure 34) was insignificant when assayed with the Kras target but showed a modest rate enhancement in the HER2 assays. The activity of all Zinzyme motifs, including the fully stabilized "0 ribose" (RPI 19727) are well above background noise level degradation. Zinzyme with only two ribose positions (RPI 19293) are sufficient to restore "wild-type" activity. Motifs containing 3 (RPI 19729), 4 (RPI 19730) or 5 ribose (RPI 19731) positions demonstrated a greater extent of cleavage and profiles almost identical to the 2 ribose motif. Applicant has thus demonstrated that a Zinzyme with no ribonucleotides present at any position can catalyze efficient RNA cleavage activity. Thus, Zinzyme enzymatic nucleic acid molecules do not require the presence of 2'-OH group within the molecule for catalytic activity.

Example 18: Activity of reduced ribose containing Class II (zinzyme) nucleic acid catalysts to inhibit HER2 gene expression

A cell proliferation assay for testing reduced ribo class II (zinzyme) nucleic acid catalysts (50-400 nM) targeting HER2 site 972 was performed as described in example 19. The results of this study are summarized in Figure 35. These results indicate significant inhibition of HER2 gene expression using stabilized Class II (zinzyme) motifs, including two ribo (RPI 19293), one ribo (RPI 19728), and non-ribo (RPI 19727) containing nucleic acid catalysts.

10 Applications

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The use of NTP's described in this invention have several research and commercial applications. These modified nucleotide triphosphates can be used for in vitro selection (evolution) of oligonucleotides with novel functions. Examples of in vitro selection protocols are incorporated herein by reference (Joyce, 1989, Gene, 82, 83-87; Beaudry et al., 1992, Science 257, 635-641; Joyce, 1992, Scientific American 267, 90-97; Breaker et al., 1994, TIBTECH 12, 268; Bartel et al., 1993, Science 261:1411-1418; Szostak, 1993, TIBS 17, 89-93; Kumar et al., 1995, FASEB J., 9, 1183; Breaker, 1996, Curr. Op. Biotech., 7, 442).

Additionally, these modified nucleotide triphosphates can be employed to generate modified oligonucleotide combinatorial chemistry libraries. Several references for this technology exist (Brenner et al., 1992, PNAS 89, 5381-5383, Eaton, 1997, Curr. Opin. Chem. Biol. 1, 10-16), which are all incorporated herein by reference.

Diagnostic uses

Enzymatic nucleic acid molecules of this invention may be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of specific RNA in a cell. The close relationship between enzymatic nucleic acid molecule activity and the structure of the target RNA allows the detection of mutations in any region of the molecule which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple enzymatic nucleic acid molecules described in this invention, one may map nucleotide changes which are important to RNA structure and function in vitro, as well as in cells and tissues. Cleavage of target RNAs with enzymatic nucleic acid

molecules may be used to inhibit gene expression and define the role (essentially) of specified gene products in the progression of disease. In this manner, other genetic targets may be defined as important mediators of the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combinational therapies (e.g., multiple enzymatic nucleic acid molecules targeted to different genes, enzymatic nucleic acid molecules coupled with known small molecule inhibitors, radiation or intermittent treatment with combinations of enzymatic nucleic acid molecules and/or other chemical or biological molecules). Other in vitro uses of enzymatic nucleic acid molecules of this invention are well known in the art, and include detection of the presence of mRNAs associated with related conditions. Such RNA is detected by determining the presence of a cleavage product after treatment with a enzymatic nucleic acid molecule using standard methodology.

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In a specific example, enzymatic nucleic acid molecules which can cleave only wildtype or mutant forms of the target RNA are used for the assay. The first enzymatic nucleic acid molecule is used to identify wild-type RNA present in the sample and the second 15 enzymatic nucleic acid molecule will be used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant RNA will be cleaved by both enzymatic nucleic acid molecules to demonstrate the relative enzymatic nucleic acid molecule efficiencies in the reactions and the absence of cleavage of the "nontargeted" RNA species. The cleavage products from the synthetic substrates will also serve to generate size markers for the analysis of wild type and mutant RNAs in the sample population. Thus each analysis can involve two enzymatic nucleic acid molecules, two substrates and one unknown sample which can be combined into six reactions. The presence of cleavage products can be determined using an RNAse protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype is adequate to establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels will be adequate and will decrease the cost of the initial diagnosis. Higher mutant form to

wild-type ratios will be correlated with higher risk whether RNA levels are compared qualitatively or quantitatively.

Additional Uses

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Potential usefulness of sequence-specific enzymatic nucleic acid molecules of the instant invention can have many of the same applications for the study of RNA that DNA restriction endonucleases have for the study of DNA (Nathans et al., 1975 Ann. Rev. Blochem. 44:273). For example, the pattern of restriction fragments can be used to establish sequence relationships between two related RNAs, and large RNAs could be specifically cleaved to fragments of a size more useful for study. The ability to engineer sequence specificity of the enzymatic nucleic acid molecule is ideal for cleavage of RNAs of unknown sequence. Applicant describes the use of nucleic acid molecules to down-regulate gene expression of target genes in bacterial, microbial, fungal, viral, and eukarvotic systems including plant, or mammalian cells.

All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising",

"consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

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In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

Thus, additional embodiments are within the scope of the invention and within the following claims

Table 1

TABLE 1

Characteristics of naturally occurring ribozymes

Group I Introns

- Size: ~150 to >1000 nucleotides.
- Requires a U in the target sequence immediately 5' of the cleavage site.
- Binds 4-6 nucleotides at the 5'-side of the cleavage site.
- Reaction mechanism: attack by the 3'-OH of guanosine to generate cleavage products with 3'-OH and 5'-guanosine.
- Additional protein cofactors required in some cases to help folding and maintainance of the active structure.
- Over 300 known members of this class. Found as an intervening sequence in Tetrahymena thermophila rRNA, fungal mitochondria, chloroplasts, phage T4, blue-green algae, and others.
- Major structural features largely established through phylogenetic comparisons, mutagenesis, and biochemical studies [^{1,11}].
- Complete kinetic framework established for one ribozyme [iii, iv, v, vi].
- Studies of ribozyme folding and substrate docking underway [vii, viii, ix].
- Chemical modification investigation of important residues well established [x,xi].
- The small (4-6 nt) binding site may make this ribozyme too non-specific for targeted RNA cleavage, however, the Tetrahymena group I intron has been used to repair a "defective" β-galactosidase message by the ligation of new β-galactosidase sequences onto the defective message [⁵⁰¹].

RNAse P RNA (M1 RNA)

- Size: ~290 to 400 nucleotides.
- RNA portion of a ubiquitous ribonucleoprotein enzyme.
- Cleaves tRNA precursors to form mature tRNA [xiii].
- Reaction mechanism: possible attack by M²⁺-OH to generate cleavage products with 3'-OH and 5'-phosphate.
- RNAse P is found throughout the prokaryotes and eukaryotes. The RNA subunit has been sequenced from bacteria, yeast, rodents, and primates.
- Recruitment of endogenous RNAse P for therapeutic applications is possible through hybridization of an External Guide Sequence (EGS) to the target RNA [xiv,xw]
- Important phosphate and 2' OH contacts recently identified [xvi,xvii]

Group II Introns

- Size: >1000 nucleotides.
- Trans cleavage of target RNAs recently demonstrated [xviii,xix].

Table 1

- Sequence requirements not fully determined.
- Reaction mechanism: 2'-OH of an internal adenosine generates cleavage products with 3'-OH and a "lariat" RNA containing a 3'-5' and a 2'-5' branch point.
- Only natural ribozyme with demonstrated participation in DNA cleavage [xx,xxi] in addition to RNA cleavage and ligation.
- Major structural features largely established through phylogenetic comparisons [xxii].
- Important 2' OH contacts beginning to be identified [xxiii]
- Kinetic framework under development [xxiv]

Neurospora VS RNA

- Size: ~144 nucleotides.
- Trans cleavage of hairpin target RNAs recently demonstrated [xxv].
- Sequence requirements not fully determined.
- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.
- Binding sites and structural requirements not fully determined.
 - Only 1 known member of this class. Found in Neurospora VS RNA.

Hammerhead Ribozyme

(see text for references)

- Size: ~13 to 40 nucleotides.
- Requires the target sequence UH immediately 5' of the cleavage site.
- Binds a variable number nucleotides on both sides of the cleavage site.
- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.
- 14 known members of this class. Found in a number of plant pathogens (virusoids) that use RNA as the infectious agent.
- Essential structural features largely defined, including 2 crystal structures [xxvi,xxvii]
- Minimal ligation activity demonstrated (for engineering through in vitro selection) [xxviii]
- Complete kinetic framework established for two or more ribozymes [xxix].
- Chemical modification investigation of important residues well established [xxx].

Hairpin Ribozyme

- Size: ~50 nucleotides.
- Requires the target sequence GUC immediately 3' of the cleavage site.
- Binds 4-6 nucleotides at the 5'-side of the cleavage site and a variable number to the 3'side of the cleavage site.
- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.
- 3 known members of this class. Found in three plant pathogen (satellite RNAs of the tobacco ringspot virus, arabis mosaic virus and chicory yellow mottle virus) which uses RNA as the infectious agent.
- Essential structural features largely defined [xxxi,xxxii,xxxiii,xxxiv]

Table 1

- Ligation activity (in addition to cleavage activity) makes ribozyme amenable to
 engineering through in vitro selection [xxxv]
- Complete kinetic framework established for one ribozyme [xxxvi].
- Chemical modification investigation of important residues begun [xxxviii].

Hepatitis Delta Virus (HDV) Ribozyme

- Size: ~60 nucleotides.
- Trans cleavage of target RNAs demonstrated [xxxix].
- Binding sites and structural requirements not fully determined, although no sequences 5'
 of cleavage site are required. Folded ribozyme contains a pseudoknot structure [xi].
- Reaction mechanism: attack by 2'-OH 5' to the scissile bond to generate cleavage products with 2',3'-cyclic phosphate and 5'-OH ends.
- Only 2 known members of this class. Found in human HDV.
- Circular form of HDV is active and shows increased nuclease stability [xli]

- Lisacek, Frederique; Diaz, Yolande; Michel, Francois. Automatic identification of group I intron cores in genomic DNA sequences. J. Mol. Biol. (1994), 235(4), 1206-17.
- #. Herschlag, Daniel, Cech, Thomas R. Catalysis of RNA cleavage by the Tetrahymena thermophila ribozyme. 1. Kinetic description of the reaction of an RNA substrate complementary to the active site. Biochemistry (1990), 29(44), 10159-71.
- * Herschlag, Daniel; Cecht, Thomas R. Catalysis of RNA cleavage by the Tetrahymena thermophila ribozyme. 2. Kinetic description of the reaction of an RNA substrate that forms a mismatch at the active site. Biochemistry (1990), 29(44), 1017-280.
- v. Knitt, Deborah S.; Herschlag, Daniel. pH Dependencies of the Tetrahymena Ribozyme Reveal an Unconventional Origin of an Apparent pKa. Biochemistry (1996), 35(5), 1560-70.
- Bevilacqua, Philip C.; Sugimoto, Naoki; Turner, Douglas H.. A mechanistic framework for the second step of splicing catalyzed by the Tetrahymena ribozyme. Biochemistry (1996), 35(2), 648-58.
- vii . Li, Yi; Bevilacqua, Philip C.; Mathews, David; Turner, Douglas H.. Thermodynamic and
- activation parameters for binding of a pyrene-labeled substrate by the Tetrahymena ribozyme: docking is not diffusion-controlled and is driven by a favorable entropy change. Biochemistry (1995), 34(44), 14394-9.
- Banerjee, Aloke Raj, Turner, Douglas H.. The time dependence of chemical modification reveals slow steps in the folding of a group I ribozyme. Biochemistry (1995), 34(19), 6504-12.
- Zarrinkar, Patrick P.; Williamson, James R.. The P9.1-P9.2 peripheral extension helps guide
- folding of the Tetrahymena ribozyme. Nucleic Acids Res. (1996), 24(5), 584-8.

 * Strobel, Scott A.; Cech, Thomas R. Minor groove recognition of the conserved G.cntdot U pair at
- the Tetrahyle Court A. Cost. Thomas R. Simos (Washington, D. C.) (1995), 267(5198), 675-9.
- s. Strobel, Scott A.; Cech, Thomas R., Exocyclic Amine of the Conserved C.cntdot U Pair at the Cleavage Site of the Tetrahymena Ribozyme Contributes to 5'-Splice Site Selection and Transition State Stabilization. Biochemistry (1996), 35(4), 1201-11.
- ^{xii}. Sullenger, Bruce A.; Cech, Thomas R.. Ribozyme-mediated repair of defective mRNA by targeted trans-splicing. Nature (London) (1994), 371(6498), 619-22.
- Robertson, H.D.; Altman, S.; Smith, J.D. J. Biol. Chem., 247, 5243-5251 (1972).
- xiv. Forster, Anthony C.; Altman, Sidney. External guide sequences for an RNA enzyme. Science (Washington, D. C., 1883-) (1990), 249(4970), 783-6.
- xy. Yuan, Y.; Hwang, E. S.; Altman, S. Targeted cleavage of mRNA by human RNase P. Proc. Natl. Acad. Sci. USA (1992) 89, 8006-10.
- ivi . Harris, Michael E.; Pace, Norman R.. Identification of phosphates involved in catalysis by the

[.] Michel, Francois; Westhof, Eric. Slippery substrates. Nat. Struct. Biol. (1994), 1(1), 5-7.

Table 1

ribozyme RNase P RNA. RNA (1995), 1(2), 210-18.

- Pan, Tao; Loria, Andrew; Zhong, Kun. Probing of tertiary interactions in RNA: 2-hydroxyl-base contacts between the RNase P RNA and pre-tRNA. Proc. Natl. Acad. Sci. U. S. A. (1995), 92(26), 12510-14.
- xviii Pyle, Anna Marie; Green, Justin B.. Building a Kinetic Framework for Group II Intron Ribozyme Activity: Quantitation of Interdomain Binding and Reaction Rate. Biochemistry (1994), 33(9), 2716-25.
- Michels, William J. Jr.; Pyle, Anna Marie. Conversion of a Group II Intron into a New Multiple-Turnover Ribozyme that Selectively Cleaves Oligonucleotides: Elucidation of Reaction Mechanism and Structure/Function Relationships. Biochemistry (1995), 34(9), 2965-77.
- Zimmerly, Steven; Guo, Huatao; Eskes, Robert; Yang, Jian; Perlman, Philip S.; Lambowitz, Alan M.. A group II intron RNA is a catalytic component of a DNA endonuclease involved in intron mobility. Cell (Cambridge, Mass.) 1995, 83(4), 529-38.
- Griffin, Edmund A., Jr.; Qin, Zhifeng: Michels, Williams J., Jr.; Pyle, Anna Marie. Group II intron ribozymes that cleave DNA and RNA linkages with similar efficiency, and lack contacts with substrate 2'-hydroxyl groups. Chem. Biol. 1995.) 2(11), 761-70.
- xxii . Michel, Francois, Ferat, Jean Luc. Structure and activities of group II introns. Annu. Rev. Biochem. (1995), 64, 435-61.
- Biochem. (1995), 64, 435-61.

 ***iii . Abramovitz, Dana L.; Friedman, Richard A.; Pyle, Anna Marie. Catalytic role of 2'-hydroxyl
- groups within a group II intron active site. Science (Washington, D. C.) (1996), 271(5254), 1410-13.

 **av* Daniels, Danette L.; Michels, William J., Jr.; Pyle, Anna Marie. Two competing pathways for self-splicing by group II introns: a quantitative analysis of in vitro reaction rates and products. J. Mol. Biol. (1996), 256(1), 31-49.
- xw . Guo, Hans C. T.; Collins, Richard A.. Efficient trans-cleavage of a stem-loop RNA substrate by a ribozyme derived from Neurospora VS RNA. EMBO I. (1995), 14(2), 368-76.
- xxvi. Scott, W.G., Finch, J.T., Aaron, K. The crystal structure of an all RNA hammerhead ribozyme: Aproposed mechanism for RNA catalytic cleavage. Cell, (1995), 81, 991-1002.
- xvii . McKay, Structure and function of the hammerhead ribozyme: an unfinished story. RNA, (1996), 2, 395-403.
- xxviii . Long, D., Uhlenbeck, O., Hertel, K. Ligation with hammerhead ribozymes. US Patent No. 5,633,133.
- *** Hertel, K.J., Herschlag, D., Uhlenbeck, O. A kinetic and thermodynamic framework for the hammerhead ribozyme reaction. Biochemistry, (1994) 33, 3374-3385. Beigelman, L., et al., Chemical modifications of hammerhead ribozymes. J. Biol. Chem., (1995) 270, 25702-25708.
- xxx Beigelman, L., et al., Chemical modifications of hammerhead ribozymes. J. Biol. Chem., (1995) 270, 25702-25708.
- ****i. Hampel, Arnold; Tritz, Richard; Hicks, Margaret; Cruz, Phillip. 'Hairpin' catalytic RNA model: evidence for helixes and sequence requirement for substrate RNA. Nucleic Acids Res. (1990), 18(2), 299-304.
- xxxii . Chowrira, Bharat M.; Berzal-Herranz, Alfredo; Burke, John M.. Novel guanosine requirement for catalysis by the hairpin ribozyme. Nature (London) (1991), 354(6351), 320-2.
- Berzal-Herranz, Alfredo; Joseph, Simpson; Chowrira, Bharat M.; Butcher, Samuel E.; Burke, John M.. Essential nucleotide sequences and secondary structure elements of the hairpin ribozyme. EMBO J. (1993), 12(6), 2567-73.
- Joseph, Simpson; Berzal-Herranz, Alfredo; Chowrira, Bharat M.; Butcher, Samuel E.. Substrate selection rules for the hairpin ribozyme determined by in vitro selection, mutation, and analysis of mismatched substrates. Genes Dev. (1993), 7(1), 130-8.
- xxxv Berzal-Herranz, Alfredo; Joseph, Simpson; Burke, John M.. In vitro selection of active hairpin ribozymes by sequential RNA-catalyzed cleavage and ligation reactions. Genes Dev. (1992), 6(1), 129-34. xxvi. Hegg, Lisa A.; Fedor, Martha J.. Kinetics and Thermodynamics of Intermolecular Catalysis by Hairpin Ribozymes. Biochemistry (1995), 34(48), 15813-28.
- xxxvii . Grasby, Jane A.; Mersmann, Karin; Singh, Mohinder; Gait, Michael J.. Purine Functional Groups in Essential Residues of the Hairpin Ribozyme Required for Catalytic Cleavage of RNA. Biochemistry

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Table 1

(1995), 34(12), 4068-76.

Schmidt, Sabine; Beigelman, Leonid; Karpeisky, Alexander; Usman, Nassim; Sorensen, Ulrik S.; Gait, Michael J. Base and sugar requirements for RNA cleavage of essential nucleoside residues in internal loop B of the hairpin ribozyme: implications for secondary structure. Nucleic Acids Res. (1996), 24(4), 573-81.

xxxix. Perrotta, Anne T.; Been, Michael D. Cleavage of oligoribonucleotides by a ribozyme derived from the hepatitis .delta. virus RNA sequence. Biochemistry (1992), 31(1), 16-21.

^{al}. Perrotta, Anne T.; Been, Michael D.. A pseudoknot-like structure required for efficient selfcleavage of hepatitis delta virus RNA. Nature (London) (1991), 350(6317), 434-6.

^{ati}. Puttaraju, M.; Perrotta, Anne T.; Been, Michael D.. A circular trans-acting hepatitis delta virus ribozyme. Nucleic Acids Res. (1993), 21(18), 4253-8.

Table 2:

Table 2

A. 2.5 µmol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA Wait Time* 2'- O-methyl	Walt Time* 2'- O-methyl	Wait Time* RNA
Phosphoramidites	6.5	163 µL	45 sec	2.5 min	7.5 min
S-Ethyl Tetrazole	23.8	238 µL	45 sec	2.5 min	7.5 min
Acetic Anhydride	100	233 µL	5 sec	5 sec	5 sec
N-Methyl Imidazole	186	233 µL	5 sec	5 sec	5 sec
TCA	176	2.3 mL	21 sec	21 sec	21 sec
lodine	11.2	1.7 mL	45 sec	45 sec	45 sec
Beaucage	12.9	645 µL	100 sec	300 sec	300 sec
Acetonitrile	NA	6.67 mL	NA	NA	NA

B. 0.2 µmol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time ⁺ DNA	Wait Time* 2'- O-methyl	Wait Time* RNA
Phosphoramidites	15	31 µL	45 sec	233 sec	465 sec
S-Ethyl Tetrazole	38.7	31 pL	45 sec	233 min	465 sec
Acetic Anhydride	655	124 pL	5 sec	5 sec	5 sec
N-Methyl Imidazole	1245	124 pL	5 sec	5 sec	5 sec
TCA	200	732 µL	10 sec	10 sec	10 sec
lodine	20.6	244 pL	15 sec	15 sec	15 sec
Beaucage	7.7	232 µL	100 sec	300 sec	300 sec

Table 2

Acetonitrile	A N	2.64 mL NA	Υ V	N A	
	Ü	C. 0.2 µmol Synthesis Cycle 96 well Instrument	vell Instrument		
Reagent	Equivalents DNA/2'-O-methyl/Ribo	Amount DNA/2'-O-methyl/Ribo	Wait Time* DNA	Wait Time* 2'-O- methyl	Wait Time* Ribo
Phosphoramidites	22/33/66	40/60/120 µL	90 sec	180 sec	360sec
S-Ethyl Tetrazole	70/105/210	40/60/120 µL	90 sec	180 min	360 sec
Acetic Anhydride	265/265/265	20/20/50 hL	10 sec	10 sec	10 sec
N-Methyl Imidazole	502/502/502	20/20/20 hL	10 sec	10 sec	10 sec
TCA	238/475/475	250/500/500 µL	15 sec	15 sec	15 sec
lodine	6.8/6.8/6.8	30/80/80 hL	30 sec	30 sec	30 sec
Beaucage	34/51/51	80/120/120	100 sec	200 sec	200 sec
Acetonitrile	NA	1150/1150/1150 µL	NA	NA	NA

* Wait time does not include contact time during delivery.

Table 3: Human PTP-1B Hammerhead Ribozyme and Target Sequence

Nt. Position	Ribozyme Sequence	Seq. ID Nos.	Substrate Sequence	Seq. 1D Nos.
15	UGCCGCUC CUGAUGAG X CGAA AGGCUGCG	1	CGCGGCCT A GAGCGGCA	529
72	AUCUCCAU CUGAUGAG X CGAA ACGGGCCA	2	TGGCCCGT C ATGGAGAT	530
92	UCUGCUCG CUGAUGAG X CGAA ACUCCUUU	3	AAAGGAGT T CGAGCAGA	531
93	AUCUGCUC CUGAUGAG X CGAA AACUCCUU	4	AAGGAGTT C GAGCAGAT	532
102	GACUUGUC CUGAUGAG X CGAA AUCUGCUC	5	GAGCAGAT C GACAAGTC	533
110	AGCUCCCG CUGAUGAG X CGAA ACUUGUCG	6	CGACAAGT C CGGGAGCT	534
129	UCCUGGUA CUGAUGAG X CGAA AUGGCCGC	7	GCGGCCAT T TACCAGGA	535
130	AUCCUGGU CUGAUGAG X CGAA AAUGGCCG	8	COGCCATT T ACCAGGAT	536
131	UAUCCUGG CUGAUGAG X CGAA AAAUGGCC	9	GGCCATTT A CCAGGATA	537
139	AUGUCGGA CUGAUGAG X CGAA AUCCUGGU	10	ACCAGGAT A TOOGACAT	538
141	UCAUGUCG CUGAUGAG X CGAA AUAUCCUG	11	CAGGATAT C CGACATGA	539
161	UACAUGGG CUGAUGAG X CGAA AGUCACUG	12	CAGTGACT T CCCATGTA	540
162	CUACAUGG CUGAUGAG X CGAA AAGUCACU	1.3	AGTGACTT C CCATGTAG	541
169	GGCCACUC CUGAUGAG X CGAA ACAUGGGA	14	TCCCATGT A GAGTGGCC	542
183	UUCUUAGG CUGAUGAG X CGAA AGCUUGGC	15	GCCAAGCT T CCTAAGAA	543
184	GUUCUUAG CUGAUGAG X CGAA AAGCUUGG	16	CCAAGCT C CTAAGAAC	544
187	UUUGUUCU CUGAUGAG X CGAA AGGAAGCU	17	AGCTTCCT A AGAACAAA	545
205	UCUGUACC CUGAUGAG X CGAA AUUUCGGU	18	ACCGAAAT A GGTACAGA	546
209	CGUCUCUG CUGAUGAG X CGAA ACCUAUUU	19	AAATAGGT A CAGAGACG	547
219	AAGGGACU CUGAUGAG X CGAA ACGUCUCU	20	AGAGACGT C AGTCCCTT	548
223	GUCAAAGG CUGAUGAG X CGAA ACUGACGU	21	ACGTCAGT C CCTTTGAC	549
227	UAUGGUCA CUGAUGAG X CGAA AGGGACUG	22	CAGTCCCT T TGACCATA	550
228	CUAUGGUC CUGAUGAG X CGAA AAGGGACU	23	AGTCCCTT T GACCATAG	551
235	AAUCCGAC CUGAUGAG X CGAA AUGGUCAA	24	TTGACCAT A GTCGGATT	552
238	UJUJAJUCC CUGAUGAG X CGAA ACUAUGGU	25	ACCATAGT C GGATTAAA	553
243	UGUAGUUU CUGAUGAG X CGAA AUCCGACU	26	AGTOGGAT T AAACTACA	554
244	AUGUAGUU CUGAUGAG X CGAA AAUCCGAC	27	GTCGGATT A AACTACAT	555
249	UCUUGAUG CUGAUGAG X CGAA AGUUUAAU	28	ATTAGACT A CATCAGA	556
253	AUCUUCUU CUGAUGAG X CGAA AUGUAGUU	29	AACTACAT C AAGAAGAT	557
262	AUAGUCAU CUGAUGAG X CGAA AUCUUCUU	3.0	AAGAAGAT A ATGACTAT	558
269	CGUUGAUA CUGAUGAG X CGAA AGUCAUUA	31	TAATGACT A TATCAACG	559
271	AGCGUUGA CUGAUGAG X CGAA AUAGUCAU	32	ATGACTAT A TCAACGCT	560
273	CUAGCGUU CUGAUGAG X CGAA AUAUAGUC	33	GACTATAT C AACGCTAG	561
280	UAUCAAAC CUGAUGAG X CGAA AGCGUUGA	34	TCAACGCT A GTTTGATA	562
283	UUUUAUCA CUGAUGAG X CGAA ACUAGCGU	35	ACCCTACT T TGATAAAA	563
284	UUUUUAUC CUGAUGAG X CGAA AACUAGCG	36	CGCTAGTT T GATAAAA	564
288	UCCAUUUU CUGAUGAG X CGAA AUCAAACU	37	AGTTTGAT A AAAATGGA	565
313	AAGAAUGU CUGAUGAG X CGAA ACUCCUUU	3.8	AAAGGAGT T ACATTCTT	566
314	UAAGAAUG CUGAUGAG X CGAA AACUCCUU	39	AAGGAGTT A CATTCTTA	567
318	UGGGUAAG CUGAUGAG X CGAA AUGUAACU	40	AGTTACAT T CTTACCCA	568
319	CUGGGUAA CUGAUGAG X CGAA AUGUAACU	41	GTTACATT C TTACCCAG	569
321	CCCUGGGU CUGAUGAG X CGAA AGAAUGUAAC	41	TACATTCT T ACCCAGGG	570
		42		
322	GCCCUGGG CUGAUGAG X CGAA AAGAAUGU	1	ACATTOTT A CCCAGGGC	571
334	GUUAGGCA CUGAUGAG X CGAA AGGGCCCU	44	AGGGCCCT T TGCCTAAC	572

Table 3

335	UGUUAGGC CUGAUGAG X CGAA AAGGGCCC	45	GGGCCCTT T GCCTAACA	573
340	GCAUGUGU CUGAUGAG X CGAA AGGCAAAG	46	CTTTGCCT A ACACATGC	574
352	CCAAAAGU CUGAUGAG X CGAA ACCGCAUG	47	CATGCGGT C ACTTTTGG	575
356	UCUCCCAA CUGAUGAG X CGAA AGUGACCG	48	CGGTCACT T TTGGGAGA	576
357	AUCUCCCA CUGAUGAG X CGAA AAGUGACC	49	GGTCACTT T TGGGAGAT	577
358	CAUCUCCC CUGAUGAG X CGAA AAAGUGAC	50	GTCACTTT T GGGAGATG	578
393	AGCAUGAC CUGAUGAG X CGAA ACACCCCU	51	AGGGGTGT C GTCATGCT	579
396	UUGAGCAU CUGAUGAG X CGAA ACGACACC	52	GGTGTCGT C ATGCTCAA	580
402	ACUCUGUU CUGAUGAG X CGAA AGCAUGAC	53	GTCATGCT C AACAGAGT	581
424	UUUUAACG CUGAUGAG X CGAA ACCUUUCU	54	AGAAAGGT T CGTTAAAA	582
425	AUUUUAAC CUGAUGAG X CGAA AACCUUUC	55	GAAAGGTT C GTTAAAAT	583
428	CGCAUUUU CUGAUGAG X CGAA ACGAACCU	56	AGGTTCGT T AAAATGCG	584
429	GCGCAUUU CUGAUGAG X CGAA AACGAACC	57	GGTTCGTT A AAATGCGC	585
443	GUGGCCAG CUGAUGAG X CGAA AUUGUGCG	58	CGCACAAT A CTGGCCAC	586
474	UCUUCAAA CUGAUGAG X CGAA AUCAUCUC	59	GAGATGAT C TTTGAAGA	587
476	UGUCUUCA CUGAUGAG X CGAA AGAUCAUC	60	GATGATCT T TGAAGACA	588
477	GUGUCUUC CUGAUGAG X CGAA AAGAUCAU	61	ATGATCTT T GAAGACAC	589
490	UAAUUUCA CUGAUGAG X CGAA AUUUGUGU	62	ACACAAAT T TGAAATTA	590
491	UUAAUUUC CUGAUGAG X CGAA AAUUUGUG	63	CACAAATT T GAAATTAA	591
497	UCAAUGUU CUGAUGAG X CGAA AUUUCAAA	64	TTTGAAAT T AACATTGA	592
498	AUCAAUGU CUGAUGAG X CGAA AAUUUCAA	65	TTGAAATT A ACATTGAT	593
503	CAGAGAUC CUGAUGAG X CGAA AUGUUAAU	66	ATTAACAT T GATCTCTG	594
507	UCUUCAGA CUGAUGAG X CGAA AUCAAUGU	67	ACATTGAT C TCTGAAGA	595
509	UAUCUUCA CUGAUGAG X CGAA AGAUCAAU	68	ATTGATCT C TGAAGATA	596
517	UGACUUGA CUGAUGAG X CGAA AUCUUCAG	69	CTGAAGAT A TCAAGTCA	597
519	UAUGACUU CUGAUGAG X CGAA AUAUCUUC	70	GAAGATAT C AAGTCATA	598
524	UAUAAUAU CUGAUGAG X CGAA ACUUGAUA	71	TATCAAGT C ATATTATA	599
527	CUGUAUAA CUGAUGAG X CGAA AUGACUUG	72	CAAGTCAT A TTATACAG	600
529	CACUGUAU CUGAUGAG X CGAA AUAUGACU	73	AGTCATAT T ATACAGTG	601
530	GCACUGUA CUGAUGAG X CGAA AAUAUGAC	74	GTCATATT A TACAGTGC	602
532	UCGCACUG CUGAUGAG X CGAA AUAAUAUG	75	CATATTAT A CAGTGCGA	603
546	UCCAAUUC CUGAUGAG X CGAA AGCUGUCG	76	CGACAGCT A GAATTGGA	604
551	GGUUUUCC CUGAUGAG X CGAA AUUCUAGC	77	GCTAGAAT T GGAAAACC	605
561	UGGGUUGU CUGAUGAG X CGAA AGGUUUUC	78	GAAAACCT T ACAACCCA	606
562	UUGGGUUG CUGAUGAG X CGAA AAGGUUUU	79	AAAACCTT A CAACCCAA	607
577	GAUCUCUC CUGAUGAG X CGAA AGUUUCUU	80	AAGAAACT C GAGAGATC	608
585	AAAUGUAA CUGAUGAG X CGAA AUCUCUCG	81	CGAGAGAT C TTACATTT	609
587	GGAAAUGU CUGAUGAG X CGAA AGAUCUCU	82	AGAGATCT T ACATTTCC	610
588	UGGAAAUG CUGAUGAG X CGAA AAGAUCUC	83	GAGATOTT A CATTTOCA	611
592	AUAGUGGA CUGAUGAG X CGAA AUGUAAGA	84	TCTTACAT T TCCACTAT	612
593	UAUAGUGG CUGAUGAG X CGAA AAUGUAAG	85	CTTACATT T CCACTATA	613
594	GUAUAGUG CUGAUGAG X CGAA AAAUGUAA	86	TTACATTT C CACTATAC	614
599	AUGUGGUA CUGAUGAG X CGAA AGUGGAAA	87	TTTCCACT A TACCACAT	615
601	CCAUGUGG CUGAUGAG X CGAA AUAGUGGA	88	TCCACTAT A CCACATGG	616
617	GGACUCCA CUGAUGAG X CGAA AGUCAGGC	89	GCCTGACT T TGGAGTCC	617
618	GGGACUCC CUGAUGAG X CGAA AAGUCAGG	90	CCTGACTT T GGAGTCCC	618
624	GAUUCAGG CUGAUGAG X CGAA ACUCCAAA	91	TTTGGAGT C CCTGAATC	619

Table 3

632	AGGCUGGU CUGAUGAG X CGAA AUUCAGGG	92	CCCTGAAT C ACCAGCCT	620
641	UCAAGAAU CUGAUGAG X CGAA AGGCUGGU	93	ACCAGCCT C ATTCTTGA	621
644	AGUUCAAG CUGAUGAG X CGAA AUGAGGCU	94	AGCCTCAT T CTTGAACT	622
645	AAGUUCAA CUGAUGAG X CGAA AAUGAGGC	95	GCCTCATT C TTGAACTT	623
647	GAAAGUUC CUGAUGAG X CGAA AGAAUGAG	96	CTCATTCT T GAACTTTC	624
653	UGAAAAGA CUGAUGAG X CGAA AGUUCAAG	97	CTTGAACT T TCTTTTCA	625
654	UUGAAAAG CUGAUGAG X CGAA AAGUUCAA	98	TTGAACTT T CTTTTCAA	626
. 655	UUUGAAAA CUGAUGAG X CGAA AAAGUUCA	99	TGAACTTT C TTTTCAAA	627
657	ACUUUGAA CUGAUGAG X CGAA AGAAAGUU	100	AACTTTCT T TTCAAAGT	628
658	GACUUUGA CUGAUGAG X CGAA AAGAAAGU	101	ACTITCTT T TCAAAGTC	629
659	GGACUUUG CUGAUGAG X CGAA AAAGAAAG	102	CTTTCTTT T CAAAGTCC	630
660	CGGACUUU CUGAUGAG X CGAA AAAAGAAA	103	TTTCTTTT C AAAGTCCG	631
666	GACUCUCG CUGAUGAG X CGAA ACUUUGAA	104	TTCAAAGT C CGAGAGTC	632
674	GUGACCCU CUGAUGAG X CGAA ACUCUCGG	105	CCGAGAGT C AGGGTCAC	633
680	GGCUGAGU CUGAUGAG X CGAA ACCCUGAC	106	GTCAGGGT C ACTCAGCC	634
705	UCCGGGCU CUGAUGAG X CGAA AGUGACCC UGCACCAC CUGAUGAG X CGAA ACGGGCCC	107	GGGTCACT C AGCCCGGA GGGCCCGT T GTGGTGCA	635
705	GACCUGCC CUGAUGAG X CGAA AUGCCUGC	109	GCAGGCAT C GGCAGGTC	637
737	AGGUUCCA CUGAUGAG X CGAA ACCUGCCG	110	CGGCAGGT C TGGAACCT	638
746	CCAGACAG CUGAUGAG X CGAA ACCUGCCG	111	TGGAACCT T CTGTCTGG	639
747	GCCAGACA CUGAUGAG X CGAA AAGGUUCC	112	GGAACCTT C TGTCTGGC	640
751	AUCAGCCA CUGAUGAG X CGAA ACAGAAGG	113	CCTTCTGT C TGGCTGAT	641
760	GAGGCAGG CUGAUGAG X CGAA AUCAGCCA	114	TGGCTGAT A CCTGCCTC	642
768	AUCAGCAA CUGAUGAG X CGAA AGGCAGGU	115	ACCTGCCT C TTGCTGAT	643
770	CCAUCAGC CUGAUGAG X CGAA AGAGGCAG	116	CTGCCTCT T GCTGATGG	644
796	AACGGAAG CUGAUGAG X CGAA AGGGUCUU	117	AAGACCCT T CTTCCGTT	645
797	CAACGGAA CUGAUGAG X CGAA AAGGGUCU	118	AGACCCTT C TTCCGTTG	646
799	AUCAACGG CUGAUGAG X CGAA AGAAGGGU	119	ACCCTTCT T CCGTTGAT	647
800	UAUCAACG CUGAUGAG X CGAA AAGAAGGG	120	CCCTTCTT C CGTTGATA	648
804	UUGAUAUC CUGAUGAG X CGAA ACGGAAGA	121	TCTTCCGT T GATATCAA	649
808	UUUCUUGA CUGAUGAG X CGAA AUCAACGG	122	CCGTTGAT A TCAAGAAA	650
810	ACUUUCUU CUGAUGAG X CGAA AUAUCAAC	123	GTTGATAT C AAGAAAGT	651
824	UCAUUUCU CUGAUGAG X CGAA ACAGCACU	124	AGTGCTGT T AGAAATGA	652
825	CUCAUUUC CUGAUGAG X CGAA AACAGCAC	125	GTGCTGTT A GAAATGAG	653
839	CCAUCCGA CUGAUGAG X CGAA ACUUCCUC	126	GAGGAAGT T TCGGATGG	654
840	CCCAUCCG CUGAUGAG X CGAA AACUUCCU	127	AGGAAGTT T CGGATGGG	655
841	CCCCAUCC CUGAUGAG X CGAA AAACUUCC	128	GGAAGTTT C GGATGGGG	656
855	GCUGUCUG CUGAUGAG X CGAA AUCAGCCC	129	GGGCTGAT C CAGACAGC	657
878	GGUAGGAG CUGAUGAG X CGAA AGCGCAGC	130	GCTGCGCT T CTCCTACC	658
879	AGGUAGGA CUGAUGAG X CGAA AAGCGCAG	131	CTGCGCTT C TCCTACCT	659
881	CCAGGUAG CUGAUGAG X CGAA AGAAGCGC	132	GCGCTTCT C CTACCTGG	660
884	CAGCCAGG CUGAUGAG X CGAA AGGAGAAG	133	CTTCTCCT A CCTGGCTG	661
897	GCACCUUC CUGAUGAG X CGAA AUCACAGC	134	GCTGTGAT C GAAGGTGC	662
911	CCAUGAUG CUGAUGAG X CGAA AUUUGGCA	135	TGCCAAAT T CATCATGG	663
912	CCCAUGAU CUGAUGAG X CGAA AAUUUGGC	136	GCCAAATT C ATCATGGG	664
915	UCCCCCAU CUGAUGAG X CGAA AUGAAUUU	137	AAATTCAT C ATGGGGGA	665
926	GCACGGAA CUGAUGAG X CGAA AGUCCCCC	138	GGGGGACT C TTCCGTGC	666

Table 3

928	CUGCACGG CUGAUGAG X CGAA AGAGUCCC	139	GGGACTCT T CCGTGCAG	667
929	CCUGCACG CUGAUGAG X CGAA AAGAGUCC	140	GGACTCTT C CGTGCAGG	668
940	CUUCCACU CUGAUGAG X CGAA AUCCUGCA	141	TGCAGGAT C AGTGGAAG	669
954	UCGUGGGA CUGAUGAG X CGAA AGCUCCUU	142	AAGGAGCT T TCCCACGA	670
955	CUCGUGGG CUGAUGAG X CGAA AAGCUCCU	143	AGGAGCTT T CCCACGAG	671
956	CCUCGUGG CUGAUGAG X CGAA AAAGCUCC	144	GGAGCTTT C CCACGAGG	672
988	UGGGGGGA CUGAUGAG X CGAA AUGCUCGG	145	CCGAGCAT A TCCCCCCA	673
990	GGUGGGGG CUGAUGAG X CGAA AUAUGCUC	146	GAGCATAT C CCCCCACC	674
1000	UGGCCGGG CUGAUGAG X CGAA AGGUGGGG	147	CCCCACCT C CCCGGCCA	675
1020	GGCUCCAG CUGAUGAG X CGAA AUUCGUUU	148	AAACGAAT C CTGGAGCC	676
1052	UUGGGAAG CUGAUGAG X CGAA ACUCCCUG	149	CAGGGAGT T CTTCCCAA	677
1053	UUUGGGAA CUGAUGAG X CGAA AACUCCCU	150	AGGGAGTT C TTCCCAAA	678
1055	GAUUUGGG CUGAUGAG X CGAA AGAACUCC	151	GGAGTTCT T CCCAAATC	679
1056	UGAUUUGG CUGAUGAG X CGAA AAGAACUC	152	GAGTTCTT C CCAAATCA	680
1063	CCACUGGU CUGAUGAG X CGAA AUUUGGGA	153	TCCCAAAT C ACCAGTGG	681
1096	GCAGUCUU CUGAUGAG X CGAA AUCCUCCU	154	AGGAGGAT A AAGACTGC	682
1110	UCUUCCUU CUGAUGAG X CGAA AUGGGGCA	155	TGCCCCAT C AAGGAAGA	683
1133	CGGCAUUU CUGAUGAG X CGAA AGGGGCUU	156	AAGCCCCT T AAATGCCG	684
1134	GCGGCAUU CUGAUGAG X CGAA AAGGGGCU	157	AGCCCCTT A AATGCCGC	685
1148	CGAUGCCG CUGAUGAG X CGAA AGGGUGCG	158	CGCACCCT A CGGCATCG	686
1155	AUGCUUUC CUGAUGAG X CGAA AUGCCGUA	159	TACGGCAT C GAAAGCAT	687
1168	AGUGUCUU CUGAUGAG X CGAA ACUCAUGC	160	GCATGAGT C AAGACACT	688
1182	CGACUUCU CUGAUGAG X CGAA ACUUCAGU	161	ACTGAAGT T AGAAGTCG	689
1183	CCGACUUC CUGAUGAG X CGAA AACUUCAG	162	CTGAAGTT A GAAGTCGG	690
1189	CACGACCC CUGAUGAG X CGAA ACUUCUAA	163	TTAGAAGT C GGGTCGTG	691
1194	CCCCCAC CUGAUGAG X CGAA ACCCGACU	164	AGTCGGGT C GTGGGGGG	692
1207	ACCUCGAA CUGAUGAG X CGAA ACUUCCCC	165	GGGGAAGT C TTCGAGGT	693
1209	GCACCUCG CUGAUGAG X CGAA AGACUUCC	166	GGAAGTCT T CGAGGTGC	694
1210	GGCACCUC CUGAUGAG X CGAA AAGACUUC	167	GAAGTCTT C GAGGTGCC	695
1229	UGGCUGGG CUGAUGAG X CGAA AGGCAGCC	168	GGCTGCCT C CCCAGCCA	696
1250	CGGGCAGU CUGAUGAG X CGAA ACGGCUCC	169	GGAGCCGT C ACTGCCCG	697
1285	CUUCCAGU CUGAUGAG X CGAA ACUCAGUG	170	CACTGAGT T ACTGGAAG	698
1286	GCUUCCAG CUGAUGAG X CGAA AACUCAGU	171	ACTGAGTT A CTGGAAGC	699
1298	UGACCAGG CUGAUGAG X CGAA AGGGCUUC	172	GAAGCCCT T CCTGGTCA	700
1299	UUGACCAG CUGAUGAG X CGAA AAGGGCUU	173	AAGCCCTT C CTGGTCAA	701
1305	CACAUGUU CUGAUGAG X CGAA ACCAGGAA	174	TTCCTGGT C AACATGTG	702
1321	GAGGACCG CUGAUGAG X CGAA AGCCACGC	175	GCGTGGCT A CGGTCCTC	703
1326	GCCGUGAG CUGAUGAG X CGAA ACCGUAGC	176	GCTACGGT C CTCACGGC	704
1329	CCGGCCGU CUGAUGAG X CGAA AGGACCGU	177	ACGGTCCT C ACGGCCGG	705
1342	GCAGAGGU CUGAUGAG X CGAA AGCGCCGG	178	CCGGCGCT T ACCTCTGC	706
1343	AGCAGAGG CUGAUGAG X CGAA AAGCGCCG	179	CGGCGCTT A CCTCTGCT	707
1347	CUGUAGCA CUGAUGAG X CGAA AGGUAAGC	180	GCTTACCT C TGCTACAG	708
1352	GGAACCUG CUGAUGAG X CGAA AGCAGAGG	181	CCTCTGCT A CAGGTTCC	709
1358	UGAACAGG CUGAUGAG X CGAA ACCUGUAG	182	CTACAGGT T CCTGTTCA	710
1359	UUGAACAG CUGAUGAG X CGAA AACCUGUA	183	TACAGGTT C CTGTTCAA	711
1364	UGCUGUUG CUGAUGAG X CGAA ACAGGAAC	184	GTTCCTGT T CAACAGCA	712
1365	UUGCUGUU CUGAUGAG X CGAA AACAGGAA	185	TTCCTGTT C AACAGCAA	713

Table 3

1379	GGUCAGGC CUGAUGAG X CGAA AUGUGUUG	186	CAACACAT A GCCTGACC	714
1390	GAGUGGAG CUGAUGAG X CGAA AGGGUCAG	187	CTGACCCT C CTCCACTC	715
1393	GUGGAGUG CUGAUGAG X CGAA AGGAGGGU	188	ACCCTCCT C CACTCCAC	716
1398	UGGAGGUG CUGAUGAG X CGAA AGUGGAGG	189	CCTCCACT C CACCTCCA	717
1404	AGUGGGUG CUGAUGAG X CGAA AGGUGGAG	190	CTCCACCT C CACCCACT	718
1415	CAGAGGCG CUGAUGAG X CGAA ACAGUGGG	191	CCCACTGT C CGCCTCTG	719
1421	UGCGGGCA CUGAUGAG X CGAA AGGCGGAC	192	GTCCGCCT C TGCCCGCA	720
1446	AUGCCUGC CUGAUGAG X CGAA AGUCGGGC	193	GCCCGACT A GCAGGCAT	721
1463	CCCUUACC CUGAUGAG X CGAA ACCGCGGC	194	GCCGCGGT A GGTAAGGG	722
1467	GCGGCCCU CUGAUGAG X CGAA ACCUACCG	195	CGGTAGGT A AGGGCCGC	723
1486	CGGCUCUC CUGAUGAG X CGAA ACGCGGUC	196	GACCGCGT A GAGAGCCG	724
1511	GCAGAACC CUGAUGAG X CGAA ACGUCCGU	197	ACGGACGT T GGTTCTGC	725
1515	UAGUGCAG CUGAUGAG X CGAA ACCAACGU	198	ACGTTGGT T CTGCACTA	726
1516	UUAGUGCA CUGAUGAG X CGAA AACCAACG	199	CGTTGGTT C TGCACTAA	727
1523	AUGGGURU CUGAUGAG X CGAA AGUGCAGA	200	TCTGCACT A AAACCCAT	728
1532	CCGGGGAA CUGAUGAG X CGAA AUGGGUUU	201	AAACCCAT C TTCCCCGG	729
1534	AUCCGGGG CUGAUGAG X CGAA AGAUGGGU	202	ACCORTOT T CCCCGGAT	730
1535	CAUCCGGG CUGAUGAG X CGAA AAGAUGGG	203	CCCATCTT C CCCGGATG	731
1549	AGGGGUGA CUGAUGAG X CGAA ACACACAU	203	ATGTGTGT C TCACCCCT	732
1551	UGAGGGGU CUGAUGAG X CGAA AGACACAC	205	GTGTGTCT C ACCCCTCA	733
1558	AAAAGGAU CUGAUGAG X CGAA AGGGGUGA	206	TCACCCCT C ATCCTTTT	734
1561	AGUAAAAG CUGAUGAG X CGAA AUGAGGGG	207	CCCCTCAT C CTTTTACT	735
1564	AAAAGUAA CUGAUGAG X CGAA AGGAUGAG	207	CTCATCCT T TTACTTT	736
			TCATCCTT T TACTTTT	737
1565	AAAAAGUA CUGAUGAG X CGAA AAAGGAUGA CAAAAAGU CUGAUGAG X CGAA AAAGGAUG	209	CATCCTT T ACTTTTG	737
1567	GCAAAAAG CUGAUGAG X CGAA AAAAGGAU	210	ATCCTTT A CTTTTGC	739
		211	CTTTTACT T TTTGCCCC	740
1570	GGGGCAAA CUGAUGAG X CGAA AGUAAAAG AGGGGCAA CUGAUGAG X CGAA AAGUAAAA	212	TTTTACT T TTTGCCCC	740
1572	AAGGGGCA CUGAUGAG X CGAA AAGUAAAA AAGGGGCA CUGAUGAG X CGAA AAAGUAAA	213	TTTACTT T TIGCCCCT	741
_				742
1573	GAAGGGGC CUGAUGAG X CGAA AAAAGUAA	215	TTACTTTT T GCCCCTTC	
1580	CAAAGUGG CUGAUGAG X CGAA AGGGGCAA	216	TTGCCCCT T CCACTTTG	744
1581	UCAAAGUG CUGAUGAG X CGAA AAGGGGCA	217	TGCCCCTT C CACTTTGA	745 .
1586	GGUACUCA CUGAUGAG X CGAA AGUGGAAG	218	CTTCCACT T TGAGTACC	746
1587	UGGUACUC CUGAUGAG X CGAA AAGUGGAA	219	TTCCACTT T GAGTACCA	747
1592	GGAUUUGG CUGAUGAG X CGAA ACUCAAAG	220	CTTTGAGT A CCAAATCC	748
1599	GGCUUGUG CUGAUGAG X CGAA AUUUGGUA	221	TACCAAAT C CACAAGCC	749
1610	CCUCAAAA CUGAUGAG X CGAA AUGGCUUG	222	CAAGCCAT T TTTTGAGG	750
1611	UCCUCAAA CUGAUGAG X CGAA AAUGGCUU	223	AAGCCATT T TTTGAGGA	751
1612	CUCCUCAA CUGAUGAG X CGAA AAAUGGCU	224	AGCCATTT T TTGAGGAG	752
1613	UCUCCUCA CUGAUGAG X CGAA AAAAUGGC	225	GCCATTTT T TGAGGAGA	753
1614	CUCUCCUC CUGAUGAG X CGAA AAAAAUGG	226	CCATTTT T GAGGAGAG	754
1634	CAGCAUGG CUGAUGAG X CGAA ACUCUCUU	227	AAGAGAGT A CCATGCTG	755
1665	GACGGGUG CUGAUGAG X CGAA AGGCCCCU	228	AGGGCCT A CACCCGTC	756
1673	AGCCCCAA CUGAUGAG X CGAA ACGGGUGU	229	ACACCCGT C TTGGGGCT	757
1675	CGAGCCCC CUGAUGAG X CGAA AGACGGGU	230	ACCCGTCT T GGGGCTCG	758
1682	GGUGGGGC CUGAUGAG X CGAA AGCCCCAA	231	TTGGGGCT C GCCCCACC	759
1698	CCAGGAGG CUGAUGAG X CGAA AGCCCUGG	232	CCAGGGCT C CCTCCTGG	760

Table 3

1702	HIGCHICCAG CHIGALIGAG X CGAA AGGGAGCC	233	GGCTCCCT C CTGGAGCA	761
1712	CCGCCUGG CUGAUGAG X CGAA AUGCUCCA	234	TGGAGCAT C CCAGGCGG	762
1746	GCAGAUUC CUGAUGAG X CGAA AGGGGGGG	235	CCCCCCT T GAATCTGC	763
1751	UCCCUGCA CUGAUGAG X CGAA AUUCAAGG	236	CCTTGAAT C TGCAGGGA	764
1766	GGAGUGGA CUGAUGAG X CGAA AGUUGCUC	237	GAGCAACT C TCCACTCC	765
1768	AUGGAGUG CUGAUGAG X CGAA AGAGUUGC	238	GCAACTCT C CACTCCAT	766
1773	UAAAUAUG CUGAUGAG X CGAA AGUGGAGA	239	TCTCCACT C CATATTTA	767
1777	UAAAUAAA CUGAUGAG X CGAA AUGGAGUG	240	CACTCCAT A TTTATTTA	768
1779	UUUAAAUA CUGAUGAG X CGAA AUAUGGAG	241	CTCCATAT T TATTTAAA	769
1780	GUUUAAAU CUGAUGAG X CGAA AAUAUGGA	242	TCCATATT T ATTTAAAC	770
1781	UGUUUAAA CUGAUGAG X CGAA AAAUAUGG	243	CCATATTT A TTTAAACA	771
1783	AUUGUUUA CUGAUGAG X CGAA AUAAAUAU	244	ATATTTAT T TAAACAAT	772
1784	AAUUGUUU CUGAUGAG X CGAA AAUAAAUA	245	TATTTATT T AAACAATT	773
1785	AAAUUGUU CUGAUGAG X CGAA AAAUAAAU	246	ATTTATTT A AACAATTT	774
1792	GGGGAAAA CUGAUGAG X CGAA AUUGUUUA	247	TAAACAAT T TTTTCCCC	775
1793	UGGGGAAA CUGAUGAG X CGAA AAUUGUUU	248	AAACAATT T TTTCCCCA	776
1794	UUGGGGAA CUGAUGAG X CGAA AAAUUGUU	249	AACAATTT T TTCCCCAA	777
1795	UUUGGGGA CUGAUGAG X CGAA AAAAUUGU	250	ACAATTTT T TCCCCAAA	778
1796	CUUUGGGG CUGAUGAG X CGAA AAAAAUUG	251	CAATTTT T CCCCAAAG	779
1797	CCUUUGGG CUGAUGAG X CGAA AAAAAAUU GCACUAUG CUGAUGAG X CGAA AUGCCUUU	252 253	AATTTTTT C CCCAAAGG	780 781
1809	UAGUGCAC CUGAUGAG X CGAA AUGGAUGC	253	GCATCCAT A GTGCACTA	781
1821	GAAAAUGC CUGAUGAG X CGAA AGUGCACU	255	AGTGCACT A GCATTTTC	783
1826	UUCAAGAA CUGAUGAG X CGAA AUGCUAGU	256	ACTAGCAT T TTCTTGAA	784
1827	GUUCAAGA CUGAUGAG X CGAA AAUGCUAG	257	CTAGCATT T TCTTGAAC	785
1828	GGUUCAAG CUGAUGAG X CGAA AAAUGCUA	258	TAGCATTT T CTTGAACC	786
1829	UGGUUCAA CUGAUGAG X CGAA AAAAUGCU	259	AGCATTTT C TTGAACCA	787
1831	AUUGGUUC CUGAUGAG X CGAA AGAAAAUG	260	CATTITCT T GAACCAAT	788
1840	UAAUACAU CUGAUGAG X CGAA AUUGGUUC	261	GAACCAAT A ATGTATTA	789
1845	AAUUUUAA CUGAUGAG X CGAA ACAUUAUU	262	AATAATGT A TTAAAATT	790
1847	AAAAUUUU CUGAUGAG X CGAA AUACAUUA	263	TAATGTAT T AAAATTTT	791
1848	AAAAAUUU CUGAUGAG X CGAA AAUACAUU	264	AATGTATT A AAATTTT	792
1853	CAUCAAAA CUGAUGAG X CGAA AUUUUAAU	265	ATTAAAAT T TTTTGATG	793
1854	ACAUCAAA CUGAUGAG X CGAA AAUUUUAA	266	TTAAAATT T TTTGATGT	794
1855	GACAUCAA CUGAUGAG X CGAA AAAUUUUA	267	TAAAATTT T TTGATGTC	795
1856	UGACAUCA CUGAUGAG X CGAA AAAAUUUU	268	AAAATTTT T TGATGTCA	796
1857	CUGACAUC CUGAUGAG X CGAA AAAAAUUU	269	AAATTTTT T GATGTCAG	797
1863	GCAAGGCU CUGAUGAG X CGAA ACAUCAAA	270 271	TTTGATGT C AGCCTTGC GTCAGCCT T GCATCAAG	798 799
1869	CUUGAUGC CUGAUGAG X CGAA AGGCUGAC AAGCCCUU CUGAUGAG X CGAA AUGCAAGG	271	CCTTGCAT C AAGGGCTT	799 800
1874	UUUUGAUA CUGAUGAG X CGAA AUGCAAGG	272	CAAGGGCT T TATCAAAA	800
1882	UUUUUGAU CUGAUGAG X CGAA AGCCCUU	274	AAGGGCTT T ATCAAAA	802
1884	CUUUUUGA CUGAUGAG X CGAA AAAGCCCU	275	AGGGCTTT A TCAAAAAG	803
1886	UACUUUIU CUGAUGAG X CGAA AUAAGCCC	276	GGCTTTAT C AAAAAGTA	804
1894	UAUUAUUG CUGAUGAG X CGAA ACUUUUUG	277	CAAAAAGT A CAATAATA	805
1899	GGAUUUAU CUGAUGAG X CGAA AUUGUACU	278	AGTACAAT A ATAAATCC	806
1902	UGAGGAUU CUGAUGAG X CGAA AUUAUUGU	279	ACAATAAT A AATCCTCA	807
	TELESCOPHOCHO & COLET MOROUGO			

Table 3

1906	UACCUGAG CUGAUGAG X CGAA AUUUAUUA	280	TAATAAAT C CTCAGGTA	808
1909	UACUACCU CUGAUGAG X CGAA AGGAUUUA	281	TAAATCCT C AGGTAGTA	809
1914	CCCAGUAC CUGAUGAG X CGAA ACCUGAGG	282	CCTCAGGT A GTACTGGG	810
1917	AUUCCCAG CUGAUGAG X CGAA ACUACCUG	. 283	CAGGTAGT A CTGGGAAT	811
1934	CCAUGGCA CUGAUGAG X CGAA AGCCUUCC	284	GGAAGGCT T TGCCATGG	812
1935	CCCAUGGC CUGAUGAG X CGAA AAGCCUUC	285	GAAGGCTT T GCCATGGG	813
1954	ACUGGUCU CUGAUGAG X CGAA ACGCAGCA	286	TGCTGCGT C AGACCAGT	814
1963	CUUCCCAG CUGAUGAG X CGAA ACUGGUCU	287	AGACCAGT A CTGGGAAG	815
1981	CUGCUUAC CUGAUGAG X CGAA ACCGUCCU	288	AGGACGGT T GTAAGCAG	816
1984	CAACUGCŲ CUGAUGAG X CGAA ACAACCGU	289	ACGGTTGT A AGCAGTTG	817
1991	UAAAUAAC CUGAUGAG X CGAA ACUGCUUA	290	TAAGCAGT T GTTATTTA	818
1994	CACUAAAU CUGAUGAG X CGAA ACAACUGC	291	GCAGTTGT T ATTTAGTG	819
1995	UCACUAAA CUGAUGAG X CGAA AACAACUG	292	CAGTTGTT A TTTAGTGA	820
1997	UAUCACUA CUGAUGAG X CGAA AUAACAAC	293	GTTGTTAT T TAGTGATA	821
1998	AUAUCACU CUGAUGAG X CGAA AAUAACAA	294	TTGTTATT T AGTGATAT	822
1999	AAUAUCAC CUGAUGAG X CGAA AAAUAACA	295	TGTTATTT A GTGATATT	823
2005	ACCCACAA CUGAUGAG X CGAA AUCACUAA	296	TTAGTGAT A TTGTGGGT	824
2007	UUACCCAC CUGAUGAG X CGAA AUAUCACU	297	AGTGATAT T GTGGGTAA	825
2014	UCUCACGU CUGAUGAG X CGAA ACCCACAA	298	TTGTGGGT A ACGTGAGA	826
2027	CAUUGUUC CUGAUGAG X CGAA AUCUUCUC	299	GAGAAGAT A GAACAATG	827
2038	AUAUAUUA CUGAUGAG X CGAA AGCAUUGU	300	ACAATGCT A TAATATAT	828
2040	UUAUAUAU CUGAUGAG X CGAA AUAGCAUU	301	AATGCTAT A ATATATAA	829
2043	UCAUUAUA CUGAUGAG X CGAA AUUAUAGC	302	GCTATAAT A TATAATGA	830
2045	GUUCAUUA CUGAUGAG X CGAA AUAUUAUA	303	TATAATAT A TAATGAAC	831
2047	GUGUUCAU CUGAUGAG X CGAA AUAUAUUA	304	TAATATAT A ATGAACAC	832
2062	UUAUUAAA CUGAUGAG X CGAA ACCCACGU	305	ACGTGGGT A TTTAATAA	833
2064	UCUUAUUA CUGAUGAG X CGAA AUACCCAC	306	GTGGGTAT T TAATAAGA	834
2065	UUCUUAUU CUGAUGAG X CGAA AAUACCCA	307	TGGGTATT T AATAAGAA	835
2066	UUUCUUAU CUGAUGAG X CGAA AAAUACCC	308	GGGTATTT A ATAAGAAA	836
2069	AUGUUUCU CUGAUGAG X CGAA AUUAAAUA	309	TATTTAAT A AGAAACAT	837
2088	GACAAAGU CUGAUGAG X CGAA AUCUCACA	310	TGTGAGAT T ACTTTGTC	838
2089	GGACAAAG CUGAUGAG X CGAA AAUCUCAC	311	GTGAGATT A CTTTGTCC	839
2092	GCGGGACA CUGAUGAG X CGAA AGUAAUCU	312	AGATTACT T TGTCCCGC	840
2093	AGCGGGAC CUGAUGAG X CGAA AAGUAAUC	313	GATTACTT T GTCCCGCT	841
2096	AUAAGCGG CUGAUGAG X CGAA ACAAAGUA	314	TACTTIGT C CCGCTTAT	842
2102	AGCAGAAU CUGAUGAG X CGAA AGCGGGAC	315	GTCCCGCT T ATTCTGCT	843
2103	GAGCAGAA CUGAUGAG X CGAA AAGCGGGA	316	TCCCGCTT A TTCTGCTC	844
2105	GGGAGCAG CUGAUGAG X CGAA AUAAGCGG	317	CCGCTTAT T CTGCTCCC	845
2106	AGGGAGCA CUGAUGAG X CGAA AAUAAGCG	318	CGCTTATT C TGCTCCCT	846
2111	AUAACAGG CUGAUGAG X CGAA AGCAGAAU	319	ATTCTGCT C CCTGTTAT	847
2117	UAGCAGAU CUGAUGAG X CGAA ACAGGGAG	320	CTCCCTGT T ATCTGCTA	848
2118	CUAGCAGA CUGAUGAG X CGAA AACAGGGA	321	TCCCTGTT A TCTGCTAG	849
2120	AUCUAGCA CUGAUGAG X CGAA AUAACAGG	322	CCTGTTAT C TGCTAGAT	850
2125	ACUAGAUC CUGAUGAG X CGAA AGCAGAUA	323	TATCTGCT A GATCTAGT	851
2129	GAGAACUA CUGAUGAG X CGAA AUCUAGCA	324	TGCTAGAT C TAGTTCTC	852
2131	UUGAGAAC CUGAUGAG X CGAA AGAUCUAG	325	CTAGATCT A GTTCTCAA	853
2134	UGAUUGAG CUGAUGAG X CGAA ACUAGAUC	326	GATCTAGT T CTCAATCA	854
		1		

Table 3

2135	GUGAUUGA CUGAUGAG X CGAA AACUAGAU	327	ATCTAGTT C TCAATCAC	855
2137	CAGUGAUU CUGAUGAG X CGAA AGAACUAG	328	CTAGTTCT C AATCACTG	856
2141	GGAGCAGU CUGAUGAG X CGAA AUUGAGAA	329	TTCTCAAT C ACTGCTCC	857
2148	ACACGGGG CUGAUGAG X CGAA AGCAGUGA	330	TCACTGCT C CCCCGTGT	858
2159	CAUUCUAA CUGAUGAG X CGAA ACACACGG	331	CCGTGTGT A TTAGAATG	859
2161	UGCAUUCU CUGAUGAG X CGAA AUACACAC	332	GTGTGTAT T AGAATGCA	860
2162	AUGCAUUC CUGAUGAG X CGAA AAUACACA	333	TGTGTATT A GAATGCAT	861
2173	GAAGACCU CUGAUGAG X CGAA ACAUGCAU	334	ATGCATGT A AGGTCTTC	862
2178	CACAAGAA CUGAUGAG X CGAA ACCUUACA	335	TGTAAGGT C TTCTTGTG	863
2180	GACACAAG CUGAUGAG X CGAA AGACCUUA	336	TAAGGTCT T CTTGTGTC	864
2181	GGACACAA CUGAUGAG X CGAA AAGACCUU	337	AAGGTCTT C TTGTGTCC	865
2183	CAGGACAC CUGAUGAG X CGAA AGAAGACC	338	GGTCTTCT T GTGTCCTG	855
2188	UUCAUCAG CUGAUGAG X CGAA ACACAAGA	339	TCTTGTGT C CTGATGAA	867
2201	CAAGCACA CUGAUGAG X CGAA AUUUUUCA	340	TGAAAAAT A TGTGCTTG	868
2208	CUCAUUUC CUGAUGAG X CGAA AGCACAUA	341	TATGTGCT T GAAATGAG	869
2222	AGAGAUCA CUGAUGAG X CGAA AGUUUCUC	342	GAGAAACT T TGATCTCT	870
2223	CAGAGAUC CUGAUGAG X CGAA AAGUUUCU	343	AGAAACTT T GATCTCTG	871
2227	UAAGCAGA CUGAUGAG X CGAA AUCAAAGU	344	ACTITGAT C TCTGCTTA	872
2229	AGUAAGCA CUGAUGAG X CGAA AGAUCAAA	345	TTTGATCT C TGCTTACT	873
2234	ACAUUAGU CUGAUGAG X CGAA AGCAGAGA	346	TCTCTGCT T ACTAATGT	874
2235	CACAUUAG CUGAUGAG X CGAA AAGCAGAG	347	CTCTGCTT A CTAATGTG	875
2238	GGGCACAU CUGAUGAG X CGAA AGUAAGCA	348	TGCTTACT A ATGTGCCC	876
2252	UGGACUUG CUGAUGAG X CGAA ACAUGGGG	349	CCCCATGT C CAAGTCCA	877
2258	GCAGGUUG CUGAUGAG X CGAA ACUUGGAC	350	GTCCAAGT C CAACCTGC	878
2283	CAUGUAAU CUGAUGAG X CGAA AUCAGGUC	351	GACCTGAT C ATTACATG	879
2286	AGCCAUGU CUGAUGAG X CGAA AUGAUCAG	352	CTGATCAT T ACATGGCT	880
2287	CAGCCAUG CUGAUGAG X CGAA AAUGAUCA	353	TGATCATT A CATGGCTG	881
2300	GGCUUAGG CUGAUGAG X CGAA ACCACAGC	354	GCTGTGGT T CCTAAGCC	882
2301	AGGCUUAG CUGAUGAG X CGAA AACCACAG	355	CTGTGGTT C CTAAGCCT	883
2304	AACAGGCU CUGAUGAG X CGAA AGGAACCA	356	TGGTTCCT A AGCCTGTT	884
2312	ACUUCAGC CUGAUGAG X CGAA ACAGGCUU	357	AAGCCTGT T GCTGAAGT	885
2321	GCGACAAU CUGAUGAG X CGAA ACUUCAGC	358	GCTGAAGT C ATTGTCGC	885
2324	UGAGCGAC CUGAUGAG X CGAA AUGACUUC	359	GAAGTCAT T GTCGCTCA	887
2327	- UGCUGAGC CUGAUGAG X CGAA ACAAUGAC	360	GTCATTGT C GCTCAGCA	888
2331	CUAUUGCU CUGAUGAG X CGAA AGCGACAA	361	TTGTCGCT C AGCAATAG	889
2338	CUGCACCC CUGAUGAG X CGAA AUUGCUGA	362	TCAGCAAT A GGGTGCAG	890
2348	UCCUGGAA CUGAUGAG X CGAA ACUGCACC	363	GGTGCAGT T TTCCAGGA	891
2349	UUCCUGGA CUGAUGAG X CGAA AACUGCAC	364	GTGCAGTT T TCCAGGAA	892
2350	AUUCCUGG CUGAUGAG X CGAA AAACUGCA	365	TGCAGTTT T CCAGGAAT	893
2351	UAUUCCUG CUGAUGAG X CGAA AAAACUGC	356	GCAGTTTT C CAGGAATA	894
2359	CAAAUGCC CUGAUGAG X CGAA AUUCCUGG	367	CCAGGAAT A GGCATTTG	895
2365	AUUAGGCA CUGAUGAG X CGAA AUGCCUAU	368	ATAGGCAT T TGCCTAAT	896
2366	AAUUAGGC CUGAUGAG X CGAA AAUGCCUA	369	TAGGCATT T GCCTAATT	897
- 2371	CCAGGAAU CUGAUGAG X CGAA AGGCAAAU	370	ATTTGCCT A ATTCCTGG	898
2374	AUGCCAGG CUGAUGAG X CGAA AUUAGGCA	371	TGCCTAAT T CCTGGCAT	899
2375	CAUGCCAG CUGAUGAG X CGAA AAUUAGGC	372	GCCTAATT C CTGGCATG	900
2389	AGUCACUA CUGAUGAG X CGAA AGUGUCAU	3 73	ATGACACT C TAGTGACT	901

Table 3

2391	GAAGUCAC CUGAUGAG X CGAA AGAGUGUC	374	GACACTCT A GTGACTTC	902
2398	UCACCAGG CUGAUGAG X CGAA AGUCACUA	375	TAGTGACT T CCTGGTGA	903
2399	CUCACCAG CUGAUGAG X CGAA AAGUCACU	376	AGTGACTT C CTGGTGAG	904
2419	UGUACCAG CUGAUGAG X CGAA ACAGGCUG	377	CAGCCTGT C CTGGTACA	905
2425	CCCUGCUG CUGAUGAG X CGAA ACCAGGAC	378	GTCCTGGT A CAGCAGGG	906
2435	UACAGCAA CUGAUGAG X CGAA ACCCUGCU	379	AGCAGGGT C TTGCTGTA	907
2437	GUUNCAGC CUGAUGAG X CGAA AGACCCUG	380	CAGGGTCT T GCTGTAAC	908
2443	GUCUGAGU CUGAUGAG X CGAA ACAGCAAG	381	CTTGCTGT A ACTCAGAC	909
2447	GAAUGUCU CUGAUGAG X CGAA AGUUACAG	382	CTGTAACT C AGACATTC	910
2454	ACCCUUGG CUGAUGAG X CGAA AUGUCUGA	383	TCAGACAT T CCAAGGGT	911
2455	UACCCUUG CUGAUGAG X CGAA AAUGUCUG	384	CAGACATT C CAAGGGTA	912
2463	GCUUCCCA CUGAUGAG X CGAA ACCCUUGG	385	CCAAGGGT A TGGGAAGC	913
2475	GGUGUGAA CUGAUGAG X CGAA AUGGCUUC	386	GAAGCCAT A TTCACACC	914
2477	GAGGUGUG CUGAUGAG X CGAA AUAUGGCU	387	AGCCATAT T CACACCTC	915
2478	UGAGGUGU CUGAUGAG X CGAA AAUAUGGC	388	GCCATATT C ACACCTCA	916
2485	CAGAGCGU CUGAUGAG X CGAA AGGUGUGA	389	TCACACCT C ACGCTCTG	917
2491	CAUGUCCA CUGAUGAG X CGAA AGCGUGAG	390	CTCACGCT C TGGACATG	918
2502	CUUCCCUA CUGAUGAG X CGAA AUCAUGUC	391	GACATGAT T TAGGGAAG	919
2503	GCUUCCCU CUGAUGAG X CGAA AAUCAUGU	392	ACATGATT T AGGGAAGC	920
2504	UGCUUCCC CUGAUGAG X CGAA AAAUCAUG	393	CATGATTT A GGGAAGCA	921
2536	UGAUCCCA CUGAUGAG X CGAA AGGUGGGG	394	CCCCACCT T TGGGATCA	922
2537	CUGAUCCC CUGAUGAG X CGAA AAGGUGGG	395	CCCACCTT T GGGATCAG	923
2543	CGGAGGCU CUGAUGAG X CGAA AUCCCAAA	396	TTTGGGAT C AGCCTCCG	924
2549	GAAUGGCG CUGAUGAG X CGAA AGGCUGAU	397	ATCAGCCT C CGCCATTC	925
2556	CGACUUGG CUGAUGAG X CGAA AUGGCGGA	398	TCCGCCAT T CCAAGTCG	926
2557	UCGACUUG CUGAUGAG X CGAA AAUGGCGG	399	CCGCCATT C CAAGTCGA	927
2563	AGAGUGUC CUGAUGAG X CGAA ACUUGGAA	400	TTCCAAGT C GACACTCT	928
2570	CUCAAGAA CUGAUGAG X CGAA AGUGUCGA	401	TCGACACT C TTCTTGAG	929
2572	UGCUCAAG CUGAUGAG X CGAA AGAGUGUC	402	GACACTCT T CTTGAGCA	930
2573	CUGCUCAA CUGAUGAG X CGAA AAGAGUGU	403	ACACTETT C TTGAGCAG	931
2575	GUCUGCUC CUGAUGAG X CGAA AGAAGAGU	404	ACTCTTCT T GAGCAGAC	932
2590	CUCUUCCA CUGAUGAG X CGAA AUCACGGU	405	ACCGTGAT T TGGAAGAG	933
2591	UCUCUUCC CUGAUGAG X CGAA AAUCACGG	406	CCGTGATT T GGAAGAGA	934
2622	GUUUCAAG CUGAUGAG X CGAA AGUGUGGU	407	ACCACACT T CTTGAAAC	935
2623	UGUUUCAA CUGAUGAG X CGAA AAGUGUGG	408	CCACACTT C TTGAAACA	936
2625	GCUGUUUC CUGAUGAG X CGAA AGAAGUGU	409	ACACTTCT T GAAACAGC	937
2646	GCCUAAAG CUGAUGAG X CGAA ACCGUCAC	410	GTGACGGT C CTTTAGGC	938
2649	GCUGCCUA CUGAUGAG X CGAA AGGACCGU	411	ACGGTCCT T TAGGCAGC	939
2650	GGCUGCCU CUGAUGAG X CGAA AAGGACCG	412 .	CGGTCCTT T AGGCAGCC	940
2651	AGGCUGCC CUGAUGAG X CGAA AAAGGACC	413	GGTCCTTT A GGCAGCCT	941
2668	GGGACAGA CUGAUGAG X CGAA ACGGCGGC	414	GCCGCCGT C TCTGTCCC	942
2670	CCGGGACA CUGAUGAG X CGAA AGACGGCG	415	CGCCGTCT C TGTCCCGG	943
2674	UGAACCGG CUGAUGAG X CGAA ACAGAGAC	416	GTCTCTGT C CCGGTTCA	944
2680	GCAAGGUG CUGAUGAG X CGAA ACCGGGAC	417	GTCCCGGT T CACCTTGC	945
2681	GGCAAGGU CUGAUGAG X CGAA AACCGGGA	418	TCCCGGTT C ACCTTGCC	946
2686	CUCUCGGC CUGAUGAG X CGAA AGGUGAAC	419	GTTCACCT T GCCGAGAG	947
2703	GUGGGGCA CUGAUGAG X CGAA ACGCGCCU	420	AGGCGCGT C TGCCCCAC	948

Table 3

2715	CAGGGUUU CUGAUGAG X CGAA AGGGUGGG	421	CCCACCCT C AAACCCTG	949
2741	AGAGUCGU CUGAUGAG X CGAA AGCACCAU	422	ATGGTGCT C ACGACTCT	950
2748	UGCAGGAA CUGAUGAG X CGAA AGUCGUGA	423	TCACGACT C TTCCTGCA	951
2750	UUUGCAGG CUGAUGAG X CGAA AGAGUCGU	424	ACGACTCT T CCTGCAAA	952
2751	CUUUGCAG CUGAUGAG X CGAA AAGAGUCG	425	CGACTCTT C CTGCAAAG	953
2774	UUAAUGUG CUGAUGAG X CGAA AGGUCUUC	426	GAAGACCT C CACATTAA	954
2780	AGCCACUU CUGAUGAG X CGAA AUGUGGAG	427	CTCCACAT T AAGTGGCT	955
2781	AAGCCACU CUGAUGAG X CGAA AAUGUGGA	428	TCCACATT A AGTGGCTT	956
2789	AUGUUAAA CUGAUGAG X CGAA AGCCACUU	429	AAGTGGCT T TTTAACAT	957
2790	CAUGUUAA CUGAUGAG X CGAA AAGCCACU	430	AGTGGCTT T TTAACATG	958
2791	UCAUGUUA CUGAUGAG X CGAA AAAGCCAC	431	GTGGCTTT T TAACATGA	959
2792	UUCAUGUU CUGAUGAG X CGAA AAAAGCCA	432	TGGCTTTT T AACATGAA	960
2793	UUUCAUGU CUGAUGAG X CGAA AAAAAGCC	433	GGCTTTTT A ACATGAAA	961
2816	UCGGGAGC CUGAUGAG X CGAA ACAGCUGC	434	GCAGCTGT A GCTCCCGA	962
2820	UAGCUCGG CUGAUGAG X CGAA AGCUACAG	435	CTGTAGCT C CCGAGCTA	963
2828	CAAGAGAG CUGAUGAG X CGAA AGCUCGGG	436	CCCGAGCT A CTCTCTTG	964
2831	UGGCAAGA CUGAUGAG X CGAA AGUAGCUC	437	GAGCTACT C TCTTGCCA	965
2833	GCUGGCAA CUGAUGAG X CGAA AGAGUAGC	438	GCTACTCT C TTGCCAGC	966
2835	AUGCUGGC CUGAUGAG X CGAA AGAGAGUA	439	TACTOTOT T GCCAGCAT	967
2844	AAUGUGAA CUGAUGAG X CGAA AUGCUGGC	440	GCCAGCAT T TTCACATT	968
2845	AAAUGUGA CUGAUGAG X CGAA AAUGCUGG	441	CCAGCATT T TCACATTT	969
2846	AAAAUGUG CUGAUGAG X CGAA AAAUGCUG	442	CAGCATTT T CACATTTT	970
2847	CAAAAUGU CUGAUGAG X CGAA AAAAUGCU	443	AGCATTTT C ACATTTTG	971
2852	AAAGGCAA CUGAUGAG X CGAA AUGUGAAA	444	TTTCACAT T TTGCCTTT	972
2853	GAAAGGCA CUGAUGAG X CGAA AAUGUGAA	445	TTCACATT T TGCCTTTC	973
2854	AGAAAGGC CUGAUGAG X CGAA AAAUGUGA	446	TCACATTT T GCCTTTCT	974
2859	CCACGAGA CUGAUGAG X CGAA AGGCAAAA	447	TTTTGCCT T TCTCGTGG	975
2860	ACCACGAG CUGAUGAG X CGAA AAGGCAAA	448	TTTGCCTT T CTCGTGGT	976
2861	UACCACGA CUGAUGAG X CGAA AAAGGCAA	449	TTGCCTTT C TCGTGGTA	977
2863	UCUACCAC CUGAUGAG X CGAA AGAAAGGC	450	GCCTTTCT C GTGGTAGA	978
2869	CUGGCUUC CUGAUGAG X CGAA ACCACGAG	451	CTCGTGGT A GAAGCCAG	979
2879	UUUCUCUG CUGAUGAG X CGAA ACUGGCUU	452	AAGCCAGT A CAGAGAAA	980
2889	CACCACAG CUGAUGAG X CGAA AUUUCUCU	453	AGAGAAAT T CTGTGGTG	981
2890	CCACCACA CUGAUGAG X CGAA AAUUUCUC	454	GAGAAATT C TGTGGTGG	982
2905	ACACCUCG CUGAUGAG X CGAA AUGUUCCC	455	GGGAACAT T CGAGGTGT	983
2906	GACACCUC CUGAUGAG X CGAA AAUGUUCC	456	GGAACATT C GAGGTGTC	984
2914	UGCAGGGU CUGAUGAG X CGAA ACACCUCG	457	CGAGGTGT C ACCCTGCA	985
2928	CCUCACCA CUGAUGAG X CGAA AGCUCUGC	458	GCAGAGCT A TGGTGAGG	986
2944	CUAAGCCU CUGAUGAG X CGAA AUCCACAC	459	GTGTGGAT A AGGCTTAG	987
2950	UGGCACCU CUGAUGAG X CGAA AGCCUUAU	460	ATAAGGCT T AGGTGCCA	988
2951	CUGGCACC CUGAUGAG X CGAA AAGCCUUA	461	TAAGGCTT A GGTGCCAG	989
2965	AGAAUGCU CUGAUGAG X CGAA ACAGCCUG	462	CAGGCTGT A AGCATTCT	990
2971	CAGCUCAG CUGAUGAG X CGAA AUGCUUAC	463	GTAAGCAT T CTGAGCTG	991
2972	CCAGCUCA CUGAUGAG X CGAA AAUGCUUA	464	TAAGCATT C TGAGCTGG	992
2983	AAAACAAC CUGAUGAG X CGAA AGCCAGCU	465	AGCTGGCT T GTTGTTTT	993
2986	UUAAAAAC CUGAUGAG X CGAA ACAAGCCA	466	TGGCTTGT T GTTTTTAA	994
2989	GACUUAAA CUGAUGAG X CGAA ACAACAAG	467	CTTGTTGT T TTTAAGTC	995

Table 3

2990	GGACUUAA CUGAUGAG X CGAA AACAACAA	468	TTGTTGTT T TTAAGTCC	996
2991	AGGACUUA CUGAUGAG X CGAA AAACAACA	469	TGTTGTTT T TAAGTCCT	997
2992	CAGGACUU CUGAUGAG X CGAA AAAACAAC	470	GTTGTTTT T AAGTCCTG	998
2993	ACAGGACU CUGAUGAG X CGAA AAAAACAA	471	TTGTTTTT A AGTCCTGT	999
2997	AUAUACAG CUGAUGAG X CGAA ACUUAAAA	472	TTTTAAGT C CTGTATAT	1000
3002	CAUACAUA CUGAUGAG X CGAA ACAGGACU	473	AGTCCTGT A TATGTATG	1001
3004	UACAUACA CUGAUGAG X CGAA AUACAGGA	474	TCCTGTAT A TGTATGTA	1002
3008	CUACUACA CUGAUGAG X CGAA ACAUAUAC	475	GTATATGT A TGTAGTAG	1003
3012	CAAACUAC CUGAUGAG X CGAA ACAUACAU	476	ATGTATGT A GTAGTTTG	1004
3015	ACCCAAAC CUGAUGAG X CGAA ACUACAUA	477	TATGTAGT A GTTTGGGT	1005
3018	CACACCCA CUGAUGAG X CGAA ACUACUAC	478	GTAGTAGT T TGGGTGTG	1006
3019	ACACACCC CUGAUGAG X CGAA AACUACUA	479	TAGTAGTT T GGGTGTGT	1007
3028	ACUAUAUA CUGAUGAG X CGAA ACACACCC	480	GGGTGTGT A TATATAGT	1008
3030	CUACUAUA CUGAUGAG X CGAA AUACACAC	481	GTGTGTAT A TATAGTAG	1009
3032	UGCUACUA CUGAUGAG X CGAA AUAUACAC	482	GTGTATAT A TAGTAGCA	1010
3034	AAUGCUAC CUGAUGAG X CGAA AUAUAUAC	483	GTATATAT A GTAGCATT	1011
3037	UGAAAUGC CUGAUGAG X CGAA ACUAUAUA	484	TATATAGT A GCATTTCA	1012
3042	CAUUUUGA CUGAUGAG X CGAA AUGCUACU	485	AGTAGCAT T TCAAAATG	1013
3043	CCAUUUUG CUGAUGAG X CGAA AAUGCUAC	486	GTAGCATT T CAAAATGG	1014
3044	UCCAUUUU CUGAUGAG X CGAA AAAUGCUA	487	TAGCATTT C AAAATGGA	1015
3056	UAAACCAG CUGAUGAG X CGAA ACGUCCAU	488	ATGGACGT A CTGGTTTA	1016
3062	GGAGGUUA CUGAUGAG X CGAA ACCAGUAC	489	GTACTGGT T TAACCTCC	1017
3063	AGGAGGUU CUGAUGAG X CGAA AACCAGUA	490	TACTGGTT T AACCTCCT	1018
3064	UAGGAGGU CUGAUGAG X CGAA AAACCAGU	491	ACTGGTTT A ACCTCCTA	1019
3069	AAGGAUAG CUGAUGAG X CGAA AGGUUAAA	492	TTTAACCT C CTATCCTT	1020
3072	UCCAAGGA CUGAUGAG X CGAA AGGAGGUU	493	AACCTCCT A TCCTTGGA	1021
3074	UCUCCAAG CUGAUGAG X CGAA AUAGGAGG	494	CCTCCTAT C CTTGGAGA	1022
3077	UGCUCUCC CUGAUGAG X CGAA AGGAUAGG	495	CCTATCCT T GGAGAGCA	1023
3093	AAGGUGGA CUGAUGAG X CGAA AGCCAGCU	496	AGCTGGCT C TCCACCTT	1024
3095	ACAAGGUG CUGAUGAG X CGAA AGAGCCAG	497	CTGGCTCT C CACCTTGT	1025
3101	UGUGUAAC CUGAUGAG X CGAA AGGUGGAG	498	CTCCACCT T GTTACACA	1026
3104	UAAUGUGU CUGAUGAG X CGAA ACAAGGUG	499	CACCTTGT T ACACATTA	1027
3105	AUAAUGUG CUGAUGAG X CGAA AACAAGGU	500	ACCTTGTT A CACATTAT	1028
3111	UCUAACAU CUGAUGAG X CGAA AUGUGUAA	501	TTACACAT T ATGTTAGA	1029
3112	CUCUAACA CUGAUGAG X CGAA AAUGUGUA	502	TACACATT A TGTTAGAG	1030
3116	ACCUCUCU CUGAUGAG X CGAA ACAUAAUG	503	CATTATGT T AGAGAGGT	1031
3117	UACCUCUC CUGAUGAG X CGAA AACAUAAU	504	ATTATGTT A GAGAGGTA	1032
3125	CAGCUCGC CUGAUGAG X CGAA ACCUCUCU	505	AGAGAGGT A GCGAGCTG	1033
3136	ACAUAGCA CUGAUGAG X CGAA AGCAGCUC	506	GAGCTGCT C TGCTATGT	1034
3141	UAAGGACA CUGAUGAG X CGAA AGCAGAGC	507	GCTCTGCT A TGTCCTTA	1035
3145	GGCUUAAG CUGAUGAG X CGAA ACAUAGCA	508	TGCTATGT C CTTAAGCC	1036
3148	AUUGGCUU CUGAUGAG X CGAA AGGACAUA	509	TATGTCCT T AAGCCAAT	1037
3149	UAUUGGCU CUGAUGAG X CGAA AAGGACAU	510	ATGTCCTT A AGCCAATA	1038
3157	UGAGUAAA CUGAUGAG X CGAA AUUGGCUU	511	AAGCCAAT A TTTACTCA	1039
3159	GAUGAGUA CUGAUGAG X CGAA AUAUUGGC	512	GCCAATAT T TACTCATC	1040
3160	UGAUGAGU CUGAUGAG X CGAA AAUAUUGG	513	CCAATATT T ACTCATCA	1041
3161	CUGAUGAG CUGAUGAG X CGAA AAAUAUUG	514	CAATATTT A CTCATCAG	1042

Table 3

3164	GACCUGAU CUGAUGAG X CGAA AGUAAAI	JA 515	TATTTACT C ATCAGGTC	1043
3167	AAUGACCU CUGAUGAG X CGAA AUGAGU	AA 516	TTACTCAT C AGGTCATT	1044
3172	AAAAUAAU CUGAUGAG X CGAA ACCUGA	UG 517	CATCAGGT C ATTATTT	1045
3175	UAAAAAU CUGAUGAG X CGAA AUGACC	JG 518	CAGGTCAT T ATTTTTA	1046
3176	GUAAAAA CUGAUGAG X CGAA AAUGAC	CU 519	AGGTCATT A TTTTTTAC	1047
3178	UUGUAAAA CUGAUGAG X CGAA AUAAUG	AC 520	GTCATTAT T TTTTACAA	1048
3179	AUUGUAAA CUGAUGAG X CGAA AAUAAU	GA 521	TCATTATT T TTTACAAT	1049
3180	CAUUGUAA CUGAUGAG X CGAA AAAUAA	JG 522	CATTATTT T TTACAATG	1050
3181	CCAUUGUA CUGAUGAG X CGAA AAAAUA	AU 523	ATTATTTT T TACAATGG	1051
3182	GCCAUUGU CUGAUGAG X CGAA AAAAAU	AA 524	TTATTTT T ACAATGGC	1052
3183	GGCCAUUG CUGAUGAG X CGAA AAAAAA	JA 525	TATTTTT A CAATGGCC	1053
3199	AAAUGGUU CUGAUGAG X CGAA AUUCCA	JG 526	CATGGAAT A AACCATTT	1054
3206	UUUGUAAA CUGAUGAG X CGAA AUGGUU	JA 527	TAAACCAT T TTTACAAA	1055
3207	UUUUUGUAA CUGAUGAG X CGAA AAUGGU	JU 528	AAACCATT T TTACAAAA	1056

Input Sequence = PTRN1 (Homo sapiens protein tyrosine phosphatase, non-receptor type 1 (PTRN1) 3215 bpl
Cut Site = UH.

Table 4

Table 4: Human PTP-1B NCH Ribozyme and Target Sequence

Nt. Position	Ribozyme Sequence	Seq. ID Nos.	Substrate Sequence	Seq. ID Nos.
13	CCGCUCUA CUGAUGAG X CGAA ICCGCGUC	1057	GACGCGGC C TAGAGCGG	1781
14	GCCGCUCU CUGAUGAG X CGAA IGCCGCGU	1058	ACGCGGCC T AGAGCGGC	1782
23	GCGCCGUC CUGAUGAG X CGAA ICCGCUCU	1059	AGAGCGGC A GACGGCGC	1783
32	CGGCCCAC CUGAUGAG X CGAA ICGCCGUC	1060	GACGGCGC A GTGGGCCG	1784
39	UCCUUCUC CUGAUGAG X CGAA ICCCACUG	1061	CAGTGGGC C GAGAAGGA	1785
53	GCGGCUGC CUGAUGAG X CGAA ICGCCUCC	1062	GGAGGCGC A GCAGCCGC	1786
56	AGGGCGGC CUGAUGAG X CGAA ICUGCGCC	1063	GGCGCAGC A GCCGCCCT	1787
59	GCCAGGGC CUGAUGAG X CGAA ICUGCUGC	1064	GCAGCAGC C GCCCTGGC	1788
62	CGGGCCAG CUGAUGAG X CGAA ICGGCUGC	1065	GCAGCCGC C CTGGCCCG	1789
63	ACGGGCCA CUGAUGAG X CGAA IGCGGCUG	1066	CAGCCGCC C TGGCCCGT	1790
64	GACGGGCC CUGAUGAG X CGAA IGGCGGCU	1067	AGCCGCCC T GGCCCGTC	1791
68	CCAUGACG CUGAUGAG X CGAA ICCAGGGC	1068	GCCCTGGC C CGTCATGG	1792
69	UCCAUGAC CUGAUGAG X CGAA IGCCAGGG	1069	CCCTGGCC C GTCATGGA	1793
73	CAUCUCCA CUGAUGAG X CGAA IACGGGCC	1070	GGCCCGTC A TGGAGATG	1794
98	UGUCGAUC CUGAUGAG X CGAA ICUCGAAC	1071	GTTCGAGC A GATCGACA	1795
106	CCCGGACU CUGAUGAG X CGAA IUCGAUCU	1072	AGATCGAC A AGTCCGGG	1796
111	CAGCUCCC CUGAUGAG X CGAA IACUUGUC	1073	GACAAGTC C GGGAGCTG	1797
118	GGCCGCCC CUGAUGAG X CGAA ICUCCCGG	1074	CCGGGAGC T GGGCGGCC	1798
126	UGGUAAAU CUGAUGAG X CGAA ICCGCCCA	1075	TGGGCGGC C ATTTACCA	1799
127	CUGGUAAA CUGAUGAG X CGAA IGCCGCCC	1076	GGGCGGCC A TTTACCAG	1800
133	GAUAUCCU CUGAUGAG X CGAA IUAAAUGG	1077	CCATTTAC C AGGATATC	1801
134	GGAUAUCC CUGAUGAG X CGAA IGUAAAUG	1078	CATTTACC A GGATATCC	1802
142	UUCAUGUC CUGAUGAG X CGAA IAUAUCCU	1079	AGGATATC C GACATGAA	1803
146	UGGCUUCA CUGAUGAG X CGAA IUCGGAUA	1080	TATCCGAC A TGAAGCCA	1804
153	AAGUCACU CUGAUGAG X CGAA ICUUCAUG	1081	CATGAAGC C AGTGACTT	1805
154	GAAGUCAC CUGAUGAG X CGAA IGCUUCAU	1082	ATGAAGCC A GTGACTTC	1806
160	ACAUGGGA CUGAUGAG X CGAA IUCACUGG	1083	CCAGTGAC T TCCCATGT	1807
163	UCUACAUG CUGAUGAG X CGAA IAAGUCAC	1084	GTGACTTC C CATGTAGA	1808
164	CUCUACAU CUGAUGAG X CGAA IGAAGUCA	1085	TGACTTCC C ATGTAGAG	1809
165	ACUCUACA CUGAUGAG X CGAA IGGAAGUC	1086	GACTTCCC A TGTAGAGT	1810
177	GGAAGCUU CUGAUGAG X CGAA ICCACUCU	1087	AGAGTGGC C AAGCTTCC	1811
178	AGGAAGCU CUGAUGAG X CGAA IGCCACUC	1088	GAGTGGCC A AGCTTCCT	1812
182	UCUUAGGA CUGAUGAG X CGAA ICUUGGCC	1089	GGCCAAGC T TCCTAAGA	1813
185	UGUUCUUA CUGAUGAG X CGAA IAAGCUUG	1090	CAAGCTTC C TAAGAACA	1814
186	UUGUUCUU CUGAUGAG X CGAA IGAAGCUU	1091	AAGCTTCC T AAGAACAA	1815
193	UCGGUUUU CUGAUGAG X CGAA IUUCUUAG	1092	CTAAGAAC A AAAACCGA	1816
199	CCUAUUUC CUGAUGAG X CGAA IUUUUUGU	1093	ACAAAAAC C GAAATAGG	1817
211	GACGUCUC CUGAUGAG X CGAA IUACCUAU	1094	ATAGGTAC A GAGACGTC	1818
220	AAAGGGAC CUGAUGAG X CGAA IACGUCUC	1095	GAGACGTC A GTCCCTTT	1819
224	GGUCAAAG CUGAUGAG X CGAA IACUGACG	1096	CGTCAGTC C CTTTGACC	1820
225	UGGUCAAA CUGAUGAG X CGAA IGACUGAC	1097	GTCAGTCC C TTTGACCA	1821
226	AUGGUCAA CUGAUGAG X CGAA IGGACUGA	1098	TCAGTCCC T TTGACCAT	1822
232	CCGACUAU CUGAUGAG X CGAA IUCAAAGG	1099	CCTTTGAC C ATAGTCGG	1823

Table 4

233	UCCGACUA CUGAUGAG X CGAA IGUCAAAG	1100	CTTTGACC A TAGTCGGA	1824
248	CUUGAUGU CUGAUGAG X CGAA IUUUAAUC	1101	GATTAAAC T ACATCAAG	1825
251	CUUCUUGA CUGAUGAG X CGAA IUAGUUUA	1102	TAAACTAC A TCAAGAAG	1826
254	UAUCUUCU CUGAUGAG X CGAA IAUGUAGU	1103	ACTACATC A AGAAGATA	1827
268	GUUGAUAU CUGAUGAG X CGAA IUCAUUAU	1104	ATAATGAC T ATATCAAC	1828
274	ACUAGCGU CUGAUGAG X CGAA IAUAUAGU	1105	ACTATATC A ACGCTAGT	1829
279	AUCAAACU CUGAUGAG X CGAA ICGUUGAU	1106	ATCAACGC T AGTTTGAT	1830
303	CUCCUUUG CUGAUGAG X CGAA ICUUCUUC	1107	GAAGAAGC C CAAAGGAG	1831
304	ACUCCUUU CUGAUGAG X CGAA IGCUUCUU	1108	AAGAAGCC C AAAGGAGT	1832
305	AACUCCUU CUGAUGAG X CGAA IGGCUUCU	1109	AGAAGCCC A AAGGAGTT	1833
316	GGUAAGAA CUGAUGAG X CGAA IUAACUCC	1110	GGAGTTAC A TTCTTACC	1834
320	CCUGGGUA CUGAUGAG X CGAA IAAUGUAA	1111	TTACATTC T TACCCAGG	1835
324	GGGCCCUG CUGAUGAG X CGAA IUAAGAAU	1112	ATTCTTAC C CAGGGCCC	1836
325	AGGGCCCU CUGAUGAG X CGAA IGUAAGAA	1113	TTCTTACC C AGGGCCCT	1837
326	AAGGGCCC CUGAUGAG X CGAA IGGUAAGA	1114	TCTTACCC A GGGCCCTT	1838
331	AGGCAAAG CUGAUGAG X CGAA ICCCUGGG	1115	CCCAGGGC C CTTTGCCT	1839
332	UAGGCAAA CUGAUGAG X CGAA IGCCCUGG	1116	CCAGGGCC C TTTGCCTA	1840
333	UUAGGCAA CUGAUGAG X CGAA IGGCCCUG	1117	CAGGGCCC T TTGCCTAA	1841
338	AUGUGUUA CUGAUGAG X CGAA ICAAAGGG	1118	CCCTTTGC C TAACACAT	1842
339	CAUGUGUU CUGAUGAG X CGAA IGCAAAGG	1119	CCTTTGCC T AACACATG	1843
343	ACCGCAUG CUGAUGAG X CGAA IUUAGGCA	1120	TGCCTAAC A CATGCGGT	1844
345	UGACCGCA CUGAUGAG X CGAA IUGUUAGG	1121	CCTAACAC A TGCGGTCA	1845
353	CCCAAAAG CUGAUGAG X CGAA IACCGCAU	1122	ATGCGGTC A CTTTTGGG	1846
355	CUCCCAAA CUGAUGAG X CGAA IUGACCGC	1123	GCGGTCAC T TTTGGGAG	1847
377	UGCUUUUC CUGAUGAG X CGAA ICUCCCAC	1124	GTGGGAGC A GAAAAGCA	1848
385	GACACCCC CUGAUGAG X CGAA ICUUUUCU	1125	AGAAAAGC A GGGGTGTC	1849
397	GUUGAGCA CUGAUGAG X CGAA IACGACAC	1126	GTGTCGTC A TGCTCAAC	1850
401	CUCUGUUG CUGAUGAG X CGAA ICAUGACG	1127	CGTCATGC T CAACAGAG	1851
403	CACUCUGU CUGAUGAG X CGAA IAGCAUGA	1128	TCATGCTC A ACAGAGTG	1852
406	CAUCACUC CUGAUGAG X CGAA IUUGAGCA	1129	TGCTCAAC A GAGTGATG	1853
438	CAGUAUUG CUGAUGAG X CGAA ICGCAUUU	1130	AAATGCGC A CAATACTG	1854
440	GCCAGUAU CUGAUGAG X CGAA IUGCGCAU	1131	ATGCGCAC A ATACTGGC	1855
445	UUGUGGCC CUGAUGAG X CGAA IUAUUGUG	1132	CACAATAC T GGCCACAA	1856
449	CUUUUUGU CUGAUGAG X CGAA ICCAGUAU	1133	ATACTGGC C ACAAAAAG	1857
450	UCUUUUUG CUGAUGAG X CGAA IGCCAGUA	1134	TACTGGCC A CAAAAAGA	1858
452	CUUCUUUU CUGAUGAG X CGAA IUGGCCAG	1135	CTGGCCAC A AAAAGAAG	1859
475	GUCUUCAA CUGAUGAG X CGAA IAUCAUCU	1136	AGATGATC T TTGAAGAC	1860
484	CAAAUUUG CUGADGAG X CGAA IUCUUCAA	1137	TTGAAGAC A CAAATTTG	1861
486	UUCAAAUU CUGAUGAG X CGAA IUGUCUUC	1138	GAAGACAC A AATTTGAA	1862
501	GAGAUCAA CUGAUGAG X CGAA IUUAAUUU	1139	AAATTAAC A TTGATCTC	1863
508	AUCUUCAG CUGAUGAG X CGAA IAUCAAUG	1140	CATTGATC T CTGAAGAT	1864
510	AUAUCUUC CUGAUGAG X CGAA IAGAUCAA	1141	TTGATCTC T GAAGATAT	1865
520	AUAUGACU CUGAUGAG X CGAA IAUAUCUU	1142	AAGATATC A AGTCATAT	1866
525	GUAUAAUA CUGAUGAG X CGAA IACUUGAU	1143	ATCAAGTC A TATTATAC	1867
534	UGUCGCAC CUGAUGAG X CGAA IUAUAAUA	1144	TATTATAC A GTGCGACA	1868
542	AUUCUAGC CUGAUGAG X CGAA IUCGCACU	1145	AGTGCGAC A GCTAGAAT	1869
545	CCAAUUCU CUGAUGAG X CGAA ICUGUCGC	1146	GCGACAGC T AGAATTGG	1870

Table 4

559	GGUUGUAA CUGAUGAG X CGAA IUUUUCCA	1147	TGGAAAAC C TTACAACC	1871
560	GGGUUGUA CUGAUGAG X CGAA IGUUUUCC	1148	GGAAAACC T TACAACCC	1872
564	UCUUGGGU CUGAUGAG X CGAA IUAAGGUU	1149	AACCTTAC A ACCCAAGA	1873
567	GUUUCUUG CUGAUGAG X CGAA IUUGUAAG	1150	CTTACAAC C CAAGAAAC	1874
568	AGUUUCUU CUGAUGAG X CGAA IGUUGUAA	1151	TTACAACC C AAGAAACT	1875
569	GAGUUUCU CUGAUGAG X CGAA IGGUUGUA	1152	TACAACCC A AGAAACTC	1876
576	AUCUCUCG CUGAUGAG X CGAA IUUUCUUG	1153	CAAGAAAC T CGAGAGAT	1877 -
586	GAAAUGUA CUGAUGAG X CGAA IAUCUCUC	1154	GAGAGATC T TACATTTC	1878
590	AGUGGAAA CUGAUGAG X CGAA IUAAGAUC	1155	GATCTTAC A TTTCCACT	1879
595	GGUAUAGU CUGAUGAG X CGAA IAAAUGUA	1156	TACATTTC C ACTATACC	1880
596	UGGUAUAG CUGAUGAG X CGAA IGAAAUGU	1157	ACATTICC A CTATACCA	1881
598	UGUGGUAU CUGAUGAG X CGAA IUGGAAAU	1158	ATTTCCAC T ATACCACA	1882
603	GGCCAUGU CUGAUGAG X CGAA IUAUAGUG	1159	CACTATAC C ACATGGCC	1883
604	AGGCCAUG CUGAUGAG X CGAA IGUAUAGU	1160	ACTATACC A CATGGCCT	1884
606	UCAGGCCA CUGAUGAG X CGAA IUGGUAUA	1161	TATACCAC A TGGCCTGA	1885
611	CAAAGUCA CUGAUGAG X CGAA ICCAUGUG	1162	CACATGGC C TGACTTTG	1886
612	CCAAAGUC CUGAUGAG X CGAA IGCCAUGU	1163	ACATGGCC T GACTTTGG	1887
616	GACUCCAA CUGAUGAG X CGAA IUCAGGCC	1164	GGCCTGAC T TTGGAGTC	1888
625	UGAUUCAG CUGAUGAG X CGAA IACUCCAA	1165	TTGGAGTC C CTGAATCA	1889 -
626	GUGAUUCA CUGAUGAG X CGAA IGACUCCA	1166	TGGAGTCC C TGAATCAC	1890
627	GGUGAUUC CUGAUGAG X CGAA IGGACUCC	1167	GGAGTCCC T GAATCACC	1891
633	GAGGCUGG CUGAUGAG X CGAA IAUUCAGG	1168	CCTGAATC A CCAGCCTC	1892
635	AUGAGGCU CUGAUGAG X CGAA IUGAUUCA	1169	TGAATCAC C AGCCTCAT	1893
636	AAUGAGGC CUGAUGAG X CGAA IGUGAUUC	1170	GAATCACC A GCCTCATT	1894
639	AAGAAUGA CUGAUGAG X CGAA ICUGGUGA	1171	TCACCAGC C TCATTCTT	1895
640	CAAGAAUG CUGAUGAG X CGAA IGCUGGUG	1172	CACCAGCC T CATTCTTG	1896
642	UUCAAGAA CUGAUGAG X CGAA IAGGCUGG	1173	CCAGCCTC A TTCTTGAA	1897
646	AAAGUUCA CUGAUGAG X CGAA IAAUGAGG	1174	CCTCATTC T TGAACTTT	1898
652	GAAAAGAA CUGAUGAG X CGAA IUUCAAGA	1175	TCTTGAAC T TTCTTTTC	1899
656	CUUUGAAA CUGAUGAG X CGAA IAAAGUUC	1176	GAACTTTC T TTTCAAAG	1900
661	UCGGACUU CUGAUGAG X CGAA IAAAAGAA	1177	TTCTTTTC A AAGTCCGA	1901
667	UGACUCUC CUGAUGAG X CGAA IACUUUGA	1178	TCAAAGTC C GAGAGTCA	1902
675	AGUGACCC CUGAUGAG X CGAA IACUCUCG	1179	CGAGAGTC A GGGTCACT	1903
681	GGGCUGAG CUGAUGAG X CGAA IACCCUGA	1180	TCAGGGTC A CTCAGCCC	1904
683	CCGGGCUG CUGAUGAG X CGAA IUGACCCU	1181	AGGGTCAC T CAGCCCGG	1905
685	CUCCGGGC CUGAUGAG X CGAA IAGUGACC	1182	GGTCACTC A GCCCGGAG	1906
688	GUGCUCCG CUGAUGAG X CGAA ICUGAGUG	1183	CACTCAGC C CGGAGCAC	1907
689	CGUGCUCC CUGAUGAG X CGAA IGCUGAGU	1184 .	ACTCAGCC C GGAGCACG	1908
695	CGGGCCCG CUGAUGAG X CGAA ICUCCGGG	1185	CCCGGAGC A CGGGCCCG	1909
701	CCACAACG CUGAUGAG X CGAA ICCCGUGC	1186	GCACGGGC C CGTTGTGG	1910
702	ACCACAAC CUGAUGAG X CGAA IGCCCGUG	1187	CACGGGCC C GTTGTGGT	1911
713	CACUGCAG CUGAUGAG X CGAA ICACCACA	1188	TGTGGTGC A CTGCAGTG	1912
715	UGCACUGC CUGAUGAG X CGAA IUGCACCA	1189	TGGTGCAC T GCAGTGCA	1913
718	GCCUGCAC CUGAUGAG X CGAA ICAGUGCA	1190	TGCACTGC A GTGCAGGC	1914
723	CCGAUGCC CUGAUGAG X CGAA ICACUGCA	1191	TGCAGTGC A GGCATCGG	1915
727 -	CCUGCCGA CUGAUGAG X CGAA ICCUGCAC	1192	GTGCAGGC A TCGGCAGG	1916
733	UCCAGACC CUGAUGAG X CGAA ICCGAUGC	1193	GCATCGGC A GGTCTGGA	1917

Table 4

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738	AAGGUUCC CUGAUGAG X CGAA IACCUGCC	1194	GGCAGGTC T GGAACCTT	1918
744	AGACAGAA CUGAUGAG X CGAA IUUCCAGA	1195	TCTGGAAC C TTCTGTCT	1919
745	CAGACAGA CUGAUGAG X CGAA IGUUCCAG	1196	CTGGAACC T TCTGTCTG	1920
748	AGCCAGAC CUGAUGAG X CGAA IAAGGUUC	1197	GAACCTIC T GTCTGGCT	1921
752	UAUCAGCC CUGAUGAG X CGAA IACAGAAG	1198	CTTCTGTC T GGCTGATA	1922
756	CAGGUAUC CUGAUGAG X CGAA ICCAGACA	1199	TGTCTGGC T GATACCTG	1923
762	AAGAGGCA CUGAUGAG X CGAA IUAUCAGC	1200	GCTGATAC C TGCCTCTT	1924
763	CAAGAGGC CUGAUGAG X CGAA IGUAUCAG	1201	CTGATACC T GCCTCTTG	1925
766	CAGCAAGA CUGAUGAG X CGAA ICAGGUAU	1202	ATACCTGC C TCTTGCTG	1926
767	UCAGCAAG CUGAUGAG X CGAA IGCAGGUA	1203	TACCTGCC T CTTGCTGA	1927
769	CAUCAGCA CUGAUGAG X CGAA IAGGCAGG	1204	CCTGCCTC T TGCTGATG	1928
773	UGUCCAUC CUGAUGAG X CGAA ICAAGAGG	1205	CCTCTTGC T GATGGACA	1929
781	UUUCCUCU CUGAUGAG X CGAA IUCCAUCA	1206	TGATGGAC A AGAGGAAA	1930
793	GGAAGAAG CUGAUGAG X CGAA IUCUUUCC	1207	GGAAAGAC C CTTCTTCC	1931
794	CGGAAGAA CUGAUGAG X CGAA IGUCUUUC	1208	GAAAGACC C TTCTTCCG	1932
795	ACGGAAGA CUGAUGAG X CGAA IGGUCUUU	1209	AAAGACCC T TCTTCCGT	1933
798	UCAACGGA CUGAUGAG X CGAA IAAGGGUC	1210	GACCCTTC T TCCGTTGA	1934
801	AUAUCAAC CUGAUGAG X CGAA IAAGAAGG	1211	CCTTCTTC C GTTGATAT	1935
811	CACUUUCU CUGAUGAG X CGAA IAUAUCAA	1212	TTGATATC A AGAAAGTG	1936
821	UJUCUAAC CUGAUGAG X CGAA ICACUJUC	1213	GAAAGTGC T GTTAGAAA	1937
851	UCUGGAUC CUGAUGAG X CGAA, ICCCCAUC	1214	GATGGGGC T GATCCAGA	1938
856	GGCUGUCU CUGAUGAG X CGAA IAUCAGCC	1215	GGCTGATC C AGACAGCC	1939
857	CGGCUGUC CUGAUGAG X CGAA IGAUCAGC	1216	GCTGATCC A GACAGCCG	1940
861	UGGUCGGC CUGAUGAG X CGAA TUCUGGAU	1217	ATCCAGAC A GCCGACCA	1941
864	AGCUGGUC CUGAUGAG X CGAA ICUGUCUG	1218	CAGACAGC C GACCAGCT	1942
868	GCGCAGCU CUGAUGAG X CGAA IUCGGCUG	1219	CAGCCGAC C AGCTGCGC	1943
869	AGCGCAGC CUGAUGAG X CGAA IGUCGGCU	1220	AGCCGACC A GCTGCGCT	1944
872	AGAAGCGC CUGAUGAG X CGAA ICUGGUCG	1221	CGACCAGC T GCGCTTCT	1945
877	GUAGGAGA CUGAUGAG X CGAA ICGCAGCU	1222	AGCTGCGC T TCTCCTAC	1946
880	CAGGUAGG CUGAUGAG X CGAA IAAGCGCA	1223	TGCGCTTC T CCTACCTG	1947
	GCCAGGUA CUGAUGAG X CGAA TAGAAGCG	1223	CGCTTCTC C TACCTGC	1947
882				
883	AGCCAGGU CUGAUGAG X CGAA IGAGAAGC	1225	GCTTCTCC T ACCTGGCT	1949
886	CACAGCCA CUGAUGAG X CGAA IUAGGAGA	1226	TCTCCTAC C TGGCTGTG	1950
887	UCACAGCC CUGAUGAG X CGAA IGUAGGAG	1227	CTCCTACC T GGCTGTGA	1951
891	UĆGAUCAC CUGAUGAG X CGAA ICCAGGUA	1228	TACCTGGC T GTGATCGA	1952
906	AUGAAUUU CUGAUGAG X CGAA ICACCUUC	1229	GAAGGTGC C AAATTCAT	1953
907	GAUGAAUU CUGAUGAG X CGAA IGCACCUU	1230	AAGGTGCC A AATTCATC	1954
913	CCCCAUGA CUGAUGAG X CGAA IAAUUUGG	1231	CCAAATTC A TCATGGGG	1955
916	GUCCCCCA CUGAUGAG X CGAA IAUGAAUU	1232	AATTCATC A TGGGGGAC	1956
925	CACGGAAG CUGAUGAG X CGAA IUCCCCCA	1233	TGGGGGAC T CTTCCGTG	1957
927	UGCACGGA CUGAUGAG X CGAA IAGUCCCC	1234	GGGGACTC T TCCGTGCA	1958
930	UCCUGCAC CUGAUGAG X CGAA IAAGAGUC	1235	GACTCTTC C GTGCAGGA	1959
935	ACUGAUCC CUGAUGAG X CGAA ICACGGAA	1236	TTCCGTGC A GGATCAGT	1960
941	CCUUCCAC CUGAUGAG X CGAA IAUCCUGC	1237	GCAGGATC A GTGGAAGG	1961
953	CGUGGGAA CUGAUGAG X CGAA I CUCCUUC	1238	GAAGGAGC T TTCCCACG	1962
957	UCCUCGUG CUGAUGAG X CGAA IAAAGCUC	1239	GAGCTTTC C CACGAGGA	1963
958	GUCCUCGU CUGAUGAG X CGAA IGAAAGCU	1240	AGCTITIC C ACGAGGAC	1964
750	GUCCUCGU CUGAUGMG A CGMA IGAAAGCU	1240	AGCITICE C ACGAGGAC	1-204

Table 4

967 GGGCUCCA CUGAURAGA X CGRA IUCCUCGU 1242 ACGAGRAC C TGGAGCCC 1366 968 GGGCUCCC CUGAURAGA X CGRA IUCCUCGU 1243 CCAGGRAC C TGGAGCCC 1366 979 CGGGUGGG CUGAURAGA X CGRA IUCCCAGG 1244 CCTGGAGC C CCACCCG 1367 979 UGCGGUGG CUGAURAGA X CGRA IGCUCCA 1245 CTGGAGCCC C CCACCCGA 1367 976 CUCGGGUGG CUGAURAGA X CGRA IGCUCCA 1245 TGGAGCCC C CCACCCGA 1367 977 GCUCGGGUG CUGAURAGA X CGRA IGGCUCCA 1245 TGGAGCCC C ACCCGAGC 1379 978 UGCCCGGG CUGAURAGA X CGRA IGGCUCCA 1246 TGGAGCCC C ACCCGAGC 1379 978 UGCCCGGG CUGAURAGA X CGRA IGGGCUCC 1247 GGAGCCC C ACCCGAGCA 1379 978 UGCCCGGG CUGAURAGA X CGRA IGGGGCUC 1248 GAGCCCCC A CCCGAGCA 1377 980 UAURCUCC CUGAURAGA X CGRA IGUGGGGG 1249 GCCCCCAC C CGGAGCA 1377 981 AURUCUCC CUGAURAGA X CGRA IGUGGGGG 1259 CCCCCAC C GAGCATA 1377 981 AURUCUCC CUGAURAGA X CGRA IGUGGGGG 1250 CCCCCAC C GAGCATA 1377 982 GAGGUGGG CUGAURAGA X CGRA IGUGGGGG 1251 ACCCGAGC A TATCCCCC 1377 992 GAGGUGGG CUGAURAGA X CGRA IGUGGGGG 1252 AGCCTATC C CCCCACCT 1377 993 GAGGUGGG CUGAURAGA X CGRA IGUGGGGG 1252 AGCCTATC C CCCCACCT 1377 993 GAGGUGGG CUGAURAGA X CGRA IGGGGAUA 1255 ACCTATCC C CCCCACCT 1377 994 GGGAGGUG CUGAURAGA X CGRA IGGGGAUA 1255 ATTCCCCC C CACCCCCC 1377 995 GAGGAGGU CUGAURAGA X CGRA IGGGGAUA 1255 ATTCCCC C CACCCCCC 1377 995 GAGGAGGU CUGAURAGA X CGRA IGGGGAUA 1255 ATTCCCC C CACCCCCC 1377 996 CCGGGGA CUGAURAGA X CGRA IGGGGAUA 1255 ATTCCCC C CACCCCCC 1377 997 GGCGGGG CUGAURAGA X CGRA IGGGGGAU 1257 ATCCCCCC C ACCCCCCC 1376 998 GCCGGGGG CUGAURAGA X CGRA IGGGGGAU 1257 ATCCCCCC C ACCCCCCC 1376 999 GCCGGGGG CUGAURAGA X CGRA IGGGGGAU 1257 ATCCCCCC C ACCCCCCC 1376 1002 GGUGGCC CUGAURAGA X CGRA IGGGGGAU 1257 ATCCCCCC C ACCCCCCC 1376 1002 GGUGGCC CUGAURAGA X CGRA IGGGGGAU 1259 CCCCCACC C CCCCCCC C 1376 1003 GGUGGCC CUGAURAGA X CGRA IGGGGGAU 1259 CCCCCACC C CCCCCCC C 1376 1001 GUUUGGGGU CUGAURAGA X CGRA IGGGGGAU 1259 CCCCCCAC C CCCCCCC C 1376 1002 GGUGGCC CUGAURAGA X CGRA IGGGGGGAU 1259 CCCCCCAC C CCCCCCC C 1376 1003 GGUGGCC CUGAURAGA X CGRA IGGGGGGA 1259 CCCCCCAC C CCCCACC C CCCCCCC C 1376 1003 GGUGGCC CUGAURAGA X CGRA IGGGGGC					
968 GGGGCUCC CUGAUGAG X CGAA IGUCCUCG 1243 CGAGGACC T GGAGCCCC 196' 974 CGGGUUGG CUGAUGAG X CGAA IGUCCAGG 1244 CCTGGAGC C CCCACCCG 196' 975 UGGGGUGG CUGAUGAG X CGAA IGCUCCAG 1245 CTGGAGC C CCCACCCG 196' 976 CUCGGGUG CUGAUGAG X CGAA IGGCUCCA 1246 977 GCUCGGGUG CUGAUGAG X CGAA IGGCUCCA 1246 977 GCUCGGGUG CUGAUGAG X CGAA IGGCUCCA 1246 978 UGCUCGGG CUGAUGAG X CGAA IGGCUCCA 1247 979 UGCUCGGG CUGAUGAG X CGAA IGGGGCUC 1247 979 UGCUCGGG CUGAUGAG X CGAA IGGGGCUC 1247 980 UGCUCGGG CUGAUGAG X CGAA IGGGGCUC 1248 980 UAUGCUCC C CCCACCCG C GACCCGAC 197' 981 AUGCUCCG CUGAUGAG X CGAA IGGGGCUC 1249 981 AUGUCCGG CUGAUGAG X CGAA IGGGGCUC 1250 981 AUGUCCC C CCCACCC C GACCCAT 197' 986 GGGGGGUG CUGAUGAG X CGAA IGGGGGU 1250 CCCCCAC C GACCCAC 1 67' 981 AGGUGGG CUGAUGAG X CGAA IGGGGGU 1250 CCCCCAC C GACCCAC 1 67' 991 AGGUGGG CUGAUGAG X CGAA IGUCGGGU 1251 ACCCGAC A TATCCCCC 137' 992 GAGGUGG CUGAUGAG X CGAA IGAUGUGGG 1253 GCCATAC C CACCCCC 1 197' 992 GAGGUGG CUGAUGAG X CGAA IGAUAUGC 1253 GCCATACC C CCCACCCC 137' 993 GGCAGGUG CUGAUGAG X CGAA IGAUAUGC 1254 GCATACC C CCCACCCC 1 197' 994 GGGAGGUG CUGAUGAG X CGAA IGAUAUGC 1254 CATACCC C CCACCCCC 137' 995 GGGGAGGU CUGAUGAG X CGAA IGAGAUAUG 1255 ATATCCCC C CACCCCCC 137' 996 GGGGAGGU CUGAUGAG X CGAA IGAGGAUA 1255 ATATCCCC C CACCCCCC 137' 997 GGCGGGGG CUGAUGAG X CGAA IGGGGGAU 1257 ATCCCCC C CACCCCCC 137' 998 GCGCGGGG CUGAUGAG X CGAA IGGGGGAU 1256 ATATCCCCC C CACCCCCC 138' 999 GGCGGGGC CUGAUGAG X CGAA IGGGGGAU 1257 ATCCCCCC C CACCCCCC 138' 1001 GUGCCCG CUGAUGAG X CGAA IGGGGGAU 1257 ATCCCCC C CACCCCCC 138' 1002 GGCGGGG CUGAUGAG X CGAA IGGGGGGU 1259 CCCCCCAC C CCCCCCCC 138' 1003 GGGGGGC CUGAUGAG X CGAA IGGGGGGU 1259 CCCCCCCC C CCCCCCCC 138' 1001 GUGCCCG CUGAUGAG X CGAA IGGGGGGG 1259 CCCCCCCC C CCCCCCCC 138' 1001 GUGCCCG CUGAUGAG X CGAA IGGGGGGG 1259 CCCCCCAC C C CCCCCCCC 138' 1001 GUGCCCG CUGAUGAG X CGAA IGGGGGGG 1259 CCCCCCCC C CCCCCCC C CCCCCCCCC 138' 1002 GGCGGGC CUGAUGAG X CGAA IGGGGGGG 1259 CCCCCCCC C CCCCCCCC C CCCCCCCC C 138' 1003 GGGGGC CUGAUGAG X CGAA IGGGGGGG 1256 CGCCCCC C GGCCAC C CACACC	959	GGUCCUCG CUGAUGAG X CGAA IGGAAAGC	1241	GCTTTCCC A CGAGGACC	1965
974 COGGUIGGO CUGAUGAG X CGAA ICUCCAGG 1244 CCTCGGAGC C CCCACCCG 1961 975 UCGGGUIGG CUGAUGAG X CGAA IGCUCCA 1245 CTGGAGC C CCCACCCGA 1975 976 CUCGGGUIG CUGAUGAG X CGAA IGGGUCCA 1246 TGGAGCC C CCACCCGA 1977 977 GCUCGGGUI CUGAUGAG X CGAA IGGGCUCC 1247 GGAGCCC C CACCCGAG 1977 978 UCCCGGGUI CUGAUGAG X CGAA IGGGCUCC 1249 GACCCCCC A CCCGAGCA 1979 979 UCCCGGGUI CUGAUGAG X CGAA IGGGCUCC 1249 GACCCCCC A CCCGAGCA 1977 980 UAUGCUCC CUGAUGAG X CGAA IUGGGGUI 1249 GACCCCCC A CCGAGCAC 1977 981 AJAUGCUC CUGAUGAG X CGAA IUGGGGGUI 1249 GACCCCCCA C CGAGCATA 1977 981 AJAUGCUC CUGAUGAG X CGAA IUGGGGGUI 1251 ACCCGAGC A TATCCCC 1977 981 AGGUIGGG CUGAUGAG X CGAA IUGGGGUI 1251 ACCCGAGC A TATCCCC 1977 992 GAGGUIGG CUGAUGAG X CGAA IGAUAUGC 1252 AGCATAT C CCCCACCT C CACCCTCC 1977 993 GAGGUIGG CUGAUGAG X CGAA IGAUAUGC 1253 AGCATATC C CCCACCTC 1977 994 GGAGGUIG CUGAUGAG X CGAA IGGAUAUGC 1254 AGCATATC C CCCACCTC 1977 995 GAGGUIGG CUGAUGAG X CGAA IGGAUAUG 1254 ACCCACCTC C CACCTCC 1977 996 GAGGGUIG CUGAUGAG X CGAA IGGAUAUG 1254 ACCACTCC C CACCTCC 1977 997 GCCCGGGA CUGAUGAG X CGAA IGGAUAUG 1254 ACCACTCC C CACCTCC 1977 998 GAGGGUIG CUGAUGAG X CGAA IGGAUAUG 1255 ATRACCCC C ACCTCCC 1977 999 GAGGGUIG CUGAUGAG X CGAA IGGGGAUA 1256 TATCCCC C CACCTCCC 1977 999 GCCGGGGAGUI CUGAUGAG X CGAA IGGGGAUA 1255 TATCCCC C ACCTCCC 1977 999 GCCGGGGG CUGAUGAG X CGAA IGGGGGUI 1257 ATCCCCC C ACCTCCC 1977 999 GCCGGGGG CUGAUGAG X CGAA IGGGGGUI 1259 CCCCCACC T CCCCGGC 1981 1001 GUGGCCGG CUGAUGAG X CGAA IGGGGGUI 1259 CCCCCCAC T CCCCGGC 1981 1002 GGUGGCC CUGAUGAG X CGAA IGGGGGUI 1259 CCCCCCAC T CCCCGGC 1981 1003 GGUGGCC CUGAUGAG X CGAA IGGGGGUI 1259 CCCCCCAC T CCCGGGCC 1981 1001 GUGGCCGG CUGAUGAG X CGAA IGGGGGGUI 1259 CCCCCCAC T CCCGGGCC 1981 1001 GUGGCCGG CUGAUGAG X CGAA IGGGGGGUI 1259 CCCCCCAC T CCCGGGCC 1981 1001 GUGGCCGG CUGAUGAG X CGAA IGGGGGGUI 1259 CCCCCCAC T CCCGGGCC 1981 1001 GUGGCCGG CUGAUGAG X CGAA IGGGGGGC 1254 1007 GUUUGGUU CUGAU	967	GGGCUCCA CUGAUGAG X CGAA IUCCUCGU	1242	ACGAGGAC C TGGAGCCC	1966
975 UCGGGGGG CUGAUGAG X CGAA IGCUCCA 1246 TGGAGCC C CCACCCGA 1967 976 CUCCGGGGG CUGAUGAG X CGAA IGGCCCC 1247 GGAGCCC C CACCCGAG 197 979 UGCUCGGG CUGAUGAG X CGAA IGGGCUCC 1247 GGAGCCC C ACCCGAGC 197 979 UGCUCGGG CUGAUGAG X CGAA IGGGGCUCC 1247 GGAGCCC C ACCCGAGC 197 979 UGCUCGGG CUGAUGAG X CGAA IGGGGCUCC 1249 GGCCCCCA CCGGAGCA 197 980 UAUGCUCG CUGAUGAG X CGAA IGGGGGCC 1249 GGCCCCCA C CGGAGCAT 197 981 AUAUGCUC CUGAUGAG X CGAA IGUGGGGC 1250 CCCCCACC C GAGCATAT 197 981 AUAUGCUC CUGAUGAG X CGAA IGUGGGGC 1251 ACCCGAGC C GAGCATAT 197 982 GAGGGGG CUGAUGAG X CGAA IGUGGGGC 1251 ACCCGAGC C GAGCATAT 197 983 QGGGGGC CUGAUGAG X CGAA IGUGGGGC 1251 ACCCGAGC C GAGCATAT 197 991 AGGGGGG CUGAUGAG X CGAA IGUGGGGG 1252 ACCCTACC C GAGCATAT 197 992 GAGGUGGG CUGAUGAG X CGAA IGUGGGGG 1253 ACCCGACC C C CCACCCC T 197 993 GAGGGUGG CUGAUGAG X CGAA IGUGAUGA 1252 ACCCTACC C 197 994 GGGAGGGG CUGAUGAG X CGAA IGGGAUAU 1252 ACCCTACC C C CCACCCC C 197 995 GGGAGGGG CUGAUGAG X CGAA IGGGAUAU 1255 ATATCCCC C CACCCCC 197 996 C CGGGGAGC CUGAUGAG X CGAA IGGGGAU 1255 ATATCCCC C CACCCCCC 197 996 C CGGGAGAG CUGAUGAG X CGAA IGGGGGAU 1255 ATATCCCC C CACCCCCC 197 999 GCCGGGGA CUGAUGAG X CGAA IGGGGGAU 1257 ATCCCCCC ACCCCCCG 198 1999 GCCGGGGG CUGAUGAG X CGAA IGGGGGAU 1257 ATCCCCCC ACCCCCC 198 1001 GUGGCCCG CUGAUGAG X CGAA IGGGGGAU 1257 ATCCCCCC ACCCCCCC 198 1002 GGUGGCCC CUGAUGAG X CGAA IGGGGGAU 1257 ATCCCCCC ACCCCCC C 1000 1002 GGUGGCCC CUGAUGAG X CGAA IGGGGGAU 1259 CCCCCCAC C TCCCCGGC 188 1001 GUGGCCCG CUGAUGAG X CGAA IGGGGGGAU 1260 CCCACCCC C CCCCCCC C 1000 1002 GGUGGCCC CUGAUGAG X CGAA IGGGGGGAU 1261 CCACCCCC C CCCCCCC C 1000 1002 GGUGGCCC CUGAUGAG X CGAA IGGGGGGAU 1261 CCACCCCC C CCCCCCC C 1000 1002 GGUGGCCC CUGAUGAG X CGAA IGGGGGGAU 1261 CCACCCCC C CCCCCCC C 1000 1003 GGGGGC CUGAUGAG X CGAA IGGGGGGAU 1261 CCACCCCC C CCCCCAC C 198 1001 GUCGUUGC CUGAUGAG X CGAA IGGGGGGC 1262 CACCCACC 188 1001 GUCGCUGC CUGAUGAG X CGAA IGGGGGCC 1262 CACCCACC C 188 1001 GUCGCUGC CUGAUGAG X CGAA IGGGGGCC 1262 CACCCACC C 188 1001 GCCCCCA C CCCACCCC C CCCCCCC C CCCCCACC C 188 1001	968	GGGGCUCC CUGAUGAG X CGAA IGUCCUCG	1243	CGAGGACC T GGAGCCCC	1967
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978 UGCUCGGG CUGAUGAG X CGAA IOGGGCUC 1248 GAGCCCCC A CCCGAGCA 197: 980 UAUGCUCC CUGAUGAG X CGAA IOGGGGGC 1249 GCCCCCAC C GAGCCATA 197: 981 AUAGCUCC CUGAUGAG X CGAA IGUGGGGG 1250 CCCCCAC C GAGCCATA 197: 981 AUAGCUC CUGAUGAG X CGAA ICUGGGGG 1250 CCCCCAC C GAGCCATA 197: 981 AGGUGGGC CUGAUGAG X CGAA ICUGGGGG 1251 ACCCGACC C GAGCCATA 197: 991 AGGUGGGC CUGAUGAG X CGAA ICUGGGGG 1251 ACCCGACC C GAGCCATA 197: 991 AGGUGGGC CUGAUGAG X CGAA IAUAGCU 1252 AGCATATC C CCCCACCT 197: 992 GAGGUGGC CUGAUGAG X CGAA IGAUAUGCU 1253 GCATATC C CCCCACCT 197: 992 GAGGUGGC CUGAUGAG X CGAA IGAUAUGCU 1253 GCATATC C CCCCACCTC 197: 993 GCAGGUGG CUGAUGAG X CGAA IGAUAUGCU 1255 ACTATCCC C CACCTCCC 197: 994 GAGGUGGC CUGAUGAG X CGAA IGAUAUGCU 1255 ATATCCCC C CACCTCCC 197: 995 GCGGAGGUG CUGAUGAG X CGAA IGAGAUAU 1255 ATATCCCC C CACCTCCC 198: 996 CCCGGGGGG CUGAUGAG X CGAA IGGGGGAU 1255 ATATCCCC C ACCTCCCC 198: 996 GCCGGGGG CUGAUGAG X CGAA IGGGGGGA 1259 ATCCCCCC A CCTCCCCG 198: 998 GCCCGGGGG CUGAUGAG X CGAA IGGGGGGA 1259 CCCCCACC T CCCCGGGC 198: 1002 GGGGGGGC CUGAUGAG X CGAA IGGGGGGA 1259 CCCCCACC T CCCCGGGC 188: 1002 GGGGGGGC CUGAUGAG X CGAA IGGGGGGA 1259 CCCCCACC T CCCCGGGC 198: 1003 GGGGGGCC CUGAUGAG X CGAA IGGGGGGA 1259 CCCCCACC T CCCCGGGC 188: 1003 GGGUGGCC CUGAUGAG X CGAA IGGGGGGA 1261 CCACCTC C CGGCCACC 198: 1003 GGGUGGCC CUGAUGAG X CGAA IGAGGUGG 1261 CCACCTC C CGGCCACC 198: 1007 GGUUGGCC CUGAUGAG X CGAA IGAGGUGG 1261 CCACCTC C CGGCCACC 198: 1007 GGUUGGCC CUGAUGAG X CGAA IGAGGUGG 1261 CCACCTC C CGGCCACC 198: 1007 GGUUGGCC CUGAUGAG X CGAA IGAGGUGG 1261 CCACCTC C CGGCCACC 198: 1008 CGUUGGGG CCGCCAUGAGGA X CGAA IGAGGUGG 1261 CCACCCC C CACCCACC 198: 1008 CGUUGGGC CUGAUGAG X CGAA IGAGGGGG 1264 CCCCACCC C CACACCAC 198: 1008 CGUUGGGC CUGAUGAG X CGAA IGCCCGGG 1264 CCCCACCC C CACACCAC 198: 1008 CGUUGGC CUGAUGAG X CGAA IGCCCGGG 1264 CCCCACCC C CACACCAC 198: 1008 CGUUGGC CUGAUGAG X CGAA IGCCCGGG 1264 CCCCACCC C CACACCAC 198: 1010 UUCCCUUC CUGAUGAG X CGAA IGCCCCC CCCCCCCC C CACACCAC 199: 1010 UUCCCUUC CUGAUGAG X CGAA IGCCCCC CCCCCCCCC CCACACCAC 199: 1010	976	CUCGGGUG CUGAUGAG X CGAA IGGCUCCA	1246	TGGAGCCC C CACCCGAG	1970
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981	978	UGCUCGGG CUGAUGAG X CGAA IGGGGCUC	1248	GAGCCCCC A CCCGAGCA	1972
996 GGGGGGAUA CUGAUGAG X CGAA IGUCGGGG 1251 ACCCCAGC A TATCCCCC 1979 991 AGGUGGGC CUGAUGAG X CGAA IGAAUGCC 1253 GCCTATCC C CCCACCTC 1977 992 GAGGUGGC CUGAUGAG X CGAA IGAAUGCC 1253 GCCTATCC C CCCACCTC 1977 993 GGAGGUG CUGAUGAG X CGAA IGAAUGCC 1255 GCCTATCC C CCCACCTC 1977 994 GGGAGGUG CUGAUGAG X CGAA IGAGAUAUC 1255 ATATCCCC C CCACCTCC 1977 995 GGGAGGUG CUGAUGAG X CGAA IGAGAUAU 1255 ATATCCCCC C CACCTCCC 1977 996 GGGAGGUG CUGAUGAG X CGAA IGAGGAUAU 1255 ATATCCCCC C CACCTCCC 1879 997 GGCGGGGG CUGAUGAG X CGAA IGAGGGGAU 1256 ATATCCCCC C CACCTCCC 1880 998 GCCGGGGG CUGAUGAG X CGAA IGGGGGGA 1259 ATCCCCCC C ACCTCCCCG 1981 999 GGCCGGGG CUGAUGAG X CGAA IGGGGGGA 1259 ATCCCCCC C CACCTCCCG 1981 1001 GUGGCCGG CUGAUGAG X CGAA IGGGGGGG 1259 CCCCCACC T CCCCGGGC 1881 1002 GGUGGCCC CUGAUGAG X CGAA IGGGGGGG 1259 CCCCCACC T CCCCGGGC 1881 1003 GGGUGGCC CUGAUGAG X CGAA IGGGGGGG 1261 CCCACCTC C CGGCCACC 1981 1003 GGGUGGCC CUGAUGAG X CGAA IGGGGGGG 1261 CCCACCTC C CGGCCACC 1981 1007 GGUUGGCC CUGAUGAG X CGAA IGGGGGGG 1261 CCCACCTC C CGGCCACC 1981 1008 CGUUGUGG CUGAUGAG X CGAA IGGGGGGG 1261 CCCACCTC C CGGCCACC 1981 1009 GGUUGGCC CUGAUGAG X CGAA IGCCGGGG 1264 CCCCACCTC C GGCCACCC 1981 1010 GUGUUCUC CUGAUGAG X CGAA IGCCGGGG 1264 CCCCACCTC C GGCCACCC 1981 1011 AUUCGUUU CUGAUGAG X CGAA IGCCGGGG 1265 CCGGCCAC C CAAACCGAA 1981 1012 GAUUCGUU CUGAUGAG X CGAA IGCCGGGG 1266 CCGCCACC C CAAACCGAA 1981 1012 GUGGCUCC CUGAUGAG X CGAA IGCGCCG 1266 CCGCCACC C CAAACCGA 1981 1012 GUGGCUCC CUGAUGAG X CGAA IGCGCCG 1266 CCGCCACC C CAAACCGA 1981 1012 GUGGCUCC CUGAUGAG X CGAA IGCGCCG 1266 CCGCCACC C CAAACCGA 1981 1012 GUGGCUCC CUGAUGAG X CGAA IGCGCCG 1266 CCGCCACC C CAAACCGA 1981 1012 GUGGCUCC CUGAUGAG X CGAA IGCGCCG 1266 CCGCCACC C CAAACCGA 1991 1012 GUGGCUCC CUGAUGAG X CGAA IGCGCCG 1266 CCGCACC C CAAACCGA 1991 1026 CACCCACC CUGAUGAG X CGAA IGCUCCC 1267 GGCCACC C CAAACCGA 1991 1027 GUGGCUCC CUGAUGAG X CGAA IGCUCCC 1267 GGCCACC C CAAACCGA 1991 1028 CAUUGUGU CUGAUGAG X CGAA IGCUCCC 1271 CCGGACCC C CAAACCGA 1991 1031 UCCCCAU CUGAUGAG X CGAA IGCUCCC 1271 CCGGACC C CAA	980	UAUGCUCG CUGAUGAG X CGAA IUGGGGGC	1249	GCCCCCAC C CGAGCATA	1973
991 AGGUGGGG CUGAUGAG X CGAA IAJAUGCU 1252 AGGATATC C CCCACCT 1976 992 GAGGUGGG CUGAUGAG X CGAA IAJAUGCU 1253 GCATATC C CCCACCTC 1977 993 GAGGUGGG CUGAUGAG X CGAA IAGAUAUGC 1253 994 GGAGGUGG CUGAUGAG X CGAA IAGAUAUGC 1254 CATATCCC C CCACCTCC 1977 995 GGAGGGG CUGAUGAG X CGAA IAGAUAUGC 1255 ATATCCCC C CACCTCCC 1979 996 GGCGGGGG CUGAUGAG X CGAA IAGAGGAUAU 1255 ATATCCCC C CACCTCCC 1979 997 GGGAGGGU CUGAUGAG X CGAA IAGAGGAUAU 1255 ATATCCCC C ACCTCCC 1979 998 GCCGGGGA CUGAUGAG X CGAA IAGAGGAUA 1257 ATACCCCC A CCTCCCCG 198 998 GCCGGGGG CUGAUGAG X CGAA IAGAGGGGG 1259 CCCCCACC T CCCCCGGC 198 1999 GCCGGGGG CUGAUGAG X CGAA IAGAUGAG 1259 CCCCCACC T CCCCCGGC 198 1001 GUGGCCG CUGAUGAG X CGAA IAGAUGAG 1259 CCCCACCT C CCGGCCAC 188 1002 GGUGGCCC CUGAUGAG X CGAA IAGAUGAG 1260 CCCACCTC C CGGCCACC 188 1003 GGUGGCCC CUGAUGAG X CGAA IAGAUGAG 1261 CCACCTCC C CGGCCACC 188 1007 GUUUGGGUC CUGAUGAG X CGAA IAGAUGAG 1261 CCACCTCC C CGGCCACC 188 1008 CQUUUGGG CUGAUGAG X CGAA IAGAUGAG 1261 CCACCTCC C GGGCCACC 188 1010 UUCGUUUG CUGAUGAG X CGAA IAGAUGAG 1264 CCCCCGGC C ACCCAAAC 189 1010 UUCGUUUG CUGAUGAG X CGAA IAGAUGAG 1264 CCCCGGGC C ACCCAAAC 189 1011 AUUCGUUU CUGAUGAG X CGAA IAGACGGGG 1265 CCGGCCC C CAAACGAAC 189 1012 GAUUCGGU CUGAUGAG X CGAA IAGACGGGG 1265 CCGGCCC C CAAACGAAC 189 1011 AUUCGUUU CUGAUGAG X CGAA IAGACGGGG 1265 CCGGCCC C CAAACGAAC 189 1012 GAUUCGGU CUGAUGAG X CGAA IAGUCGCG 1265 CCGGCCAC C CAAACGAAC 189 1012 GAUUCGGU CUGAUGAG X CGAA IAGUCGCC 1267 GCCCACC C CAAACGAA 189 1012 GAUUCGGU CUGAUGAG X CGAA IAGUCGCC 1267 GCCCACC C AAACGAAT 189 1021 UUCGCUU CUGAUGAG X CGAA IAGUCGCC 1267 GCCCACC C CAAACGAA 189 1022 GCAUUGGG CUGAUGAG X CGAA IAGUCGCC 1267 GCCCACC C AAACGAAT 189 1023 GAUUCCCU CUGAUGAG X CGAA IAGUCGCC 1267 GCCCACC C AAACGAAT 189 1024 CAAUGUGG CUGAUGAG X CGAA IAGUCGCC 1267 GCGCACC C AAACGAAT 189 1026 CCACCC CUGAUGAG X CGAA IAGUCGCC 1267 GCGCCACC C AAACGAAT 189 1027 CCCAUGC CUGAUGAG X CGAA IAGUCGCC 1267 GCGCCACC C AAACGAAT 189 1028 CAUUCUCCU CUGAUGAG X CGAA IAGUCCC 1272 GGAACCC C CAAACGAAT 189 1031 UUCCCCU CUGAUGAG X CGAA IAGUU	981	AUAUGCUC CUGAUGAG X CGAA IGUGGGGG	1250	CCCCCACC C GAGCATAT	1974
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995 GOGGAGGI CUGAUGGA X CGAA IGGGGAJA 1256 TATCCCCC C ACCTCCCC 1386 996 COGGGAGG CUGAUGGA X CGAA IGGGGAJA 1257 ATCCCCCC A ACCTCCCCC 188. 998 GCCGGGGA CUGAUGGA X CGAA IUGGGGGG 1258 CCCCCCAC C TCCCCGGC 188. 999 GCCGGGGA CUGAUGGA X CGAA IUGGGGGG 1259 CCCCCAC C TCCCCGGCC 188. 1001 GUGGCGG CUGAUGGA X CGAA IAGGUGGG 1259 CCCCCCCC C CCGGGCCAC 188. 1002 GUGUGCCG CUGAUGGA X CGAA IAGGUGGG 1261 CCCACCTC C CGGCCACC 188. 1003 GGGUGGCC CUGAUGGA X CGAA IGGAGGGA 1262 CACCTCCC C GGCCACC 188. 1007 GUUUGGG CUGAUGGA X CGAA IGCCGGGA 1263 TCCCCGGCC C ACCCAAAC 188. 1010 UUCGUUUG CUGAUGGA X CGAA IGCCGGGA 1264 CCCCGGCC C CAAACGAA 188. 1011 UUCGUUUG CUGAUGGA X CGAA IGGUGGCC 1265 CGGCCACC C AAACGAA 189. 1012 GUGCUCCA CUGAUGGA X CGAA IGGUGGCC 1267 GGCCACCC A AACGAAT 199. 1021 UGGCUCCA CUGAUGGA X CGAA IGUCCGC 1269 ACGAATC C T GGAGCCA	993	GGAGGUGG CUGAUGAG X CGAA IGGAUAUG	1254	CATATCCC C CCACCTCC	1978
996 CGGGGAGG CUGAUGAG X CGAA IGGGGGAU 1257 ATCCCCCC A CCTCCCCG 198. 998 GCCGGGGA CUGAUGAG X CGAA IGGGGGGAU 1259 CCCCCCAC C TCCCCGGGC 198. 1999 GCCGGGGG CUGAUGAG X CGAA IGGGGGGG 1259 CCCCCAC C TCCCCGGGC 198. 1001 GUGGCCGG GUGAUGAG X CGAA IAGGUGGG 1259 CCCCACCT C CCCGGGCC 198. 1002 GGUGGCC GUGAUGAG X CGAA IAGGUGGG 1250 CCCACCTC C CGGGCCAC 198. 1003 GGUGGCC CUGAUGAG X CGAA IAGGUGGG 1261 CCACCTC C GGGCCACC 198. 1007 GUTUNGGGU CUGAUGAG X CGAA IGGGGGG 1262 CACCCAAAC 198. 1008 CGUUUGGG CUGAUGAG X CGAA IGGGGGG 1264 CCCCGGGC A CCCAAAC 198. 1019 UUCGUUUG CUGAUGAG X CGAA IGCGGGG 1264 CCCCGGCC C CACCCAAAC 198. 1010 UUCGUUUG CUGAUGAG X CGAA IGCGGGG 1265 CCGGCCAC C CAAACGAAC 198. 1011 AUUCGUUU CUGAUGAG X CGAA IGGGCGG 1265 CCGGCCAC C CAAACGAAC 198. 1012 GAUUCGUU CUGAUGAG X CGAA IGGGCGG 1265 CCGGCCAC C CAAACGAAC 199. 1012 GAUUCGUU CUGAUGAG X CGAA IAGUCGCG 1265 CCGGCCAC C CAAACGAAC 199. 1021 UGGCUCCC CUGAUGAG X CGAA IAGUCGCG 1267 GGCCACCC A AACGAAT 199. 1022 GGGGCCC CUGAUGAG X CGAA IAGUCGUU 1268 AACGAAT C 199. 1028 CAUUGUGU CUGAUGAG X CGAA IAGUCGU 1269 AACGAAC T TGGAGCCA 199. 1029 CCAUUGUC CUGAUGAG X CGAA IAGUCGU 1269 AACGAAC T TGGAGCCA 199. 1029 CCAUUGUC CUGAUGAG X CGAA IAGUCGU 1269 AACGAAC T TGGAGCCA 199. 1028 CAUUGUG CUGAUGAG X CGAA IAGUCGU 1269 AACGAAC T TGGAGCCA 199. 1029 CCAUUGUC CUGAUGAG X CGAA IAGUCGU 1269 AACGAAC T TGGAGCCA 199. 1031 UCCCCAUUG CUGAUGAG X CGAA IAGUCGUC 1272 GGAGCCAC A AACGAAT 199. 1031 UCCCCAUUG CUGAUGAG X CGAA IAGUCCCC 1272 GGAGCCAC A CACAATGG 199. 1031 UCCCCAUUG CUGAUGAG X CGAA IAGUCCCC 1272 GGAGCCAC A CACAATGG 199. 1033 UUCCCCU CUGAUGAG X CGAA IAGUCCCC 1272 GGAGCCAC A CACAATGG 199. 1034 CAAUGUCC CUGAUGAG X CGAA IAGUUCCC 1272 GGAGCCAC A CACAATGG 199. 1035 UUCCCAUUG CUGAUGAG X CGAA IAGUUCCC 1274 GGAAAGAC A CACAATGG 199. 1036 CACCCAC C CACAAGAG X CGAA IAGUUCCC 1274 GGAAAGAC C CACAATGG 199. 1037 UUCCCCU CUGAUGAG X CGAA IAGUUCCC 1274 GGAAAGAC C CACAATGG 199. 1036 CACCCAC C CACAAGGAC C CAAACGAC C CACAAGGAC C CAC	994	GGGAGGUG CUGAUGAG X CGAA IGGGAUAU	1255	ATATCCCC C CACCTCCC	1979
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999 GCCCCGGC CUGAUGAG X CGAA IGUIGGGG 1259 CCCCCACC T CCCCGGCC 198: 1001 GUIGCCCG CUGAUGAG X CGAA IAGGUIGG 1261 CCCACCCT C CCCGGCCC 138: 1002 GCUGGCCC CUGAUGAG X CGAA IAGGUIGG 1261 CCCACCCT C CCCGGCCC 138: 1003 GGUIGGCC CUGAUGAG X CGAA IGAGGUIGG 1261 CCACCTCC C CGGCCACC 138: 1007 GUIUUGGG CUGAUGAG X CGAA IGAGGUIGG 1262 CACCTCCC C GGCCACCC 138: 1008 CCUUUGGG CUGAUGAG X CGAA IGCCGGGA 128: 1009 CCUUUGGG CUGAUGAG X CGAA IGCCGGGG 1264 CCCCGGCC C ACCCAAACC 138: 1010 UUCCGUUUG CUGAUGAG X CGAA IGCCCGGG 1264 CCCCGGCC C ACCCAAACC 138: 1011 AUUCGUUU CUGAUGAG X CGAA IGCCCGGG 1265 CCGGCCAC C CAAACCGAA 139: 1012 GAUUCGUU CUGAUGAG X CGAA IGCCCGGG 1265 CCGGCCAC C CAAACCGAA 139: 1012 GAUUCGUU CUGAUGAG X CGAA IGCGCCG 1266 CCGGCCAC C CAAACCGAA 139: 1012 GGUUCCC CUGAUGAG X CGAA IGCGCCG 1266 CCGCCACC C CAAACCGA 139: 1022 GUIGGCUCC CUGAUGAG X CGAA IGCCCGG 1266 CCGCCACC C CAAACCGA 139: 1023 CAUUGUUU CUGAUGAG X CGAA IGCUCCG 1269 ACGAATC C TGGACCCA 139: 1024 CCCAUUGUU CUGAUGAG X CGAA IGCUCCG 1269 ACGAATC C TGGACCCA 139: 1029 CCAUUGUU CUGAUGAG X CGAA IGCUCCG 1270 CCTGGACC A CACACATG 139: 1029 CCAUUGUU CUGAUGAG X CGAA IGCUCCG 1271 CTGGAGCC A CACACATG 139: 1031 UUCCCAU CUGAUGAG X CGAA IUGUCCC 1272 GGAGCCAC C ACACACTG 139: 1031 UUCCCCAU CUGAUGAG X CGAA IUGUCCC 1274 GGAACCC A CAATGGGA 139: 1045 GAACUCC CUGAUGAG X CGAA IACUUCC 1274 GGAACCC A CAATGGGA 139: 1045 GAACUCC CUGAUGAG X CGAA IACUUCC 1274 GGAACCC A CAATGGGA 139: 1057 GUGAUUU CUGAUGAG X CGAA IACUUCC 1274 GGAACCC A CAATGGGA 139: 1058 AUUUCCCAU CUGAUGAG X CGAA IACUUCC 1275 GGAGCTC T CCCAAAC 139: 1059 UGGUGAUU CUGAUGAG X CGAA IACUUCC 1276 GGAGCTC T TCCCAAAT 139: 1051 GUCCCAUUC CUGAUGAG X CGAA IACUUCC 1276 GGAGCTC C CAAATCAC 200: 1057 UGCCCAUC CUGAUGAG X CGAA IGAACCAC 1276 GGAGCTC C CAAATCAC 200: 1058 GUCCCCUC CUGAUGAG X CGAA IGAAUGA	996	· CGGGGAGG CUGAUGAG X CGAA IGGGGGAU	1257	ATCCCCCC A CCTCCCCG	1981
1001	998	GCCGGGGA CUGAUGAG X CGAA IUGGGGGG	1258	CCCCCCAC C TCCCCGGC	1982
1002	999	GGCCGGGG CUGAUGAG X CGAA IGUGGGGG	1259	CCCCCACC T CCCCGGCC	1983
1003	1001	GUGGCCGG CUGAUGAG X CGAA IAGGUGGG	1260	CCCACCTC C CCGGCCAC	1984
1007 GUJUGGGU CUGAUGAG X CGAA ICCGGGGA 1263 TCCCCGGC C ACCCAAAC 1981	1002	GGUGGCCG CUGAUGAG X CGAA IGAGGUGG	1261	CCACCTCC C CGGCCACC	1985
1008	1003	GGGUGGCC CUGAUGAG X CGAA IGGAGGUG	1262	CACCTCCC C GGCCACCC	1986
1011	1007	GUUUGGGU CUGAUGAG X CGAA ICCGGGGA	1263	TCCCCGGC C ACCCAAAC	1987
1011	1008	CGUUUGGG CUGAUGAG X CGAA IGCCGGGG	1264	CCCCGGCC A CCCAAACG	1988
1012	1010	UUCGUUUG CUGAUGAG X CGAA IUGGCCGG	1265	CCGGCCAC C CAAACGAA	1989
1021	1011	AUUCGUUU CUGAUGAG X CGAA IGUGGCCG	1266	CGGCCACC C AAACGAAT	1990
1922 GUGGCÜCC CUGAUGAG X CGAA IGAUUCGU 1269 ACGAATCC T GGAGCCAC 199: 1028 CAUUGUGU CUGAUGAG X CGAA ICUCCAGG 1270 CCTGGAGC C ACACAATG 199: 1039 CCAUUGUGU CUGAUGAG X CGAA IGCUCCAG 1271 CCTGGAGC C ACACAATG 199: 1031 UCCCCAUGU CUGAUGAG X CGAA IGCUCCAG 1271 CCTGGAGC C ACACAATG 199: 1033 UUUCCCAU CUGAUGAG X CGAA IUGUGCCU 1273 AGCCACA C A CAATGGGA 199: 1045 GAACUCCC CUGAUGAG X CGAA ICAUUCCC 1274 GGAAATGC A GGGGATTC 199: 1054 AUUUGGGA CUGAUGAG X CGAA IACAUCCC 1274 GGAAATGC A GGGGATTC 199: 1057 GUGAUUC CUGAUGAG X CGAA IACAUCCC 1275 GGGAGTTC T TCCCAAAT 199: 1058 GGUGAUUU CUGAUGAG X CGAA IACAGACC 1276 AGTTCTC C CAAATCAC 200: 1059 UGGUGAUU CUGAUGAG X CGAA IGGAAGAA 1276 ATTCTCC C AAATCACC 200: 1059 UGGUGAUU CUGAUGAG X CGAA IGGAGAAA 1277 GTTCTTCC C AAATCACC 200: 1056 CACCCACU CUGAUGAG X CGAA IGGAGAGA 1279 CCCAAATCA C AGTGGGG 1064 CCACCAGG CUGAUGAG X CGAA IGGAUGAUU 1280 CCAAATCAC C AGTGGGTG 200: 1056 CACCCACU CUGAUGAG X CGAA IGGAUGUU 1280 CAAATCAC C AGTGGGTG 200: 1057 UCACCCAC CUGAUGAG X CGAA IGUCUCUU 1281 AAATCACC A GGGGGAT 200: 1068 UCCUCCUU CUGAUGAG X CGAA IGUCUCUU 1282 GAAGAGAC C CAGGAGGAT 200: 1069 AUCCUCC CUGAUGAG X CGAA IGUCUCUU 1282 AAGAGACC C AGGAGGAT 200: 1069 AUCCUCC CUGAUGAG X CGAA IGUCUCUU 1281 AAATCACC A GGGGGAT 200: 1068 UCCUCCUC CUGAUGAG X CGAA IGUCUCUU 1282 AAGAGACC C AGGAGGAT 200: 1070 AUCCUCC CUGAUGAG X CGAA IGUCUCUU 1281 AAGAGACC C AGGAGGAT 200: 1070 AUCCUCC CUGAUGAG X CGAA IGUCUCUU 1281 AAGAGACC C AGGAGGAT 200: 1070 AUCCUCC CUGAUGAG X CGAA IGUCUCUU 1281 AAGAGACC C AGGAGGAT 200:	1012	GAUUCGUU CUGAUGAG X CGAA IGGUGGCC	1267	GGCCACCC A AACGAATC	1991
1028	1021	UGGCUCCA CUGAUGAG X CGAA IAUUCGUU	1268	AACGAATC C TGGAGCCA	1992
1029 CCAUUGUG CUGAUGAG X CGAA IGCUCCAG 1271 CTGGAGCC A CACAATGG 1991 1031 UCCCCAUUG CUGAUGAG X CGAA IGCGCUCC 1272 GGAGCCAC A CAATGGGA 1991 1033 UUUCCCAU CUGAUGAG X CGAA IGCGCUCC 1273 AGCCACAC A ATGGGAAA 1999 1045 GAACUCCC CUGAUGAG X CGAA ICAUUCCC 1274 GGAAATGC A GGGAGTTC 1991 1057 AUUUGGGA CUGAUGAG X CGAA IACACACC 1275 GGGAGTTC T TCCCAAAT 1991 1057 GUGAUUG CUGAUGAG X CGAA IGAAGAAC 1276 AGTTCTTC C CAAATCAC 2000 1058 GGUGAUUU CUGAUGAG X CGAA IGAAGAAC 1276 AGTTCTTC C CAAATCAC 2000 1059 UGGUGAUU CUGAUGAG X CGAA IGAAGAAC 1277 GTTCTTCC C AAATCAC 2000 1066 CCCACUGG CUGAUGAG X CGAA IGUGUUU 1280 CCAAATCAC C AGTGGGTG 2000 1067 UCACCCAC CUGAUGAG X CGAA IUGAUUU 1280 CAAATCAC C AGTGGGTG 2000 1068 UCCUCCCUG CUGAUGAG X CGAA IUGAUUU 1281 AAATCAC C AGTGGGTG 2000 1069 UCCUCCCUG CUGAUGAG X CGAA IUGAUUU 1281 AAATCAC C AGTGGGTG 2000 1069 UCCUCCCUG CUGAUGAG X CGAA IUGUGUUU 1281 AAATCAC C AGTGGGTG 2000 1069 AUCUCCUC CUGAUGAG X CGAA IUGUGUUU 1282 GAAGAGAC C CAGGAGGAT 2000 1069 UCCUCCUC CUGAUGAG X CGAA IUGUGUUU 1282 GAAGAGAC C CAGGAGGAT 2000 1069 UCCUCCUC CUGAUGAG X CGAA IUGUGUUU 1282 GAAGAGAC C CAGGAGGAT 2000 1069 AUCUCCUC CUGAUGAG X CGAA IUGUUUU 1282 GAAGAGAC C CAGGAGGAT 2000 1070 AUCUCCUC CUGAUGAG X CGAA IUGUUUU 1282 AAGAGACC C AGGAGGAT 2000 1070 AUCUCCUC CUGAUGAG X CGAA IUGUUUU 1284 AAGAGACC A GGGAGATA 2000 1070 AUCUCCC CUGAUGAG X CGAA IUCUUUU 1285 ATAAAGAC T A GCCCCATC 2000 1100 AUCUCCC CUGAUGAG X CGAA IUCUUUU 1285 ATAAAGAC T A GCCCCATC 2000 1110 AUCUCCC CUGAUGAG X CGAA IUCUUUU 1285 ATAAAGAC T A GCCCCATC 2000 1110 AUCUCCC CUGAUGAG X CGAA IUCUUUU 1285 ATAAAGAC T A GCCCCATC 2000 1110 AUCUCCC CUGAUGAG X CGAA IUCUUUU 1285 ATAAAGAC T A GCCCCATC 2000	1022	GUGGCUCC CUGAUGAG X CGAA IGAUUCGU	1269	ACGAATCC T GGAGCCAC	1993
1031	1028	CAUUGUGU CUGAUGAG X CGAA ICUCCAGG	1270	CCTGGAGC C ACACAATG	1994
1033	1029	CCAUUGUG CUGAUGAG X CGAA IGCUCCAG	1271	CTGGAGCC A CACAATGG	1995
1045	1031	UCCCAUUG CUGAUGAG X CGAA IUGGCUCC	1272	GGAGCCAC A CAATGGGA	1996
1054	1033	UUUCCCAU CUGAUGAG X CGAA IUGUGGCU	1273	AGCCACAC A ATGGGAAA	1997
1057 GUGAUJUG CUGAUGAG X CGAA TAAGAACU 1276 AGTTCTTC C CAAATCAC 2001	1045	GAACUCCC CUGAUGAG X CGAA ICAUUUCC	1274	GGAAATGC A GGGAGTTC	1998
1058 GGUGAUUU CUGAUGAG X CGAA IGAAGAAC 1277 GTTCTTCC C AAATCACC 200: 1059 UGGUGAUU CUGAUGAG X CGAA IGGAAGAA 1278 TTCTTCCC A AATCACC 200: 1064 CCCACUGG CUGAUGAG X CGAA IAUTUGAGG 1279 CCCAAATCA C CCAAGGG CIGAAGGAG X CGAA IAUTUGAGG 1279 CCCAAATCA C CCAGGGGG 200: 1065 CACCCACC CUGAUGAG X CGAA IGUGAUUU 1280 CAAATCAC C AGTGGGTG 200: 1067 UCACCCAC CUGAUGAG X CGAA IGUGUCUU 1281 AAATCAC A GTGGGTG 200: 1086 UCCUCCUU CUGAUGAG X CGAA IGUCUCUU 1282 GAAGAGAC C CAGGAGGA 200: 1087 AUCCUCC CUGAUGAG X CGAA IGUCUCUU 1283 AAGGACC C AGGAGGAT 200: 1088 UAUCCUCC CUGAUGAG X CGAA IGUCUCUU 1284 AAGAGACC A GGAGGATA 200: 1088 UAUCCUCC CUGAUGAG X CGAA IGUCUCUU 1285 ATAAAGAC C AGGAGGAT 200: 1088 UAUCCUCC CUGAUGAG X CGAA IGUCUCUU 1285 ATAAAGAC C AGGAGGAT 200: 1088 UAUCCUCC CUGAUGAG X CGAA IGUCUCUU 1285 ATAAAGAC C AGGAGGAT 200: 1088 UAUCCUCC CUGAUGAG X CGAA IGUCUCUU 1285 ATAAAGAC T GCCCCATC 200: 1088 CACCCATC 200: 1088 CACCATC 200: 1088 CACCCATC 200: 1088 CAC	1054				1999
1059	1057	GUGAUUUG CUGAUGAG X CGAA IAAGAACU	1276		2000
1054 CCCACUGG CUGAUGAG X CGAA TAUTUUGGG 1279 CCCAAATC A CCACTGGG 200: 1056 CACCCACU CUGAUGAG X CGAA TUGAUUUG 1280 CAAATCAC C AGTGGGTG 200- 1067 UGACCAC CUGAUGAG X CGAA TUGUGUUUC 1281 AAATCAC C AGTGGGTG 200- 1086 UCCUCCUG CUGAUGAG X CGAA TUCUCUUC 1282 GAAGAGAC C CAGGAGGA 200- 1087 ADCCUCCU CUGAUGAG X CGAA TUCUCUUC 1283 AAGAGAC C AGGAGGAT 200- 1088 UAUCUCCC CUGAUGAG X CGAA TGUCUCU 1284 AGGAACC A GGAGGAT 200- 1088 UAUCUCCC CUGAUGAG X CGAA TGUCUCU 1284 AGGAACC A GGAGGAT 200- 1089 CAUCUCC CUGAUGAG X CGAA TUCUUUUU 1285 ATAAGAC T GCCCCATC 200- 1090 CACCCACC CUGAUGAG X CGAA TUCUUUUU 1285 ATAAGAC T GCCCCATC 200-	1058	GGUGAUUU CUGAUGAG X CGAA IGAAGAAC			2001
1056 CACCCACU CUGAUGAG X CGAA IUGAUUU 1280 CAAATCAC C AGTOGGTG 200- 1067 UGACCCAC CUGAUGAG X CGAA IGUGAUUU 1281 AAATCAC C AGTOGGTG 200- 1086 UGCUCCOG CUGAUGAG X CGAA IUGCUCUC 1282 GAAGAGAC C CAGGAGGA 200- 1087 AUCCUCCU CUGAUGAG X CGAA IUGCUCUU 1283 AAGAGAC C CAGGAGGAT 200- 1088 UJUCCUCC CUGAUGAG X CGAA IUGCUCUC 1284 AAGAGACC C AGGAGGAT 200- 1103 GAUGGGGC CUGAUGAG X CGAA IUGCUCUC 1284 AAGAGACC AGGAGGAT 200- 1103 GAUGGGGC CUGAUGAG X CGAA IUGCUCUC 1284 AAGAGACC AGGAGGAT 200- 1104 CAUCGGGC CUGAUGAG X CGAA IUGCUCUC 1284 AAGAGACC AGGAGGAT 200- 1105 CAACCCAC C COCCAC CACCAC C COCCAC C COCCAC C C COCCAC C C C	1059				2002
1067 UCACCCAC CUGAUGAG X CGAA IGUGAUUU 1281 AAATCACC A GTOGGTGA 2001					2003
1086 UCCUCCUG CUGAUGAG X CGAA IUCUCUUC 1282 GAAGAGAC C CAGGAGGA 2006 1087 ADCCUCCU CUGAUGAG X CGAA IGUCUCUU 1283 AAGAGACC A AGGAGGAT 2007 1088 UAUCUCCC CUGAUGAG X CGAA IGGUCUCU 1294 AGGAACCC A GGAGATA 2007 1097 10					2004
1087 AUCCUCCU CUGAUGAG X CGAA IGUCUCUU 1283 AAGAGACC C AGGAGGAT 200° 1088 UAUCCUCC CUGAUGAG X CGAA IGGUCUCU 1284 AGAGACCC A GGAGGATA 200° 1102 GAUGGGG CUGAUGAG X CGAA IUCUUUAU 1285 ATAAAGAC T GCCCATC 200°			1		2005
1088 UAUCCUCC CUGAUGAG X CGAA IGGUCUCU 1284 AGAGACCC A GGAGGATA 2001 1102 GAUGGGGC CUGAUGAG X CGAA IUCUUUAU 1285 ATAAAGAC T GCCCCATC 2003	1086		1282		2006
1102 GAUGGGGC CUGAUGAG X CGAA IUCUUUAU 1285 ATAAAGAC T GCCCCATC 2008					2007
	1088	UAUCCUCC CUGAUGAG X CGAA IGGUCUCU	1284		2008
1105 CUUGAUGG CUGAUGAG X CGAA ICAGUCUU 1286 AAGACTGC C CCATCAAG 2010					2009
					2010
1106 CCUUGAUG CUGAUGAG X CGAA IGCAGUCU 1287 AGACTGCC C CATCAAGG 201	1106	CCUUGAUG CUGAUGAG X CGAA IGCAGUCU	1287	AGACTGCC C CATCAAGG	2011

1107	UCCUUGAU CUGAUGAG X CGAA IGGCAGUC	1288	GACTGCCC C ATCAAGGA	2012
1108	UUCCUUGA CUGAUGAG X CGAA IGGGCAGU	1289	ACTGCCCC A TCAAGGAA	2013
1111	UUCUUCCU CUGAUGAG X CGAA IAUGGGGC	1290	GCCCCATC A AGGAAGAA	2014
1129	AUUUAAGG CUGAUGAG X CGAA ICUUCCUU	1291	AAGGAAGC C CCTTAAAT	2015
1130	CAUUUAAG CUGAUGAG X CGAA IGCUUCCU	1292	AGGAAGCC C CTTAAATG	2016
1131	GCAUUUAA CUGAUGAG X CGAA IGGCUUCC	1293	GGAAGCCC C TTAAATGC	2017
1132	GGCAUUUA CUGAUGAG X CGAA IGGGCUUC	1294	GAAGCCCC T TAAATGCC	2018
1140	UAGGGUGC CUGAUGAG X CGAA ICAUUUAA	1295	TTAAATGC C GCACCCTA	2019
1143	CCGUAGGG CUGAUGAG X CGAA ICGGCAUU	1296	AATGCCGC A CCCTACGG	2020
1145	UGCCGUAG CUGAUGAG X CGAA IUGCGGCA	1297	TGCCGCAC C CTACGGCA	2021
1146	AUGCCGUA CUGAUGAG X CGAA IGUGCGGC	1298	GCCGCACC C TACGGCAT	2022
1147	GAUGCCGU CUGAUGAG X CGAA IGGUGCGG	1299	CCGCACCC T ACGGCATC	2023
1153	GCUUUCGA CUGAUGAG X CGAA ICCGUAGG	1300	CCTACGGC A TCGAAAGC	2024
1162	UUGACUCA CUGAUGAG X CGAA ICUUUCGA	1301	TCGAAAGC A TGAGTCAA	2025
1169	CAGUGUCU CUGAUGAG X CGAA IACUCAUG	1302	CATGAGTC A AGACACTG	2026
1174	AACUUCAG CUGAUGAG X CGAA IUCUUGAC	1303	GTCAAGAC A CTGAAGTT	2027
1176	CUAACUUC CUGAUGAG X CGAA IUGUCUUG	1304	CAAGACAC T GAAGTTAG	2028
1208	CACCUCGA CUGAUGAG X CGAA IACUUCCC	1305	GGGAAGTC T TCGAGGTG	2029
1218	GCAGCCUG CUGAUGAG X CGAA ICACCUCG	1306	CGAGGTGC C CAGGCTGC	2030
1219	GGCAGCCU CUGAUGAG X CGAA IGCACCUC	1307	GAGGTGCC C AGGCTGCC	2031
1220	AGGCAGCC CUGAUGAG X CGAA IGGCACCU	1308	AGGTGCCC A GGCTGCCT	2032
1224	GGGGAGGC CUGAUGAG X CGAA ICCUGGGC	1309	GCCCAGGC T GCCTCCCC	2033
1227	GCUGGGGA CUGAUGAG X CGAA ICAGCCUG	1310	CAGGCTGC C TCCCCAGC	2034
1228	GGCUGGGG CUGAUGAG X CGAA IGCAGCCU	1311	AGGCTGCC T CCCCAGCC	2035
1230	UUGGCUGG CUGAUGAG X CGAA IAGGCAGC	1312	GCTGCCTC C CCAGCCAA	2036
1231	UUUGGCUG CUGAUGAG X CGAA IGAGGCAG	1313	CTGCCTCC C CAGCCAAA	2037
1232	CUUUGGCU CUGAUGAG X CGAA IGGAGGCA	1314	TGCCTCCC C AGCCAAAG	2038
1233	CCUUUGGC CUGAUGAG X CGAA IGGGAGGC	1315	GCCTCCCC A GCCAAAGG	2039
1236	UCCCCUUU CUGAUGAG X CGAA ICUGGGGA	1316	TCCCCAGC C AAAGGGGA	2040
1237	CUCCCCUU CUGAUGAG X CGAA IGCUGGGG	1317	CCCCAGCC A AAGGGGAG	2041
1247	GCAGUGAC CUGAUGAG X CGAA ICUCCCCU	1318	AGGGGAGC C GTCACTGC	2042
1251	UCGGGCAG CUGAUGAG X CGAA IACGGCUC	1319	GAGCCGTC A CTGCCCGA	2043
1253	UCUCGGGC CUGAUGAG X CGAA 1UGACGGC	1320	GCCGTCAC T GCCCGAGA	2044
1256	CCUUCUCG CUGAUGAG X CGAA ICAGUGAC	1321	GTCACTGC C CGAGAAGG	2045
1257	UCCUUCUC CUGAUGAG X CGAA IGCAGUGA	1322	TCACTGCC C GAGAAGGA	2046
1273	CAGUGCAU CUGAUGAG X CGAA IUCCUCGU	1323	ACGAGGAC C ATGCACTG	2047
1274	UCAGUGCA CUGAUGAG X CGAA IGUCCUCG	1324	CGAGGACC A TGCACTGA	2048
1278	UAACUCAG CUGAUGAG X CGAA ICAUGGUC	1325	GACCATGC A CTGAGTTA	2049
1280	AGUAACUC CUGAUGAG X CGAA IUGCAUGG	1326	CCATGCAC T GAGTTACT	2050
1288	GGGCUUCC CUGAUGAG X CGAA IUAACUCA	1327	TGAGTTAC T GGAAGCCC	2051
1295	CCAGGAAG CUGAUGAG X CGAA ICUUCCAG	1328	CTGGAAGC C CTTCCTGG	2052
1296	ACCAGGAA CUGAUGAG X CGAA IGCUUCCA	1329	TGGAAGCC C TTCCTGGT	2053
1297	GACCAGGA CUGAUGAG X CGAA IGGCUUCC	1330	GGAAGCCC T TCCTGGTC	2054
1300	GUUGACCA CUGAUGAG X CGAA IAAGGGCU	1331	AGCCCTTC C TGGTCAAC	2055
1301	UGUUGACC CUGAUGAG X CGAA IGAAGGGC	1332	GCCCTTCC T GGTCAACA	2056
1306	GCACAUGU CUGAUGAG X CGAA IACCAGGA	1333	TCCTGGTC A ACATGTGC	2057
1309	CACGCACA CUGAUGAG X CGAA IUUGACCA	1334	TGGTCAAC A TGTGCGTG	2058
			1	1

Table 4

1320	AGGACCGU CUGAUGAG X CGAA ICCACGCA	1335	TGCGTGGC T ACGGTCCT	2059
1327	GGCCGUGA CUGAUGAG X CGAA IACCGUAG	1336	CTACGGTC C TCACGGCC	2060
1328	CGGCCGUG CUGAUGAG X CGAA IGACCGUA	1337	TACGGTCC T CACGGCCG	2061
1330	GCCGGCCG CUGAUGAG X CGAA IAGGACCG	1338	CGGTCCTC A CGGCCGGC	2062
1335	UAAGCGCC CUGAUGAG X CGAA ICCGUGAG	1339	CTCACGGC C GGCGCTTA	2063
1341	CAGAGGUA CUGAUGAG X CGAA ICGCCGGC	1340	GCCGGCGC T TACCTCTG	2064
1345	GUAGCAGA CUGAUGAG X CGAA IUAAGCGC	1341	GCGCTTAC C TCTGCTAC	2065
1346	UGUAGCAG CUGAUGAG X CGAA IGUAAGCG	1342	CGCTTACC T CTGCTACA	2066
1348	CCUGUAGC CUGAUGAG X CGAA IAGGUAAG	1343	CTTACCTC T GCTACAGG	2067
1351	GAACCUGU CUGAUGAG X CGAA ICAGAGGU	1344	ACCTCTGC T ACAGGTTC	2068
1354	CAGGAACC CUGAUGAG X CGAA IUAGCAGA	1345	TCTGCTAC A GGTTCCTG	2069
1360	GUUGAACA CUGAUGAG X CGAA TAACCUGU	1346	ACAGGTTC C TGTTCAAC	2070
1361	UGUUGAAC CUGAUGAG X CGAA IGAACCUG	1347	CAGGTTCC T GTTCAACA	2071
1366	GUUGCUGU CUGAUGAG X CGAA IAACAGGA	1348	TCCTGTTC A ACAGCAAC	2072
1369	UGUGUUGC CUGAUGAG X CGAA IUUGAACA	1349	TGTTCAAC A GCAACACA	2073
1372	CUAUGUGU CUGAUGAG X CGAA ICUGUUGA	1350	TCAACAGC A ACACATAG	2074
1375	AGGCUAUG CUGAUGAG X CGAA IUUGCUGU	1351	ACAGCAAC A CATAGCCT	2075
1377	UCAGGCUA CUGAUGAG X CGAA IUGUUGCU	1352	AGCAACAC A TAGCCTGA	2076
1382	GAGGGUCA CUGAUGAG X CGAA ICUAUGUG	1353	CACATAGC C TGACCCTC	2077
1383	GGAGGGUC CUGAUGAG X CGAA IGCUAUGU	1354	ACATAGCC T GACCCTCC	2078
1387	UGGAGGAG CUGAUGAG X CGAA IUCAGGCU	1355	AGCCTGAC C CTCCTCCA	2079
1388	GUGGAGGA CUGAUGAG X CGAA IGUCAGGC	1356	GCCTGACC C TCCTCCAC	2080
1389	AGUGGAGG CUGAUGAG X CGAA IGGUCAGG	1357	CCTGACCC T CCTCCACT	2081
1391	GGAGUGGA CUGAUGAG X CGAA IAGGGUCA	1358	TGACCCTC C TCCACTCC	2082
1392	UGGAGUGG CUGAUGAG X CGAA IGAGGGUC	1359	GACCCTCC T CCACTCCA	2083
1394	GGUGGAGU CUGAUGAG X CGAA IAGGAGGG	1360	CCCTCCTC C ACTCCACC	2084
1395	AGGUGGAG CUGAUGAG X CGAA IGAGGAGG	1361	CCTCCTCC A CTCCACCT	2085
1397	GGAGGUGG CUGAUGAG X CGAA IUGGAGGA	1362	TCCTCCAC T CCACCTCC	2086
1399	GUGGAGGU CUGAUGAG X CGAA IAGUGGAG	1363	CTCCACTC C ACCTCCAC	2087
1400	GGUGGAGG CUGAUGAG X CGAA IGAGUGGA	1364	TCCACTCC A CCTCCACC	2088
1402	UGGGUGGA CUGAUGAG X CGAA IUGGAGUG	1365	CACTCCAC C TCCACCCA	2089
1403	GUGGGUGG CUGAUGAG X CGAA IGUGGAGU	1366	ACTCCACC T CCACCCAC	2090
1405	CAGUGGGU CUGAUGAG X CGAA IAGGUGGA	1367	TCCACCTC C ACCCACTG	2091
1406	ACAGUGGG CUĞAUGAG X CGAA IGAGGUGG	1368	CCACCTCC A CCCACTGT	2092
1408	GGACAGUG CUGAUGAG X CGAA IUGGAGGU	1369	ACCTCCAC C CACTGTCC	2093
1409	CGGACAGU CUGAUGAG X CGAA IGUGGAGG	1370	CCTCCACC C ACTGTCCG	2094
1410	GCGGACAG CUGAUGAG X CGAA IGGUGGAG	1371	CTCCACCC A CTGTCCGC	2095
1412	AGGCGGAC CUGAUGAG X CGAA IUGGGUGG	1372	CCACCCAC T GTCCGCCT	2096
1416	GCAGAGGC CUGAUGAG X CGAA IACAGUGG	1373	CCACTGTC C GCCTCTGC	2097
1419	CGGGCAGA CUGAUGAG X CGAA ICGGACAG	1374	CTGTCCGC C TCTGCCCG	2098
1420	GCGGGCAG CUGAUGAG X CGAA IGCGGACA	1375	TGTCCGCC T CTGCCCGC	2099
1422	CUGCGGGC CUGAUGAG X CGAA IAGGCGGA	1376	TCCGCCTC T GCCCGCAG	2100
1425	GCUCUGCG CUGAUGAG X CGAA ICAGAGGC	1377	GCCTCTGC C CGCAGAGC	2101
1426	GGCUCUGC CUGAUGAG X CGAA IGCAGAGG	1378	CCTCTGCC C GCAGAGCC	2102
1429	GUGGGCUC CUGAUGAG X CGAA ICGGGCAG	1379	CTGCCCGC A GAGCCCAC	2103
1434	CGGGCGUG CUGAUGAG X CGAA ICUCUGCG	1380	CGCAGAGC C CACGCCCG	2104
1435	UCGGGCGU CUGAUGAG X CGAA IGCUCUGC	1381	GCAGAGCC C ACGCCCGA	2105

1440 GUUGGUCG CUGAUGAG X CGAA IGCGUGGG 1383 GCCCCGC C C GACCTAGC 2106					
1445	1436	GUCGGGCG CUGAUGAG X CGAA IGGCUCUG	1382	CAGAGCCC A CGCCCGAC	2106
1445					
1449					
1453 CCGCGGCA CUGAUGAG X CGAA ICCUGCUA 1387 TAGCAGGC A TGCCGCGG 2111 1457 CCUACCGC CUGAUGAG X CGAA ICCUGAC 1389 GAGCATGC C GGGGTAGG 2112 1476 CGCGGGCC CUGAUGAG X CGAA ICCCUGAC 1389 GRAAGGCC C GGGGACC 2114 1476 CGCGGGCC CUGAUGAG X CGAA ICCCCUGAC 1390 AGGGCCGC C GGACCCCG 2114 1476 CGCGGGCC CUGAUGAG X CGAA ICCCGGCC 1391 AGGCGCGC C GGACCCCG 2116 1498 CCGULGGG CUGAUGAG X CGAA ICCCGGCC 1391 AGGCGGGC C GGACCCGG 2116 1498 CCGUCGG CUGAUGAG X CGAA ICCCGGCC 1392 AGGCGGGC C GGACCGCG 2116 1499 UCCGUCGG CUGAUGAG X CGAA ICCCGGCC 1394 GCCGGGGC C GGACGGG 2117 1499 UCCGUCGG CUGAUGAG X CGAA ICCCGGCC 1394 GCCGGGGC C GGACGGG 2117 1510 GUCGGUCC CUGAUGAG X CGAA ICCCGGCC 1394 GCCGGGGC C GGACGGG 2117 1510 GUCGGUCC CUGAUGAG X CGAA ICACCAGC 1395 CCGGGGCC C GGACGGG 2119 1517 UUUAGUGC CUGAUGAG X CGAA ICACCAGC 1395 CCGGGGCC C GGACGGG 2119 1518 GGAGAGAC CUGAUGAG X CGAA ICACCAGC 1397 GGTTCTGC A CTANAACC 2121 1520 GGUUUUAG CUCAUGAG X CGAA ICACCAGC 1397 GGTTCTGC A CTANAACC 2121 1521 UUGAGGAG X CGAA IUGCAGAA 1398 TTCTGCAC T TANAACC 2121 1522 GGGAAGAC CUGAUGAG X CGAA IUUUAGU 1399 ACTANAAC C ATCTTCC 2124 1523 GGGAAGAC CUGAUGAG X CGAA IUUUAGU 1399 ACTANAAC C ATCTTCC 2124 1524 GGGGAAGA CUGAUGAG X CGAA IUUUAGU 1400 CTANAACC A TCTTCCC 2125 1533 UCCGGGGG CUGAUGAG X CGAA IUUUAGU 1401 TAAAACC A TCTTCCC 2125 1534 CACCACCC CUGAUGAG X CGAA IAGAGAGA 1406 CATANAACC A TCTTCCC 2125 1535 ACAUCCG CUGAUGAG X CGAA IAGAGAG 1403 CATCTTC C CCGGATGT 2127 1526 ACAUCCG CUGAUGAG X CGAA IAGAGAG 1404 CATCTTC C CCGGATGT 2127 1536 ACAUCCG CUGAUGAG X CGAA IAGAGAG 1404 CATCTTC C C CGGATGT 2127 1537 CACCACC CUGAUGAG X CGAA IAGAGAG 1404 CATCTTC C C CGGATGT 2127 1538 ACACACC CUGAUGAG X CGAA IAGAGAG 1404 CATCTTC C C CGGATGT 2127 1539 AGAGGGGG CUGAUGAG X CGAA IAGAGAG 1404 CATCTTC C C CGGATGT 2127 1536 AAGAGAG CUGAUGAG X CGA	1445	UGCCUGCU CUGAUGAG X CGAA IUCGGGCG	1385	CGCCCGAC T AGCAGGCA	2109
1457	1449		1386		2110
1473	1453	CCGCGGCA CUGAUGAG X CGAA ICCUGCUA	1387	TAGCAGGC A TGCCGCGG	2111
1476	1457	CCUACCGC CUGAUGAG X CGAA ICAUGCCU	1388	AGGCATGC C GCGGTAGG	2112
1481	1473	GGUCCGGC CUGAUGAG X CGAA ICCCUUAC	1389	GTAAGGGC C GCCGGACC	2113
1493	1476	CGCGGUCC CUGAUGAG X CGAA ICGGCCCU	1390	AGGGCCGC C GGACCGCG	2114
1498 CCGUCCGG CURANUGAG X CGAA ICCCGGCU 1393 AGCCGGGC C CCGGACGG 2117 1499 UCCGUCCG CURANUGAG X CGAA ICCCCGGC 1394 GCCGGGCC C CGGACGGA 2118 1500 GUCCGUCC CURANUGAG X CGAA ICGCCCCGC 1395 CCCGGGCC C GGGACGGAC 2118 1517 UUUAGUUCC CURANUGAG X CGAA ICGCCCCGC 1395 CCCGGGCC C GGGACGGAC 2119 1520 GGUUUNG CURANUGAG X CGAA ICACCAC 1396 GTTGGTTC T GCACTAAAA 2120 1521 UUUAGUUCC GUCANUGAG X CGAA ICACCAC 1397 GGTTCTCC A CTAAAACC 2121 1522 URGGUTUU CUCANUGAG X CGAA ILUGUAGAA 1398 TTCTGCAC T AAAACCCA 2122 1528 GGAAGAUC GUCANUGAG X CGAA INUUUAGA 1399 ACTAAAAC C CATCTTCC 2123 1529 GGAGAGAU CUGANUGAG X CGAA INUUUAGA 1400 CTAAAACC A TCTTCCC 2125 1530 GGGGGAGA CUGANUGAG X CGAA IGUNUUAG 1401 TAAAACC A TCTTCCC 2125 1531 UCCGGGGGA CUGANUGAG X CGAA IGUNUUAG 1401 TAAAACC A TCTTCCC 2125 1532 AUCCGGG CUGANUGAG X CGAA IGAGAGA 1403 CCATCTTC C CGGATGT 2127 1536 ACACNUCCG CUGANUGAG X CGAA IGAGAGA 1403 CCATCTTC C CGGATGT 2127 1537 CACANUCCG CUGANUGAG X CGAA IGAGAGA 1405 CATCTTCC C CGGATGT 2128 1538 ACACNUCC CUGANUGAG X CGAA IGAGAGA 1405 ATCTTCCC C CGGATGT 2129 1550 GACGGGUG CUGANUGAG X CGAA IGAGAGA 1405 ATCTTCCC C CGGATGTG 2128 1551 ACACANUCC CUGANUGAG X CGAA IGAGACA 1405 ATCTTCCC C CGGATGTG 2128 1552 AUGANGGG CUGANUGAG X CGAA IGACACA 1406 TGTGTCTC A CCCCTCAT 2131 1554 GGUAGAG CUGANUGAG X CGAA IGAGACA 1407 TGTGTCTC A CCCCTCAT 2131 1555 AAGGANGA CUGANUGAG X CGAA IGAGACA 1408 TGTCCAC C CTAATCCT 2132 1555 AAGGANGA CUGANUGAG X CGAA IGAGACA 1409 GTTCCAC C C CTAATCCT 2133 1556 AAGGANGA CUGANUGAG X CGAA IGAGACA 1409 GTTCCAC C C TCATCCTT 2134 1557 AAGGANGA CUGANUGAG X CGAA IGAGAGA 1410 TCTCACC C C TCATCCTT 2135 1559 AAGANGA CUGANUGAG X CGAA IGAGAGAG 1411 CTCACCCC C C TCATCCTT 2135 1559 AAGGANGA CUGANUGAG X CGAA IGAGAGAG 1411 CTCACCCC T C TCTCCTT 2136 1559 AAGANGAG CUGANUGAG X CGAA IGAGAGAG 1411 CTC	1481	CUCUACGC CUGAUGAG X CGAA IUCCGGCG	1391	CGCCGGAC C GCGTAGAG	2115
1499	1493	CGGGGCCC CUGAUGAG X CGAA ICUCUCUA	1392	TAGAGAGC C GGGCCCCG	2116
1517	1498	CCGUCCGG CUGAUGAG X CGAA ICCCGGCU	1393	AGCCGGGC C CCGGACGG	2117
1517	1499	UCCGUCCG CUGAUGAG X CGAA IGCCCGGC	1394	GCCGGGCC C CGGACGGA	2118
1522 USGGUULU CUQAUGAG X CGAA ICAGAACC 1397 GOTTCTGC A CTAMAACC 2121 1522 USGGUULU CUQAUGAG X CGAA ILUGAGAA 1398 TTCTGCAC T AAMACCCA 2122 1528 GGAAGAU CUGAUGAG X CGAA ILUGUUAGU 1399 ACTAMAAC C ACTCTTCC 2123 1529 GGGAAGAU CUGAUGAG X CGAA IGUUUUAGU 1490 CTAMAACC C ATCTTCCC 2124 1529 GGGAAGAU CUGAUGAG X CGAA IGUUUUAGU 1400 CTAMAACC C ATCTTCCC 2124 1520 GGGAAGA CUGAUGAG X CGAA IGUUUUAGU 1401 TAMAACCC A TCTTCCCC 2125 1533 UCCGGGGA CUGAUGAG X CGAA IAUGAGUU 1402 AACCCATC T TCCCCGGAA 2126 1536 ACAUCCGG CUGAUGAG X CGAA IAUGAGUU 1402 AACCCATC T TCCCCGGAA 2127 1537 CACCULCC GUGAUGAG X CGAA IAUGAGUU 1404 CATCTTCC C COGATGT 2127 1538 ACACAUCC GUGAUGAG X CGAA IGACAGAA 1404 CATCTTCC C COGATGT 2129 1539 ACACAUCC GUGAUGAG X CGAA IGACAGAA 1405 ATCTTCCC C GAATGTG 2129 1550 GAOGOGUG CUGAUGAG X CGAA IGACACA 1407 TGTGTCT C CCCCCTCT 2131 1554 GGAUGAG CUGAUGAG X CGAA IGACACA 1407 TGTGTCT C CCCCCCTC 2131 1555 AGGUAGAG CUGAUGAG X CGAA IGACACA 1409 GTCTCAC C CCTCATCC 2132 1555 AAGGUAG CUGAUGAG X CGAA IGACACA 1409 GTCTCAC C CCTCATCC 2132 1556 AAGGUAG CUGAUGAG X CGAA IGACACA 1409 GTCTCAC C C CTCATCC 2132 1557 AAAGGAUG CUGAUGAG X CGAA IGACAGA 1410 TCTCACC C C TCATCCT 2134 1558 AAGGUAG CUGAUGAG X CGAA IGACAGA 1410 TCTCACC C C TCATCCT 2134 1559 UAAAAGGA CUGAUGAG X CGAA IGACAGA 1411 CTCCACCC C TCATCCT 2136 1552 AAGUAAA CUGAUGAG X CGAA IGACAGA 1411 CTCCACCC C TCATCCT 2136 1553 AAAGGAUG CUGAUGAG X CGAA IGACAGA 1411 CTCCACCC C TCATCCT 2136 1554 AAGGAUG CUGAUGAG X CGAA IGACAGA 1411 CTCTCACC C C TCATCCT 2136 1556 AAGGAUGA CUGAUGAG X CGAA IGACAGA 1411 CTCTCACC C C TCTTCTT 2137 1557 AAGGAUG CUGAUGAG X CGAA IGACAGA 1414 CCTCTCACC C TTTTCATT 2137 1558 AAGUAAA CUGAUGAG X CGAA IGACAGA 1415 CCTCTTCC C TTTTCATT 2137 1559 AAGUAAA CUGAUGAG X CGAA IGACAGA 1415 CCTCTTCC C TTTTCATT 2137 1559 AAGUAAA CU	1500	GUCCGUCC CUGAUGAG X CGAA IGGCCCGG	1395	CCGGGCCC C GGACGGAC	2119
1522	1517	UUUAGUGC CUGAUGAG X CGAA IAACCAAC	1396	GTTGGTTC T GCACTAAA	2120
1528 GGANGAUG CUGAUGAG X CGAR IUJUUAGU 1399 ACTAAAAC C ARTTTCC 2123 1529 GGGARGAU CUGAUGAG X CGAR IUJUUAGU 1401 TAAAAACC A TCTTCCC 2124 1530 GGGARGA CUGAUGAG X CGAR IGUJUUAG 1401 TAAAAACC A TCTTCCC 2125 1531 UCCGGGGA CUGAUGAG X CGAR IAUGGGUUA 1402 AACCCATC T TCCCCGGA 2126 1536 ACAUCCG CUGAUGAG X CGAR IAUGGGU 1404 AACCCATC T TCCCCGGA 2126 1537 CACAUCCG CUGAUGAG X CGAR IAGAGAGA 1404 CATCTTCC C CGGARGT 2127 1537 CACAUCCG CUGAUGAG X CGAR IAGAGAGA 1404 CATCTTCC C CGGARGT 2128 1538 ACACAUCC CUGAUGAG X CGAR IGAGAGAU 1405 ATCTTCCC C CGGARGT 2129 1559 GAGGGGU GUGAUGAG X CGAR IACACACA 1406 TGTGTGTC A CCCCTC 2131 1550 GAGGGU GUGAUGAG X CGAR IACACACA 1406 TGTGTGTC A CCCCTCAT 2131 1551 GGAUGAG CUGAUGAG X CGAR IAGACACA 1407 TGTGTCTC A CCCCTCAT 2131 1552 AUGAGGG CUGAUGAG X CGAR IAGACACA 1409 GTCTCACC C CTCATCC 2132 1555 AAGGAUGA CUGAUGAG X CGAR IAGACACA 1409 GTCTCACC C CTCATCC 2132 1556 AAGGAUGA CUGAUGAG X CGAR IAGACACA 1409 GTCTCACC C CTCATCCT 2133 1556 AAGGAUGA CUGAUGAG X CGAR IAGACACA 1409 GTCTCACC C CTCATCCT 2133 1557 AAAGGAUG CUGAUGAG X CGAR IAGAGAGA 1410 TCTCACCC C TCATCCTT 2136 1558 AAGGAUGA CUGAUGAG X CGAR IAGAGAGA 1410 TCTCACCC C TCATCCTT 2136 1559 AAGGAUGA CUGAUGAG X CGAR IAGAGAGA 1411 CTCACCC C TCATCCTT 2137 1551 AAGGAUGA CUGAUGAG X CGAR IAGAGAGA 1412 CACCCCTC A TCCTTTTA 2136 1552 AAGUARAA CUGAUGAG X CGAR IAGAGAGA 1414 CCTCATCC T TTTACTTT 2137 1553 AAGUARAA CUGAUGAG X CGAR IAGAGAGA 1414 CCTCATCC T TTTACTTT 2137 1554 AAGUARAA CUGAUGAG X CGAR IAGAGAGA 1414 CCTCATCC T TTTACTTT 2137 1556 GUGGAGAG CUGAUGAG X CGAR IAGAGAGA 1414 CCTCATCC T TTTACTTT 2138 1559 GGGAAGA CUGAUGAG X CGAR IAGAGAGA 1416 CTTTTCC C C TTTCCCT 2141 1576 GUGGAGAG CUGAUGAG X CGAR IAGAGAGA 1417 TTTTCC C C TTTCCCT 2141 1577 AGUGGAG CUGAUGAG X CGAR IAGAGAGAG 1418 TTTTCCC C C TTCCACT 2141 1578 AAG	1520	GGUUUUAG CUGAUGAG X CGAA ICAGAACC	1397	GGTTCTGC A CTAAAACC	2121
1529 GOGARGAU CUGAUGAG X CGAA IGUIUUUA 1400 CTAAAACC C ATCTTCCC 2124 1530 GOGGAAGA CUGAUGAG X CGAA IGUIUUUA 1401 TAAAAACC A TCTTCCCC 2125 1531 UCCGOGGA CUGAUGAG X CGAA IAAGAGGA 1402 AACCCATC T TCCCCCGAA 2126 1536 ACAUCCG CUGAUGAG X CGAA IAAGAGGA 1403 CCATCTTC C CCGGATGT 2127 1537 CACAUCCG CUGAUGAG X CGAA IAGAGAGA 1404 CATCTTCC C CGGATGT 2127 1538 ACACLICC CUGAUGAG X CGAA IAGAGAGA 1405 ATCTTCCC C GGATGT 2127 1539 ACACLICC CUGAUGAG X CGAA IAGAGAGA 1405 ATCTTCCC C GGATGT 2129 1538 ACACLICC CUGAUGAG X CGAA IAGAGAGA 1405 ATCTTCCC C GGATGT 2129 1550 GAGGGGU CUGAUGAG X CGAA IAGACACA 1406 TGTGTGTC T CACCCCTC 2130 1552 AUBAGGGG CUGAUGAG X CGAA IAGACACA 1407 TGTGTGTC T CACCCCTC 2131 1554 GAGUGAG CUGAUGAG X CGAA IAGAGACA 1408 TGTCTCAC C CCTAATCC 2131 1555 AGAGGAG CUGAUGAG X CGAA IAGAGACA 1409 GTCTCAC C CCTAATCC 2131 1556 AAGGAUGA CUGAUGAG X CGAA IGGGGAGA 1410 TCTCACCC C TCAATCCT 2134 1557 AAAGGAUG CUGAUGAG X CGAA IAGAGACA 1410 TCTCACCC C TCAATCCT 2135 1559 UAAAAGGA CUGAUGAG X CGAA IAGAGAGA 1411 CTCACCCC T CATCCTT 2135 1559 UAAAAGGA CUGAUGAG X CGAA IAGAGAGA 1410 TCTCACCC C TCATCCTT 2135 1559 UAAAAGGA CUGAUGAG X CGAA IAGAGAGA 1411 CTCACCCC T CATCCTTT 2135 1559 UAAAAGGA CUGAUGAG X CGAA IAGAGAGA 1412 CACCCCCT A TCCTTTT 2135 1550 AAGGAUGA CUGAUGAG X CGAA IAGAGAGA 1413 CCCTCATC C TTTTACTT 2137 1551 AAGGAUGA CUGAUGAG X CGAA IAGAGAGA 1414 CCTCACCC T TTTACTT 2137 1552 AAGUAGAA CUGAUGAG X CGAA IAGAGAGA 1415 CCTCTATC C TTTTACTT 2137 1553 AAGUAGAA CUGAUGAG X CGAA IAGAGAGA 1415 CCTCTATC C TTTTACTT 2137 1554 AAGUAGAA CUGAUGAG X CGAA IGAGAGAG 1415 CCTCTTC C C TTTCCAC 2140 1557 AGGGAAGA CUGAUGAG X CGAA IGAGAGAG 1415 CCTCTTC C C TTTCCAC 2140 1577 AGGGAAGA CUGAUGAG X CGAA IGAGAGAG 1415 CTTTTTGC C C CTTCCCAC 2141 1578 AAGUGGAA CUGAUGAG X CGAA IGAGAGAG 1415 TTTTTTGC C C CTTCCAC 2141 1	1522	UGGGUUUU CUGAUGAG X CGAA IUGCAGAA	1398	TTCTGCAC T AAAACCCA	2122
1530 GGGGAAGA CUGAUGAG X CGAA IGGUUUUA 1401	1528	GGAAGAUG CUGAUGAG X CGAA IUUUUAGU	1399	ACTAMANC C CATCTTCC	2123
1533	1529	GGGAAGAU CUGAUGAG X CGAA IGUUUUAG	1400	CTAAAACC C ATCTTCCC	2124
1536 ACAUCCGG CUGAUGAG X CGAA IAAGANUG 1403 CCATCTTC C CCGGATGT 2127 1537 CACAUCCG CUGAUGAG X CGAA IGAAGANUG 1404 CATCTTCC C CGGATGT 2128 1538 ACACAUCC CUGAUGAG X CGAA IGAAGANU 1405 ATCTTCCC C GGATGTG 2128 1550 GAGGGGG CUGAUGAG X CGAA IGAAGAC 1405 ATCTTCCC C GGATGTG 2129 1550 GAGGGGG CUGAUGAG X CGAA IACACACA 1406 TGTGTGTC T CACCCCTC 2130 1551 GAGGUGAG CUGAUGAG X CGAA IGACACA 1407 TGTGTGTC T CACCCCTC 2131 1554 GGAUGAGG CUGAUGAG X CGAA IGAGACA 1408 TGTCTCAC C CCTCATCC 2132 1555 AGGAUGAG CUGAUGAG X CGAA IUGAGAC 1408 TGTCTCAC C CCTCATCC 2132 1555 AGGAUGAG CUGAUGAG X CGAA IUGAGAC 1409 GTCTCACC C CTCATCCT 2133 1557 AAAGGAUG CUGAUGAG X CGAA IGGGUGAG 1410 TCTCACCC C TCATCCTT 2135 1559 UAAAAGGA CUGAUGAG X CGAA IGGGUGAG 1411 CTCACCCC T CATCCTT 2135 1552 AAGGUAA CUGAUGAG X CGAA IGAGGAG 1411 CTCACCCC T CATCCTT 2135 1553 AAAGUAA CUGAUGAG X CGAA IGAGGAG 1413 CACCCCTC A TCCTTTA 2136 1554 AAAGUAA CUGAUGAG X CGAA IGAUGAGG 1413 CACCCCTC T TTTACTT 2137 1563 AAAGUAA CUGAUGAG X CGAA IGAUGAGG 1414 CCTCATC T TTTTACT 2137 1563 AAAGUAA CUGAUGAG X CGAA IGAUGAGG 1414 CCTCATC T TTTTACT 2139 1576 GUGAGAG CUGAUGAG X CGAA IGACAAAA 1416 CCTTTTAC T TTTTCC 2139 1577 AGUGGAAG CUGAUGAG X CGAA IGACAAAA 1417 TTTTTCC C CCTTCCAC 2140 1577 AAGUGGAA CUGAUGAG X CGAA IGACAAAA 1418 TTTTCCC C TTCCACTT 2141 1579 AAAGUGGA CUGAUGAG X CGAA IGACAAAA 1417 TTTTTCCC C TTCCACTT 2141 1579 AAGUGGAA CUGAUGAG X CGAA IGACAAAA 1417 TTTTTCCC C TTCCACTT 2141 1579 AAGUGGAA CUGAUGAG X CGAA IGACAAAA 1418 TTTTCCC C TTCCACTT 2141 1579 AAGUGGAA CUGAUGAG X CGAA IGACAAAA 1417 TTTTTCCC C TTCCACTT 2141 1579 AAGUGGAA CUGAUGAG X CGAA IGACAAAA 1418 TTTTCCC C TTCCACTT 2141 1579 AAGUGGAA CUGAUGAG X CGAA IGACAAAA 1418 TTTTCCC C TTCCACTT 2141 1583 ACUCAAA CUGAUGAG X CGAA IGACAAA 1418 TTTTCCC C TTCCACTT 2141 1579 AAGUGGAA CUGAUGAG	1530	GGGGAAGA CUGAUGAG X CGAA IGGUUUUA	1401	TAAAACCC A TCTTCCCC	2125
1537	1533	UCCGGGGA CUGAUGAG X CGAA IAUGGGUU	1402	AACCCATC T TCCCCGGA	2126 -
1536	1536	ACAUCCGG CUGAUGAG X CGAA IAAGAUGG	1403	CCATCTTC C CCGGATGT	2127
1550	1537	CACAUCCG CUGAUGAG X CGAA IGAAGAUG	1404	CATCTTCC C CGGATGTG	2128
1552 AUGAGGG CUGAUGAG X CGAA IAGACACA 4407 TGTGTCTC A CCCTCAT 21.31 1554 GGAUGAG CUGAUGAG X CGAA ILGAGACAC 1408 TGTCTCAC C CCTCATCC 21.32 1555 AGGGUAG CUGAUGAG X CGAA IGUGAGAC 1409 GTCTCACC C CTCATCCT 21.33 1556 AAGGAUGA CUGAUGAG X CGAA IGUGAGAC 1409 GTCTCACC C CTCATCCT 21.34 1557 AAAGGAUG CUGAUGAG X CGAA IGGGGUAG 1410 TCTCACCC C TCATCCTT 21.35 1559 UAAAAGGA CUGAUGAG X CGAA IGGGGUAG 1411 CTCACCCC T CATCCTT 21.36 1562 AAGUAAAA CUGAUGAG X CGAA IGAGGGUAG 1411 CCCCTCATC C TTTTACTT 21.36 1563 AAAGUAAA CUGAUGAG X CGAA IGAGAGGG 1414 CCCCTCATC C TTTTACTT 21.37 1559 GGGCAAA CUGAUGAG X CGAA IGAAGAGG 1414 CCCCATCC T TTACTTT 21.37 1563 AAAGUGAA CUGAUGAG X CGAA IGAAGAGG 1414 CCTCATCC T TTACTTT 21.37 1576 GUGGAGG CUGAUGAG X CGAA IGAAAAAA 1415 CCTTTTAC T TTTTGCCC 21.39 1576 GUGGAGG CUGAUGAG X CGAA IGAAAAAA 1417 TTTTTGCC C CTTCCACT 21.41 1577 AAGUGGAG CUGAUGAG X CGAA IGACAAAA 1418 TTTTGCCC C TCCCACT 21.41 1578 AAGUGGAA CUGAUGAG X CGAA IGACAAAA 1419 TTTTGCCC C TCCCACT 21.42 1579 AAGUGGAA CUGAUGAG X CGAA IGACAAAA 1419 TTTTGCCC C TCCCACT 21.42 1582 CUCAAAGU CUGAUGAG X CGAA IGACAAAA 1419 TTTTGCCC C TCCCACT 21.42 1583 ACUCAAAG CUGAUGAG X CGAA IGAGAGGG 1421 CCCCTTCC A CTTTGAGT 21.45 1584 GUGGUUGU CUGAUGAG X CGAA IGAGAGGG 1421 CCCCTTCC A CTTTGAGT 21.45 1585 GUGCUCAU CUGAUGAG X CGAA IGAGAGGG 1421 CCCCTTCC A CTTTGAGT 21.45 1586 GUGCUCAU CUGAUGAG X CGAA IGACAGAG 1422 CCTTCCAC T TTGAGTAC 21.46 1595 UGGCUUGU CUGAUGAG X CGAA IGACACAG 1424 TCAGATAC C AATCCAC 21.47 1595 UGGCUUGU CUGAUGAG X CGAA IGACACCA 1424 TCAGATAC C AATCCAC 21.47 1596 GUGGGUUT CUCAUGAG X CGAA IGACACCA 1424 TCAGATAC C AATCCAC 21.49 1501 AUGCCUUG CUGAUGAG X CGAA IGACACCA 1425 TCAGATAC C AATCCAC 21.49 1501 AUGCCUUG CUGAUGAG X CGAA IGACACCA 1426 TCAGATAC C AATCCAC 21.49 1501 AUGCCUUG CUGAUGAG X CGAA IGACACCA 1427 TCAGATAC	1538	ACACAUCC CUGAUGAG X CGAA IGGAAGAU	1405	ATCTTCCC C GGATGTGT	2129
1554 GGAUGAGG CUGAUGAG X CGAA IUJAGACA 1408 TOTCTCAC C CCTCATCC 2132 1555 AGGAUGAG CUGAUGAG X CGAA IGUGAGGA 1409 GTCTCACC C CTCATCCT 2133 1556 AAGGAUGA CUGAUGAG X CGAA IGUGAGGA 1410 TCTCACCC C TCATCCTT 2136 1557 AAAGGAUGA CUGAUGAG X CGAA IGGGUGAG 1411 CTCACCCC T TATCCTTT 2136 1559 UARAAGGA CUGAUGAG X CGAA IAGGGUGAG 1412 CACCCCCT A TCCTTTTA 2136 1562 AAGUARAA CUGAUGAG X CGAA IAGGGGG 1413 CCCTCATC C TTTTACTTT 2137 1553 AAAGUARAA CUGAUGAG X CGAA IAGUAGGG 1414 CCTCATC C TTTTACTTT 2137 1569 GUGGARAA CUGAUGAG X CGAA IAGUAGAG 1414 CCTCATC C TTTTACTTT 2139 1576 GUGGARAA CUGAUGAG X CGAA IAGAAGAG 1416 CCTTTTAC T TTTTGCCC 2139 1576 GUGGARAA CUGAUGAG X CGAA ICAAAAAA 1417 TTTTTGCC C CTCCACT 2140 1577 AAGUGGAA CUGAUGAG X CGAA IGCAAAAA 1417 TTTTTCCC C CTCCACT 2141 1578 AAAGUGGA CUGAUGAG X CGAA IGCAGAAA 1418 TTTTCCCC C TTCCACTT 2142 1579 AAAGUGGA CUGAUGAG X CGAA IGAGGAGAA 1419 TTTGCCC C TTCCACTT 2143 1582 CUCAAAGU CUGAUGAG X CGAA IGAGGGAG 1420 GCCCCTTC C ACTTTGAGT 2144 1563 ACCCAAAG CUGAUGAG X CGAA IGAGAGG 1421 CCCCCTCC C ACTTTGAGT 2145 1583 ACCCAAAG CUGAUGAG X CGAA IGAGAGGG 1421 CCCCCTTC C ACTTTGAGT 2146 1594 GUGGAUGA C CGAA IGAGAGGG 1421 CCCCCTTC C ACTTTGAGT 2146 1594 GUGGAUGA C CGAA IGAGAGGG 1421 CCCCCTTC C ACTTTGAGT 2147 1595 UGGGGAUT CUGAUGAG X CGAA IUGACAG 1422 CCTTCCAC T TTGAGTAC 2146 1594 GUGGGGUUT CUGAUGAG X CGAA IGAUCACA 1424 TGAGTAC C AAATCCAC 2146 1595 UGGGGUUT CUGAUGAG X CGAA IUGACAG 1424 TGAGTAC C AAATCCAC 2146 1596 UGGCUUG CUGAUGAG X CGAA IUGAUCAC 1424 TGAGTAC C AAATCCAC 2146 1596 UGGCUUGU CUGAUGAG X CGAA IUGAUCAC 1424 TGAGTAC C AAATCCAC 2146 1596 UGGCUUGU CUGAUGAG X CGAA IUGAUCAC 1424 TGAGTAC C AAATCCAC 2146 1596 UGGCUUGU CUGAUGAG X CGAA IUGAUCAC 1427 TGAGTAC C AAATCCAC 2149 1596 1496 1496 1496 1496 1496 1496 1496 1496 1496 1496 1496 1496	1550	GAGGGGUG CUGAUGAG X CGAA IACACACA	1406	TGTGTGTC T CACCCCTC	2130
1555 AGGAIRAG CUGAUGAG X CGAA IGUCAGAC 1409 GTCTCACC C CTCATCCT 2131 1556 AAGGAIRA CUCAUGAG X CGAA IGUGAGAC 1410 TCTCACCC C TCATCCTT 2134 1557 AAAGGAIR CUGAUGAG X CGAA IGGGUAGA 1411 CTCACCCC T CATCCTTT 2135 1559 UAAAAGGA CUGAUGAG X CGAA IAGGGUAG 1411 CTCACCCC T CATCCTTT 2135 1569 UAAAAGGA CUGAUGAG X CGAA IAGGGUAG 1412 CACCCCTC A TCCTTTAC 2136 1561 AAGURAAA CUGAUGAG X CGAA IAGGGUAG 1413 CCCTCATCC T TTTACTTT 2138 1569 GGGCAAAA CUGAUGAG X CGAA IGAGAGAG 1414 CCTCATCC T TTTACTTT 2138 1569 GGGCAAAA CUGAUGAG X CGAA IGAAAAAG 1414 CCTCATCC T TTTACTTT 2138 1576 GUGGAGG CUGAUGAG X CGAA IGAAAAAG 1416 CCTTTTAC T TTTTGCCC 2139 1577 AAGUGAAG CUGAUGAG X CGAA IGCAAAAA 1417 TTTTGCCC C CTCCACT 2141 1578 AAGUGGAA CUGAUGAG X CGAA IGCAAAAA 1418 TTTTGCCC C TTCCACT 2142 1579 AAGUGGA CUGAUGAG X CGAA IGGGCAAA 1419 TTTGCCC C TTCCACTT 2143 1582 CUCAAAGU CUGAUGAG X CGAA IAGGGCAAA 1419 TTTGCCC C TTCCACTT 2143 1583 ACUCAAAG CUGAUGAG X CGAA IGAGGGA 1420 GCCCCTTC C ACTTGAGT 2144 1586 GUGAUGAG CUGAUGAG X CGAA IGAGGGG 1421 GCCCCTTC C ACTTGAGT 2144 1589 GUGAUGAG CUGAUGAG X CGAA IUGCAAAAG 1422 CCTTCCAC T TTGAGTAC 2146 1594 GUGGAUGU CUGAUGAG X CGAA IUGCAAA 1424 TCAGATAC C AAATCCAC 2147 1595 GUGCAUCA CUGAUGAG X CGAA IUGCACA 1424 TCAGATAC C AAATCCAC 2147 1595 GUGCAUCU CUGAUGAG X CGAA IUGCACA 1424 TCAGATAC C AAATCCAC 2146 1590 UGCCUUG CUGAUGAG X CGAA IUGCACA 1424 TCAGATAC C AAATCCAC 2147 1591 AAGUGCUUG CUGAUGAG X CGAA IUGCACA 1424 TCAGATAC C AAATCCAC 2149 1591 AUGCCUUG CUGAUGAG X CGAA IUGCACA 1424 TCAGATAC C AAATCCAC 2149 1591 AUGCCUUG CUGAUGAG X CGAA IUGCACA 1424 TCAGATAC C AAATCCAC 2146 1591 AUGCCUUG CUGAUGAG X CGAA IUGCACA 1424 TCAGATAC C AAATCCAC 2146 1591 AUGCCUUG CUGAUGAG X CGAA IUGCACA 1424 TCAGATAC C AAACCCAT 2150	1552	AUGAGGG CUGAUGAG X CGAA IAGACACA	1407	TGTGTCTC A CCCCTCAT	2131
1556	1554	GGAUGAGG CUGAUGAG X CGAA IUGAGACA	1408	TGTCTCAC C CCTCATCC	2132
1557 AAAGGANG CUGANGAG X CGAA IGGGUNAG 1411 CTCACCCC T CATCCTTT 2135 1559 UAAAAAGGA CUGANGAG X CGAA IAGGGGUNAG 1412 CACCCCTC A TCCTTTA 2136 1552 AAAGGAAA CUGANGAG X CGAA IANGAGGG 1413 CCCTCATC C TTTTACTT 2137 1553 AAAGGAAA CUGANGAG X CGAA IGANGAGG 1414 CCTCATCC T TTTACTTT 2137 1559 GUGGAAAA CUGANGAG X CGAA IGANGAGG 1414 CCTCATCC T TTTACTTT 2138 1576 GUIGANGAG CUGANGAG X CGAA IGANAAAG 1416 CCTTTTAC T TTTTGCC 2139 1577 AAGGGAAA CUGANGAG X CGAA IGANAAAAG 1416 CTTTTTAC C CCTTCCACT 2141 1578 AAAGGGAA CUGANGAG X CGAA IGANAAAA 1417 TTTTTGCC C TTCCACTT 2141 1579 AAAGGGAA CUGANGAG X CGAA IGANAAA 1418 TTTTGCCC C TTCCACTT 2142 1579 AAAGGGAA CUGANGAG X CGAA IGAGCAAAA 1419 TTTGCCC C TTCCACTT 2143 1582 CUCAAAGG CUGANGAG X CGAA IAGGGGG 1420 GCCCCTTC C ACTTTGAG 2144 1583 ACUCAAAG CUGANGAG X CGAA IAGAGGGG 1421 CCCCCTTC C ACTTTGAG 2144 1584 GUIGANGAG X CGAA INGANAGG 1422 CCTTCCAC T TTGAGTAC 2146 1594 GUIGANGAG X CGAA INGANAGG 1422 CCTTCCAC T TTGAGTAC 2146 1595 UBGGAUNU CUGANGAG X CGAA INGANGAG 1424 TGAGTAC C AAATCCAC 2147 1595 UBGGAUNU CUGANGAG X CGAA INGANGGG 1424 TGAGTAC C AAATCCAC 2147 1596 UBGCUNGU CUGANGAG X CGAA INGANGGG 1424 TGAGTAC C AAATCCAC 2147 1596 UBGCUNGU CUGANGAG X CGAA INGANGGG 1427 AAATCCAC A AACCCAT 2150	1555	AGGAUGAG CUGAUGAG X CGAA IGUGAGAC	1409	GTCTCACC C CTCATCCT	2133
1559	1556	AAGGAUGA CUGAUGAG X CGAA IGGUGAGA	1410	TCTCACCC C TCATCCTT	2134
1562 AAGURANA CUGAUGAG X CGAA IAUGAGGG 1413 CCCTCATC C TTTTACTT 2137 1563 AAAGURANA CUGAUGAG X CGAA IGAUGAGG 1414 CCTCATCC T TTTACTTT 2138 1559 GGGCANA CUGAUGAG X CGAA IGANANGG 1415 CCTTTAC T TTTACTTT 2138 1576 GUGGAAG CUGAUGAG X CGAA ICANANAG 1416 CTTTTAC C C CTTCCAC 2140 1577 AAGUGGA CUGAUGAG X CGAA IGACAAAA 1417 TTTTTGCC C C TTCCACT 2141 1578 AAGUGGA CUGAUGAG X CGAA IGGCAAAA 1418 TTTTGCCC C TTCCACT 2141 1579 AAAGUGGA CUGAUGAG X CGAA IGGCAAAA 1419 TTTGCCC C TTCCACTT 2142 1579 AAAGUGGA CUGAUGAG X CGAA IGGCAAAA 1419 TTTGCCC C TTCCACTT 2143 1582 CUCAAAGU CUGAUGAG X CGAA IGAGGGG 1420 GCCCCTTC C ACTTTGAG 2144 1583 ACCCAAAG CUGAUGAG X CGAA IGAAGGGG 1421 CCCCTTC C A CTTTGAGT 2145 1583 GUACCAA CUGAUGAG X CGAA IGAGAGGG 1421 CCCCTTC C A CTTTGAGT 2145 1594 GUGGAUIU CUGAUGAG X CGAA IUGCACA 1423 TTGAGTAC C TTGAGTAC 2146 1595 UGUGGAUU CUGAUGAG X CGAA IGUACUCA 1424 TGAGTAC C ANTCCAC 2147 1595 UGUGGAUU CUGAUGAG X CGAA IGUACUCA 1424 TGAGTAC C ANTCCAC 2148 1500 UGGCUUG CUGAUGAG X CGAA IGAUGUGG 1425 ACCAATC C ACAAGCCA 2149 1501 AUGGCUUG CUGAUGAG X CGAA IGAGUGUU 1425 ACCAATC C ACAAGCCA 2149 1503 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1425 ACCAATC C ACAAGCCA 2156	1557	AAAGGAUG CUGAUGAG X CGAA IGGGUGAG	1411	CTCACCCC T CATCCTTT	2135
1563 AANGURAA CUGAUGAG X CGAA IGAUGAGG 1414 CCTCATCC T TITACTTT 2138 1569 GOGCANAA CUGAUGAG X CGAA IUANAAGG 1415 CCTTTTAC T TITTGCCC 2119 1576 GUGGAGG CUGAUGAG X CGAA ICANAAGG 1416 CCTTTTAC T TITTGCCC 2129 1577 AGUGGAAG CUGAUGAG X CGAA IGCANAAGA 1416 CTTTTTGCC C C TCTCCACT 2141 1578 AAGUGGAA CUGAUGAG X CGAA IGCANAAA 1418 TTTTGCCC C TTCCACTT 2142 1579 AAAGUGGA CUGAUGAG X CGAA IGGGCANAA 1419 TTTGCCC C TTCCACTT 2143 1582 CUCANAGU CUGAUGAG X CGAA IAGGGGG 1420 GCCCCTTC C ACTTTGAG 2144 1583 ACUCAAG CUGAUGAG X CGAA IAGGGGG 1421 GCCCCTTC C ACTTTGAG 2144 1584 GUGAUGAG C CGAA IGAGAGGG 1421 CCCCTTCC A TTTGAGT 2146 1594 GUGGAUGU CUGAUGAG X CGAA IUACUCAA 1423 TTGAGTAC C ANATCCAC 2146 1595 UGGGAUU CUGAUGAG X CGAA IUACUCA 1424 TGAGTAC C ANATCCAC 2147 1595 UGGGAUU CUGAUGAG X CGAA IUACUCA 1424 TGAGTAC C ANATCCAC 2147 1596 UGGCUUGU CUGAUGAG X CGAA IUACUCA 1424 TGAGTAC C ANATCCAC 2149 1590 UGGCUUGU CUGAUGAG X CGAA IUAUCUCA 1424 TGAGTAC C ANATCCAC 2149 1591 AUGGCUUGU CUGAUGAG X CGAA IUAUCUCA 1424 TGAGTAC C ANATCCAC 2149 1591 AUGGCUUGU CUGAUGAG X CGAA IUAUCUCA 1424 TGAGTAC C ANATCCAC 2149 1591 AUGGCUUGU CUGAUGAG X CGAA IUAUCUCA 1424 TGAGTAC C ANATCCAC 2149 1591 AUGGCUUGU CUGAUGAG X CGAA IUAUCUCA 1424 TGAGTAC C ANACCCAC 2150 1501 AUGGCUUG CUGAUGAG X CGAA IUAUCUCA 1426 CCAAATC C ACAAGCCA 2150	1559	UAAAAGGA CUGAUGAG X CGAA IAGGGGUG	1412	CACCCCTC A TCCTTTTA	2136
1569 GGGCAAAA CUGAUGAG X CGAA IUANAAGG 1415 CCTTTTAC T TTTTGCCC 2139 1576 GUGAAGG CUGAUGAG X CGAA ICAAAAAG 1416 CTTTTTGC C C CTTCCAC 2140 1577 AGUGGAAG CUGAUGAG X CGAA IGACAAAAA 1417 TTTTGCC C CTTCCACT 2141 1578 AAGUGGAA CUGAUGAG X CGAA IGGCAAAAA 1418 TTTTGCC C CTTCCACT 2142 1579 AAAGUGGA CUGAUGAG X CGAA IGGCAAAA 1419 TTTGCCC C TTCCACTT 2142 1579 AAAGUGGA CUGAUGAG X CGAA IAAGCGGC 1420 GCCCCTTC C ACTTTGAG 2144 1583 ACUCAAAG CUGAUGAG X CGAA IGAAGGGG 1421 CCCCTTCC A CTTTGAGT 2145 1594 GUGGAUGU CUGAUGAG X CGAA IUGCAAAG 1422 CCTTCCAC T TTGAGTAC 2146 1595 UGUGGAUU CUGAUGAG X CGAA IUGCACA 1423 TTGAGTAC C AAATCCCAC 2147 1595 UGUGGAUU CUGAUGAG X CGAA IUGCACA 1424 TGAGTAC C AAATCCAC 2148 1500 UGGCUUG CUGAUGAG X CGAA IAUUUGG 1425 ACCAAATC C ACAAGCCA 2149 1501 AUGGCUUG CUGAUGAG X CGAA IUGCAUUU 1425 ACCAAATC C ACAAGCCA 2150 1603 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CAACCCATT 2151 1604 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CAACCCATT 2151 1606 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CAACCCATT 2151 1607 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CAACCCATT 2151 1608 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CAACCCATT 2151 1609 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CACCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CACCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CACCATTT 2151 1601 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CAACCCATT 2151 1602 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CACCATTT 2151 1603 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CAACCATTT 2151 1604 AUGCCUCAU CAACCAC A CAACCATT 2151 1606 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CAACCATT 2151 1607 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CACCATTT 2151 1608 AAAUGGCU CUGAUG	1562	AAGUAAAA CUGAUGAG X CGAA IAUGAGGG	1413	CCCTCATC C TTTTACTT	2137
1576 GUSGAAGG CUGAUGAG X CGAA ICAAAAAG 1416 CTTTTTGC C CCTTCCAC 2140 1577 AGUGGAAG CUGAUGAG X CGAA IGCAAAAAA 1417 TTTTTGCC C CTTCCACT 2141 1578 AAGUGGA CUGAUGAG X CGAA IGCACAAA 1418 TTTTGCCC C TTCCACTT 2142 1579 AAAGUGGA CUGAUGAG X CGAA IGGCAAAA 1419 TTTGCCC C TTCCACTT 2143 1582 CUCAAAGG CUGAUGAG X CGAA IGGAGAAA 1419 TTTGCCC T TCCACTTT 2143 1583 ACUCAAA CUGAUGAG X CGAA IGAAAGGG 1421 CCCCTTC C ACTTTGAG 2144 1583 AGUCACAA CUGAUGAG X CGAA IGAAAGGG 1421 CCCCTTC C A CTTTGAGT 2145 1584 GUGAUGAG CUGAUGAG X CGAA IUGCAGA 1423 CTTCCAC T TTGAGTAC 2146 1594 GUGGAUGU CUGAUGAG X CGAA IUACUCAA 1423 TTGAGTAC C AAATCCAC 2147 1595 UGUGGAUU CUGAUGAG X CGAA IGUACUCA 1424 TGAGTAC C AAATCCAC 2148 1600 UGGCUUG CUGAUGAG X CGAA IGAUGUGG 1425 ACCAAATC C ACAAGCCA 2149 1601 AUGGCUUG CUGAUGAG X CGAA IGAGUGG 1426 CCAAATCC A CAAACCCA 2156 1603 AAAUGGCU CUGAUGAG X CGAA IUACUGAUUU 1425 ACCAAATC A CAAACCCAT 2150	1563	AAAGUAAA CUGAUGAG X CGAA IGAUGAGG	1414	CCTCATCC T TTTACTTT	2138
1577	1569	GGGCAAAA CUGAUGAG X CGAA IUAAAAGG	1415	CCTTTTAC T TTTTGCCC	2139
1578 AAGUIGAA CUGAUGAG X CGAA IGGCAAAA 1418 TITTOCCC C TTCCACTT 2142 1579 AAAGUIGAA CUGAUGAG X CGAA IGGCAAAA 1419 TTTGCCC C TTCCACTT 2143 1582 CUCAAAGU CUGAUGAG X CGAA IAAGGGGC 1420 GCCCCTTC C ACTITIGAG 2144 1583 ACUCAAAG CUGAUGAG X CGAA IGAAGGGG 1421 CCCCTTCC A CTTTGAGT 2145 1585 GUACUCAA CUGAUGAG X CGAA IUGAAAGG 1422 CCTTCCAC T TTGAGTAC 2145 1594 GUIGGAUJU CUGAUGAG X CGAA IUGCACA 1423 TTGAGTAC C AAATCCCAC 2147 1595 UGUGGAUU CUGAUGAG X CGAA IUGUCCA 1424 TGAGTAC C AAATCCAC 2148 1500 UGGCUUGU CUGAUGAG X CGAA IAUUUGG 1425 ACCAAATC C ACAAGCCA 2149 1501 AUGGCUUG CUGAUGAG X CGAA IAUUUGG 1426 CCAAATCC A CAAGCCAT 2150 1603 AAAUGGCU CUGAUGAG X CGAA IUGCAUUU 1427 AAATCCAC A CACCATTT 2151 1604 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1607 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1608 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1609 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1601 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1602 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1603 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1604 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1607 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1608 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1609 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGGAUU 1427 AAATCCAC A ACCCATTT 2151 1600 AUGGCUAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151	1576	GUGGAAGG CUGAUGAG X CGAA ICAAAAAG	1416	CTTTTTGC C CCTTCCAC	2140
1579 AAAGUUGA CUGAUGAG X CGAA IGGGCAAA 1419 TTTGCCCC T TCCACTTT 2143 1582 CUCAAAGU CUGAUGAG X CGAA IAAGGGGC 1420 GCCCCTTC C ACTTGAG 2144 1583 ACUCAAAG CUGAUGAG X CGAA IGAAGGGG 1421 CCCCTTCC A CTTTGAGT 2145 1585 GUACUCAA CUGAUGAG X CGAA IUGGAAGG 1422 CCTTCCAC T TTGAGTAC 2146 1594 GUSGAUTU CUGAUGAG X CGAA IUGCUCAA 1423 TTGAGTAC C AAATCCAC 2147 1595 UGGCGAUT CUGAUGAG X CGAA IGAUCUCA 1424 TGAGTACC A AATCCAC 2146 1590 UGGCUUGU CUGAUGAG X CGAA IAUTUGGI 1425 ACCAAATC C ACAAGCCA 2149 1501 ALGGCUUG CUGAUGAG X CGAA IGAUGUG 1426 CCAAATCC A CAAGCCAT 2150 1503 AAAUGGGU CUGAUGAG X CGAA IGACAUUU 1427 AAATCCAC A ACCCATTT 2151 1503 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1504 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1507 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1508 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1509 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 2151 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT 1515 1500 AAAUGGGU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A ACCCATTT	1577	AGUGGAAG CUGAUGAG X CGAA IGCAAAAA	1417	TTTTTGCC C CTTCCACT	2141
1582 CUCAAAGU CUGAUGAG X CGAA IAAGCOGC 1420 GCCCCTTC C ACTITGAG 2144 1583 ACUCAAAG CUGAUGAG X CGAA IGAAGGGG 1421 CCCCTTCC A CTITGAGT 2145 1585 GIACUCAA CUGAUGAG X CGAA IUGGAAGG 1422 CCTTCCAC T TTGAGTAC 2146 1594 GUGGAUGU CUGAUGAG X CGAA IUGCUCAA 1423 TTGAGTAC C MARTCCAC 2147 1595 UGGGAUU CUGAUGAG X CGAA IUACUCAA 1424 TGAGTAC C AAATCCAC 2148 1500 UGGCUUGU CUGAUGAG X CGAA IAUUUGGU 1425 ACCAAATC C ACAAGCCA 2149 1501 AUGGCUUG CUGAUGAG X CGAA IAUUUGGU 1425 CCAAATCC A CAAGCCA 2149 1501 AUGGCUUG CUGAUGAG X CGAA IUGGAUGU 1426 CCAAATCC A CAAGCCAT 2150 1503 AAAUGGGU CUGAUGAG X CGAA IUGGAUGU 1427 AAATCCAC A ACCCATTT 2151 1504 AUGGCUUG CUGAUGAG X CGAA IUGGAUGU 1427 AAATCCAC A ACCCATTT 2151 1507 ACCCATTT 2151 CCCCTTCCAC CCCCTTCCAC CCCCTTCCAC CCCCTTCCAC CCCCTTCCAC CCCCTTCCAC CCCCTTCCACCAC CCCCTTCCACCAC CCCCTTCCACCAC CCCCTTCCACCACCACCACCACCACCACCACCACCACCAC	1578	AAGUGGAA CUGAUGAG X CGAA IGGCAAAA	1418	TTTTGCCC C TTCCACTT	2142
1583 ACUCANAG CUGAUGAG X CGAA IGAAGGGG 1421 CCCCTTCC A CTTTGAGT 2145 1585 GUACUCAA CUGAUGAG X CGAA IUGGANGG 1422 CCTTCCAC T TTGAGTAC 2146 1594 GUGGAUJU CUGAUGAG X CGAA IUGACUCA 1423 TTGAGTAC C NATCCAC 2147 1595 UGUGGAUJU CUGAUGAG X CGAA IGUACUCA 1424 TGAGTACC A NATCCAC 2148 1600 UGGCUJGU CUGAUGAG X CGAA IAUJUGGU 1425 ACCANATC C ACAAGCCA 2149 1601 AUGGCUJG CUGAUGAG X CGAA IGAJUUGG 1426 CCANATCC A CAGCCAT 2150 1603 AAAUGGCU CUGAUGAG X CGAA IUGAJUUJ 1427 AAATCCAC A ACCCATTT 2151 1604 AAAUGGCU CUGAUGAG X CGAA IUGAJUUJ 1427 AAATCCAC A ACCCATTT 2151 1607 AAAUGGCU CUGAUGAG X CGAA IUGAJUUJ 1427 AAATCCAC A ACCCATTT 2151 1608 AAAUGGCU CUGAUGAG X CGAA IUGAJUUJ 1427 AAATCCAC A ACCCATTT 2151 1609 AAAUGGCU CUGAUGAG X CGAA IUGAJUUJ 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGAJUUJ 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGAJUUJ 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGAGUUJ 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGAGUUJ 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGAGUUJ 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGAGUUJ 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGAGUUJ 1427 AAATCCAC A ACCCATTT 2151 1600 AAAUGGCU CUGAUGAG X CGAA IUGAGUUJ 1427 AAATCCAC A ACCCATTT 1448	1579	AAAGUGGA CUGAUGAG X CGAA IGGGCAAA	1419		2143
1985 GURCUCAN CUGAUGAG X CGNA IUGGANGG 1422 CCTTCCAC T TTGAGTAC 2146 1594 GUSGAUJU CUGAUGAG X CGNA IUGCUCAN 1423 TTGAGTAC C ANATCCAC 2147 1595 USUGGAUJU CUGAUGAG X CGNA IGUACUCA 1424 TGAGTAC C ANATCCAC 2148 1690 USUGCUUGU CUGAUGAG X CGNA IAUJUUGG 1425 ACCANATC C ACANGCCA 2149 1691 AUGGCUUGU CUGAUGAG X CGNA IGUAUUUG 1426 CCANATCC A CANGCCAT 2150 1603 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1604 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1607 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1608 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1609 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1600 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1600 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1600 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1600 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1600 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1600 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1600 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1600 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1600 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1600 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 2151 1600 ANAUGGCU CUGAUGAG X CGNA IUGGAUJU 1427 ANATCCAC A ACCCATTT 1447	1582	CUCAAAGU CUGAUGAG X CGAA IAAGGGGC	1420	GCCCCTTC C ACTTTGAG	2144
1594 GUSGAUUU CUGAUGAS X CGAA IUACUCAA 1423 TTGAGTAC C AAATCCAC 2147 1595 UGUGGAUU CUGAUGAG X CGAA IGUACUCA 1424 TGAGTACC A AATCCACA 2148 1600 UGGCUUGU CUGAUGAG X CGAA IGUUUGGU 1425 ACCAAATC C A CAAGCCA 2149 1601 AUGGCUUG CUGAUGAG X CGAA IGAUUUGG 1426 CCAAATCC A CAAGCCAT 2150 1603 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A AGCCATT 2151	1583	ACUCAAAG CUGAUGAG X CGAA IGAAGGGG	1421		2145
1595 UGUGGAUU CUGAUGAG X CGAA IGUACUCA 1424 TGAGTACC A AATCCACA 2148 1600 UGGCUUGU CUGAUGAG X CGAA IAUUUGGI 1425 ACCAAATC C ACAAGCCA 2149 1691 AUGGCUUG CUGAUGAG X CGAA IGAUUUGG 1426 CCAAATCC A CAAGCCAT 2150 1603 AAAUUGGU CUGAUGAG X CGAA IUGAUUU 1427 AAATCCAC A ACCCATIT 2151	1585	GUACUCAA CUGAUGAG X CGAA IUGGAAGG	1422		
1601 UGGCUUGU CUGAUGAG X CGAA IANJUGGU 1425 ACCAAATC C ACAAGCCA 21.9 1601 AUGGCUUG CUGAUGAG X CGAA IGAJUUUG 1426 CCAAATCC A CAAGCCAT 2150 1603 AAAUGGA ACCATTT 2151 1427 AAATCCAC A ACCCATTT 2151	1594	GUGGAUUU CUGADGAG X CGAA IUACUCAA	1423	TTGAGTAC C AAATCCAC	2147
1601 AUGGCUUG CUGAUGAG X CGAA IGAUUUGG 1426 CCAAATCC A CAAGCCAT 2150 1603 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A AGCCATTT 2151	1595	UGUGGAUU CUGAUGAG X CGAA IGUACUCA	1424	TGAGTACC A AATCCACA	2148
1603 AAAUGGCU CUGAUGAG X CGAA IUGGAUUU 1427 AAATCCAC A AGCCATTT 2151	1600	UGGCUUGU CUGAUGAG X CGAA IAUUUGGU	1425	ACCAAATC C ACAAGCCA	2149
	1601	AUGGCUUG CUGAUGAG X CGAA IGAUUUGG	1426	CCAAATCC A CAAGCCAT	2150
1607 CAAAAAAU CUGAUGAG X CGAA ICUUGUGG 1428 CCACAAGC C ATTTTTTG 2152	1603	AAAUGGCU CUGAUGAG X CGAA IUGGAUUU	1427	AAATCCAC A AGCCATTT	2151
	1607	CAAAAAU CUGAUGAG X CGAA ICUUGUGG	1428	CCACAAGC C ATTTTTG	2152

Table 4

1608	UCAAAAA CUGAUGAG X CGAA IGCUUGUG	1429	CACAAGCC A TTTTTTGA	2153
1636	GCCAGCAU CUGAUGAG X CGAA IUACUCUC	1430	GAGAGTAC C ATGCTGGC	2154
1637	CGCCAGCA CUGAUGAG X CGAA IGUACUCU	1431	AGAGTACC A TGCTGGCG	2155
1641	GCGCCGCC CUGAUGAG X CGAA ICAUGGUA	1432	TACCATGC T GGCGGCGC	2156
1650	CUUCCCUC CUGAUGAG X CGAA IOGCOGCC	1433	GGCGGCGC A GAGGGAAG	2157
1663	CGGGUGUA CUGAUGAG X CGAA ICCCCUUC	1434	GAAGGGC C TACACCCG	2158
1664	ACGGGUGU CUGAUGAG X CGAA IGCCCCUU	1435	AAGGGGCC T ACACCCGT	2159
1667	AAGACGGG CUGAUGAG X CGAA IUAGGCCC	1436	GGGCCTAC A CCCGTCTT	2160
1669	CCAAGACG CUGAUGAG X CGAA IUGUAGGC	1437	GCCTACAC C CGTCTTGG	2161
1670	CCCAAGAC CUGAUGAG X CGAA IGUGUAGG	1438	CCTACACC C GTCTTGGG	2162
1674	GAGCCCCA CUGAUGAG X CGAA IACGGGUG	1439	CACCCGTC T TGGGGCTC	2163
1681	GUGGGGCG CUGAUGAG X CGAA ICCCCAAG	1440	CTTGGGGC T CGCCCCAC	2164
1685	CUGGGUGG CUGAUGAG X CGAA ICGAGCCC	1441	GGGCTCGC C CCACCCAG	2165
1686	CCUGGGUG CUGAUGAG X CGAA IGCGAGCC	1442	GGCTCGCC C CACCCAGG	2166
1687	CCCUGGGU CUGAUGAG X CGAA IGGCGAGC	1443	GCTCGCCC C ACCCAGGG	2167
1688	GCCCUGGG CUGAUGAG X CGAA IGGGCGAG	1444	CTCGCCCC A CCCAGGGC '	2168
1690	GAGCCCUG CUGAUGAG X CGAA IUGGGGCG	1445	CGCCCCAC C CAGGGCTC	2169
1691	GGAGCCCU CUGAUGAG X CGAA IGUGGGGC	1446	GCCCCACC C AGGGCTCC	2170
1692	GGGAGCCC CUGAUGAG X CGAA IGGUGGGG	1447	CCCCACCC A GGGCTCCC ·	2171
1697	CAGGAGGG CUGAUGAG X CGAA ICCCUGGG	1448	CCCAGGGC T CCCTCCTG	2172
1699	UCCAGGAG CUGAUGAG X CGAA IAGCCCUG	1449	CAGGGCTC C CTCCTGGA	2173
1700	CUCCAGGA CUGAUGAG X CGAA IGAGCCCU	1450	AGGGCTCC C TCCTGGAG	2174
1701	GCUCCAGG CUGAUGAG X CGAA IGGAGCCC	1451	GGGCTCCC T CCTGGAGC	2175
1703	AUGCUCCA CUGAUGAG X CGAA IAGGGAGC	1452	GCTCCCTC C TGGAGCAT	2176
1704	GAUGCUCC CUGAUGAG X CGAA IGAGGGAG	1453	CTCCCTCC T GGAGCATC	2177
1710	GCCUGGGA CUGAUGAG X CGAA ICUCCAGG	1454	CCTGGAGC A TCCCAGGC	2178
1713	CCCGCCUG CUGAUGAG X CGAA IAUGCUCC	1455	GGAGCATC C CAGGCGGG	2179
1714	GCCCGCCU CUGAUGAG X CGAA IGAUGCUC	1456	GAGCATCC C AGGCGGGC	2180
1715	CGCCCGCC CUGAUGAG X CGAA IGGAUGCU	1457	AGCATCCC A GGCGGGCG	2181
1726	GUCUGGCG CUGAUGAG X CGAA ICCGCCCG	1458	CGGGCGGC A CGCCAGAC	2182
1730	GGCUGUCU CUGAUGAG X CGAA ICGUGCCG	1459	CGGCACGC C AGACAGCC	2183
1731	GGGCUGUC CUGAUGAG X CGAA IGCGUGCC	1460	GGCACGCC A GACAGCCC	2184
1735	GGGGGGC CUGAUGAG X CGAA IUCUGGCG	1461	CGCCAGAC A GCCCCCCC	2185
1738	AAGGGGG CUGAUGAG X CGAA ICUGUCUG	1462	CAGACAGC C CCCCCCTT	2186
1739	CAAGGGGG CUGAUGAG X CGAA IGCUGUCU	1463	AGACAGCC C CCCCTTGA	2187
1740	UCAAGGGG CUGAUGAG X CGAA IGGCUGUC	1464		2188
1741	UUCAAGGG CUGAUGAG X CGAA IGGGCUGU	1465	ACAGCCCC C CCCTTGAA	2189
1742	AUUCAAGG CUGAUGAG X CGAA IGGGGCUG	1466	CAGCCCCC C CCTTGAAT	2190
1743	GAUUCAAG CUGAUGAG X CGAA IGGGGGCU	1467	AGCCCCCC C CTTGAATC	2191
1744	AGAUUCAA CUGAUGAG X CGAA IGGGGGGC	1468		2192
1745	CAGAUUCA CUGAUGAG X CGAA IGGGGGGG	1469	CCCCCCC T TGAATCTG	2193
1752	CUCCCUGC CUGAUGAG X CGAA IAUUCAAG	1470	CTTGAATC T GCAGGGAG	2194
1755	UUGCUCCC CUGAUGAG X CGAA ICAGAUUC	1471	GAATCTGC A GGGAGCAA	2195
1762	UGGAGAGU CUGAUGAG X CGAA ICUCCCUG	1472	CAGGGAGC A ACTCTCCA	2196
1765	GAGUGGAG CUGAUGAG X CGAA IUUGCUCC	1473	GGAGCAAC T CTCCACTC	2197
1767	UGGAGUGG CUGAUGAG X CGAA IAGUUGCU	1474	AGCAACTC T CCACTCCA	2198
1769	UAUGGAGU CUGAUGAG X CGAA IAGAGUUG	1475	CAACTCTC C ACTCCATA	2199

Table 4

1770	AUAUGGAG CUGAUGAG X CGAA IGAGAGUU	1476	AACTCTCC A CTCCATAT	2200
1772	AAAUAUGG CUGAUGAG X CGAA IUGGAGAG	1477	CTCTCCAC T CCATATTT	2201
1774	AUAAAUAU CUGAUGAG X CGAA IAGUGGAG	1478	CTCCACTC C ATATTTAT	2202
1775	AAUAAAUA CUGAUGAG X CGAA IGAGUGGA	1479	TCCACTCC A TATTTATT	2203
1789	GAAAAAU CUGAUGAG X CGAA IUUUAAAU	1480	ATTTAAAC A ATTTTTC	2204
1798	GCCUUUGG CUGAUGAG X CGAA IAAAAAAU	1481	ATTTTTC C CCAAAGGC	2205
1799	UGCCUUUG CUGAUGAG X CGAA IGAAAAAA	1482	TTTTTTCC C CAAAGGCA	2206
1800	AUGCCUUU CUGAUGAG X CGAA IGGAAAAA	1483	TTTTTCCC C AAAGGCAT	2207
1801	GAUGCCUU CUGAUGAG X CGAA IGGGAAAA	1484	. TTTTCCCC A AAGGCATC	2208
1807	ACUAUGGA CUGAUGAG X CGAA ICCUUUGG	1485	CCAAAGGC A TCCATAGT	2209
1810	UGCACUAU CUGAUGAG X CGAA IAUGCCUU	1486	AAGGCATC C ATAGTGCA	2210
1811	GUGCACUA CUGAUGAG X CGAA IGAUGCCU	1487	AGGCATCC A TAGTGCAC	2211
1818	AAUGCUAG CUGAUGAG X CGAA ICACUAUG	1488	CATAGTGC A CTAGCATT	2212
1820	AAAAUGCU CUGAUGAG X CGAA IUGCACUA	1489	TAGTGCAC T AGCATTTT	2213
1824	CAAGAAAA CUGAUGAG X CGAA ICUAGUGC	1490	GCACTAGC A TTTTCTTG	2214
1830	UUGGUUCA CUGAUGAG X CGAA IAAAAUGC	1491	GCATTITC T TGAACCAA	2215
1836	ACAUUAUU CUGAUGAG X CGAA IUUCAAGA	1492	TCTTGAAC C AATAATGT	2216
1837	UACAUUAU CUGAUGAG X CGAA IGUUCAAG	1493	CTTGAACC A ATAATGTA	2217
1864	UGCAAGGC CUGAUGAG X CGAA IACAUCAA	1494	TTGATGTC A GCCTTGCA	2218
1867	UGAUGCAA CUGAUGAG X CGAA ICUGACAU	1495	ATGTCAGC C TTGCATCA	2219
1868	UUGAUGCA CUGAUGAG X CGAA IGCUGACA	1496	TGTCAGCC T TGCATCAA	2220
1872	GCCCUUGA CUGAUGAG X CGAA ICAAGGCU	1497	AGCCTTGC A TCAAGGGC	2221
1875	AAAGCCCU CUGAUGAG X CGAA IAUGCAAG	1498	CTTGCATC A AGGGCTTT	2222
1881	UUUGAUAA CUGAUGAG X CGAA ICCCUUGA	1499	TCAAGGGC T TTATCAAA	2223
1887	GUACURUU CUGAUGAG X CGAA IAHAAAGC	1500	GCTTTATC A AAAAGTAC	2224
1896	UUUAUUAU CUGAUGAG X CGAA IUACUUUU	1501	AAAAGTAC A ATAATAAA	2225
1907	CUACCUGA CUGAUGAG X CGAA IAUUUAUU	1502	AATAAATC C TCAGGTAG	2225
1908	ACUACCUG CUGAUGAG X CGAA IGAUUUAU	1503	ATAMATIC T CAGGTAGT	2227
1910	GUACUACC CUGAUGAG X CGAA IAGGAUUU	1504	AAATCCTC A GGTAGTAC	2228
1910	CCAUTICCC CUGAUGAG X CGAA TAGGAUGU	1505	GGTAGTAC T GGGAATGG	2229
	CAUGGCAA CUGAUGAG X CGAA TOACOACC		TGGAAGGC T TTGCCATG	
1933		1506		2230
1938	AGGCCCAU CUGAUGAG X CGAA ICAAAGCC		GGCTTTGC C ATGGGCCT	-
1939	CAGGCCCA CUGAUGAG X CGAA IGCAAAGC	1508	GCTTTGCC A TGGGCCTG	2232
1945	ACGCAGCA CUGAUGAG X CGAA ICCCAUGG	1509	CCATGGGC C TGCTGCGT	2233
1946	GACGCAGC CUGAUGAG X CGAA IGCCCAUG	1510	CATGGGCC T GCTGCGTC	2234
1949	UCUGACGC CUGAUGAG X CGAA ICAGGCCC	1511	GGGCCTGC T GCGTCAGA	2235
1955	UACUGGUC CUGAUGAG X CGAA IACGCAGC	1512	GCTGCGTC A GACCAGTA	2236
1959	CCAGUACU CUGAUGAG X CGAA IUCUGACG	1513	CGTCAGAC C AGTACTGG	2237
1960	CCCAGUAC CUGAUGAG X CGAA IGUCUGAC	1514	GTCAGACC A GTACTGGG	2238
1965	UCCUUCCC CUGAUGAG X CGAA IUACUGGU	1515	ACCAGTAC T GGGAAGGA	2239
1988	AUAACAAC CUGAUGAG X CGAA ICUUACAA	1516	TTGTAAGC A GTTGTTAT	2240
2032	UAUAGCAU CUGAUGAG X CGAA IUUCUAUC	1517	GATAGAAC A ATGCTATA	2241
2037	UAUAUUAU CUGAUGAG X CGAA ICAUUGUU	1518	AACAATGC T ATAATATA	2242
2054	UACCCACG CUGAUGAG X CGAA IUUCAUUA	1519	TAATGAAC A CGTGGGTA	2243
2076	UCACAUCA CUGAUGAG X CGAA IUUUCUUA	1520	TAAGAAAC A TGATGTGA	2244
2091	CGGGACAA CUGAUGAG X CGAA IUAAUCUC	1521	GAGATTAC T TTGTCCCG	2245
2097	AAUAAGCG CUGAUGAG X CGAA IACAAAGU	1522	ACTITGIC C CGCTTATT	2246

2098	GAAUAAGC CUGAUGAG X CGAA IGACAAAG	1523	CTTTGTCC C GCTTATTC	2247
2101	GCAGAAUA CUGAUGAG X CGAA ICGGGACA	1524	TGTCCCGC T TATTCTGC	2248
2107	CAGGGAGC CUGAUGAG X CGAA IAAUAAGC	1525	GCTTATTC T GCTCCCTG	2249
2110	UAACAGGG CUGAUGAG X CGAA ICAGAAUA	1526	TATTCTGC T CCCTGTTA	2250
2112	GAUAACAG CUGAUGAG X CGAA IAGCAGAA	1527	TTCTGCTC C CTGTTATC	2251
2113	AGAUAACA CUGAUGAG X CGAA IGAGCAGA	1528	TCTGCTCC C TGTTATCT	2252
2114	CAGAUAAC CUGAUGAG X CGAA IGGAGCAG	1529	CTGCTCCC T GTTATCTG	2253
2121	GAUCUAGO CUGAUGAG X CGAA IAUAACAG	1530	CTGTTATC T GCTAGATC	2254
2124	CUAGAUCU CUGAUGAG X CGAA ICAGAUAA	1531	TTATCTGC T AGATCTAG	2255
2130	UGAGAACU CUGAUGAG X CGAA IAUCUAGC	1532	GCTAGATC T AGTTCTCA	2256
2136	AGUGAUUG CUGAUGAG X CGAA IAACUAGA	1533	TCTAGTTC T CAATCACT	2257
2138	GCAGUGAU CUGAUGAG X CGAA IAGAACUA	1534	TAGTTCTC A ATCACTGC	2258
2142	GGGAGCAG CUGAUGAG X CGAA IAUUGAGA	1535	TCTCAATC A CTGCTCCC	2259
2144	GGGGGAGC CUGAUGAG X CGAA IUGAUUGA	1536	TCAATCAC T GCTCCCCC	2260
2147	CACGGGG CUGAUGAG X CGAA ICAGUGAU	1537	ATCACTGC T CCCCCGTG	2261
2149	CACACGGG CUGAUGAG X CGAA IAGCAGUG	1538	CACTGCTC C CCCGTGTG	2262
2150	ACACACGG CUGAUGAG X CGAA IGAGCAGU	1539	ACTGCTCC C CCGTGTGT	2263
2151	UACACACG CUGAUGAG X CGAA IGGAGCAG	1540	CTGCTCCC C CGTGTGTA	2264
2152	AUACACAC CUGAUGAG X CGAA IGGGAGCA	1541	TGCTCCCC C GTGTGTAT	2265
2169	ACCUUACA CUGAUGAG X CGAA ICAUUCUA	1542	TAGAATGC A TGTAAGGT	2266
2179	ACACAAGA CUGAUGAG X CGAA IACCUUAC	1543	GTAAGGTC T TCTTGTGT	2267
2182	AGGACACA CUGAUGAG X CGAA IAAGACCU	1544	AGGTCTTC T TGTGTCCT	2268
2189	UUUCAUCA CUGAUGAG X CGAA IACACAAG	1545	CTTGTGTC C TGATGAAA	2269
2190	UUUUCAUC CUGAUGAG X CGAA IGACACAA	1546	TTGTGTCC T GATGAAAA	2270
2207	UCAUUUCA CUGAUGAG X CGAA ICACAUAU	1547	ATATGTGC T TGAAATGA	2271
2221	GAGAUCAA CUGAUGAG X CGAA IUUUCUCA	1548	TGAGAAAC T TTGATCTC	2272
2228	GUAAGCAG CUGAUGAG X CGAA IAUCAAAG	1549	CTTTGATC T CTGCTTAC	2273
2230	UAGUAAGC CUGAUGAG X CGAA IAGAUCAA	1550	TTGATCTC T GCTTACTA	2274
2233	CAUUAGUA CUGAUGAG X CGAA ICAGAGAU	1551	ATCTCTGC T TACTAATG	2275
2237	GGCACAUU CUGAUGAG X CGAA IUAAGCAG	1552	CTGCTTAC T AATGTGCC	2276
2245	GGACAUGG CUGAUGAG X CGAA ICACAUUA	1553	TAATGTGC C CCATGTCC	2277
2246	UGGACAUG CUGAUGAG X CGAA IGCACAUU	1554	AATGTGCC C CATGTCCA	2278
2247	UUGGACAU CUGAUGAG X CGAA IGGCACAU	1555	ATGTGCCC C ATGTCCAA	2279
2248	CUUGGACA CUGAUGAG X CGAA IGGGCACA	1556	TGTGCCCC A TGTCCAAG	2280
2253	UUGGACUU CUGAUGAG X CGAA IACAUGGG	1557	CCCATGTC C AAGTCCAA	2281
2254	GUUGGACU CUGAUGAG X CGAA IGACAUGG	1558	CCATGTCC A AGTCCAAC	2282
2259	GGCAGGUU CUGAUGAG X CGAA IACUUGGA	1559	TCCAAGTC C AACCTGCC	2283
2260	AGGCAGGU CUGAUGAG X CGAA IGACUUGG	1560	CCAAGTCC A ACCTGCCT	2284
2263	CACAGGCA CUGAUGAG X CGAA IUUGGACU	1561	AGTCCAAC C TGCCTGTG	2285
2264	GCACAGGC CUGAUGAG X CGAA IGUUGGAC	1562	GTCCAACC T GCCTGTGC	2286
2267	CAUGCACA CUGAUGAG X CGAA ICAGGUUG	1563	CAACCTGC C TGTGCATG	2287
2268	UCAUGCAC CUGAUGAG X CGAA IGCAGGUU	1564	AACCTGCC T GTGCATGA	2288
2273	UCAGGUCA CUGAUGAG X CGAA ICACAGGC	1565	GCCTGTGC A TGACCTGA	2289
2278	AAUGAUCA CUGAUGAG X CGAA IUCAUGCA	1566	TGCATGAC C TGATCATT	2290
2279	UAAUGAUC CUGAUGAG X CGAA IGUCAUGC	1567	GCATGACC T GATCATTA	2291
2284	CCAUGUAA CUGAUGAG X CGAA IAUCAGGU	1568	ACCTGATC A TTACATGG	2292
2289	CACAGCCA CUGAUGAG X CGAA IUAAUGAU	1569	ATCATTAC A TGGCTGTG	2293

Table 4

2294	GGAACCAC CUGAUGAG X CGAA ICCAUGUA	1570	TACATGGC T GTGGTTCC	2294
2302	CAGGCUUA CUGAUGAG X CGAA IAACCACA	1571	TGTGGTTC C TAAGCCTG	2295
2303	ACAGGCUU CUGAUGAG X CGAA IGAACCAC	1572	GTGGTTCC T AAGCCTGT	2296
2308	CAGCAACA CUGAUGAG X CGAA ICUUAGGA	1573	TCCTAAGC C TGTTGCTG	2297
2309	UCAGCAAC CUGAUGAG X CGAA IGCUUAGG	1574	CCTAAGCC T GTTGCTGA	2298
2315	AUGACUUC CUGAUGAG X CGAA ICAACAGG	1575	CCTGTTGC T GAAGTCAT	2299
2322	AGCGACAA CUGAUGAG X CGAA IACUUCAG	1576	CTGAAGTC A TTGTCGCT	2300
2330	UAUUGCUG CUGAUGAG X CGAA ICGACAAU	1577	ATTGTCGC T CAGCAATA	2301
2332	CCUAUUGC CUGAUGAG X CGAA IAGCGACA	1578	TGTCGCTC A GCAATAGG	2302
2335	CACCCUAU CUGAUGAG X CGAA ICUGAGCG	1579	CGCTCAGC A ATAGGGTG	2303
2345	UGGAAAAC CUGAUGAG X CGAA ICACCCUA	1580	TAGGGTGC A GTTTTCCA	2304
2352	CUAUUCCU CUGAUGAG X CGAA IAAAACUG	1581	CAGTTTTC C AGGAATAG	2305
2353	CCUAUUCC CUGAUGAG X CGAA IGAAAACU	1582	AGTTTTCC A GGAATAGG	2306
2363	UAGGCAAA CUGAUGAG X CGAA ICCUAUUC	1583	GAATAGGC A TTTGCCTA	2307
2369	AGGAAUUA CUGAUGAG X CGAA ICAAAUGC	1584	GCATTIGC C TAATTCCT	2308
2370	CAGGAAUU CUGAUGAG X CGAA IGCAAAUG	1585	CATTIGC C TAATICCI	2308
2376	UCAUGCCA CUGAUGAG X CGAA IAAUUAGG	1586	CCTAATTC C TGGCATGA	2309
2377	GUCAUGCC CUGAUGAG X CGAA IGAAUUAG	1587	CTAATTCC T GGCATGAC	
2377	GAGUGUCA CUGAUGAG X CGAA ICCAGGAA			2311
		1588	TTCCTGGC A TGACACTC	2312
2386	CACUAGAG CUGAUGAG X CGAA IUCAUGCC	1589	GGCATGAC A CTCTAGTG	2313
2388	GUCACUAG CUGAUGAG X CGAA IUGUCAUG	1590	CATGACAC T CTAGTGAC	2314
2390	AAGUCACU CUGAUGAG X CGAA IAGUGUCA	1591	TGACACTC T AGTGACTT	2315
2397	CACCAGGA CUGAUGAG X CGAA IUCACUAG	1592	CTAGTGAC T TCCTGGTG	2316
2400	CCUCACCA CUGAUGAG X CGAA IAAGUCAC	1593	GTGACTTC C TGGTGAGG	2317
2401	GCCUCACC CUGAUGAG X CGAA IGAAGUCA	1594	TGACTTCC T GGTGAGGC	2318
2410	ACAGGCUG CUGAUGAG X CGAA ICCUCACC	1595	GGTGAGGC C CAGCCTGT	2319
2411	GACAGGCU CUGAUGAG X CGAA IGCCUCAC	1596	GTGAGGCC C AGCCTGTC	2320
2412	GGACAGGC CUGAUGAG X CGAA IGGCCUCA	1597	TGAGGCCC A GCCTGTCC	2321
2415	CCAGGACA CUGAUGAG X CGAA ICUGGGCC	1598	GGCCCAGC C TGTCCTGG	2322
2416	ACCAGGAC CUGAUGAG X CGAA IGCUGGGC	1599	GCCCAGCC T GTCCTGGT	2323
2420	CUGUACCA CUGAUGAG X CGAA IACAGGCU	1600	AGCCTGTC C TGGTACAG	2324
2421	GCUGUACC CUGAUGAG X CGAA IGACAGGC	1601	GCCTGTCC T GGTACAGC	2325
2427	GACCCUGC CUGAUGAG X CGAA IUACCAGG	1602	CCTGGTAC A GCAGGGTC	2326
2430	CAAGACCC CUGAUGAG X CGAA ICUGUACC	1603	GGTACAGC A GGGTCTTG	2327
2436	UUACAGCA CUGAUGAG X CGAA IACCCUGC	1604	GCAGGGTC T TGCTGTAA	2328
2440	UGAGUUAC CUGAUGAG X CGAA ICAAGACC	1605	GGTCTTGC T GTAACTCA	2329
2446	AAUGUCUG CUGAUGAG X CGAA IUUACAGC	1606	GCTGTAAC T CAGACATT	2330
2448	GGAAUGUC CUGAUGAG X CGAA IAGUUACA	1607	TGTAACTC A GACATTCC	2331
2452	CCUUGGAA CUGAUGAG X CGAA IUCUGAGU	1608	ACTCAGAC A TTCCAAGG	2332
2456	AUACCCUU CUGAUGAG X CGAA IAAUGUCU	1609	AGACATTC C AAGGGTAT	2333
245.7	CAUACCCU CUGAUGAG X CGAA IGAAUGUC	1610	GACATTCC A AGGGTATG	2334
2472	GUGAAUAU CUGAUGAG X CGAA ICUUCCCA	1611	TGGGAAGC C ATATTCAC	2335
2473	UGUGAAUA CUGAUGAG X CGAA IGCUUCCC	1612	GGGAAGCC A TATTCACA	2336
2479	GUGAGGUG CUGAUGAG X CGAA IAAUAUGG	1613	CCATATTC A CACCTCAC	2337
2481	GCGUGAGG CUGAUGAG X CGAA IUGAAUAU	1614	ATATTCAC A CCTCACGC	2338
2483	GAGCGUGA CUGAUGAG X CGAA IUGUGAAU	1615	ATTCACAC C TCACGCTC	2339
2484	AGAGCGUG CUGAUGAG X CGAA IGUGUGAA	1616	TTCACACC T CACGCTCT	2340
		12020	Transmict I CACGUICI	12370

2486	CCAGAGCG CUGAUGAG X CGAA IAGGUGUG	1617	CACACCTC A CGCTCTGG	2341
2490	AUGUCCAG CUGAUGAG X CGAA ICGUGAGG	1618	CCTCACGC T CTGGACAT	2342
2492	UCAUGUCC CUGAUGAG X CGAA IAGCGUGA	1619	TCACGCTC T GGACATGA	2343
2497	CUAAAUCA CUGAUGAG X CGAA IUCCAGAG	1620	CTCTGGAC A TGATTTAG	2344
2512	GGUGUCCC CUGAUGAG X CGAA ICUUCCCU	1621	AGGGAAGC A GGGACACC	2345
2518	GCGGGGGG CUGAUGAG X CGAA IUCCCUGC	1622	GCAGGGAC A CCCCCCGC	2346
2520	GGGCGGGG CUGAUGAG X CGAA IUGUCCCU	1623	AGGGACAC C CCCCGCCC	2347
2521	GGGGCGGG CUGAUGAG X CGAA IGUGUCCC	1624	GGGACACC C CCCGCCCC	2348
2522	GGGGGCGG CUGAUGAG X CGAA IGGUGUCC	1625	GGACACCC C CCGCCCCC	2349
2523	GGGGGCG CUGAUGAG X CGAA IGGGUGUC	1626	GACACCCC C CGCCCCCC	2350
2524	UGGGGGC CUGAUGAG X CGAA IGGGGUGU	1627	ACACCCCC C GCCCCCCA	2351
2527	AGGUGGGG CUGAUGAG X CGAA ICGGGGGG	1628	CCCCCGC C CCCCACCT	2352
2528	AAGGUGGG CUGAUGAG X CGAA IGCGGGGG	1629	CCCCCGCC C CCCACCTT	2353
2529	AAAGGUGG CUGAUGAG X CGAA IGGCGGGG	1630	CCCCGCCC C CCACCTTT	2354
2530	CAAAGGUG CUGAUGAG X CGAA IGGGCGGG	1631	CCCGCCCC C CACCTTTG	2355
2531	CCAAAGGU CUGAUGAG X CGAA IGGGGCGG	1632	CCGCCCCC C ACCTTTGG	2356
2532	CCCAAAGG CUGAUGAG X CGAA IGGGGGCG	1633	CGCCCCCC A CCTTTGGG	2357
2534	AUCCCAAA CUGAUGAG X CGAA IUGGGGGG	1634	CCCCCCAC C TTTGGGAT	2358
2535	GAUCCCAA CUGAUGAG X CGAA IGUGGGGG	1635	CCCCCACC T TTGGGATC	2359
2544	GCGGAGGC CUGAUGAG X CGAA IAUCCCAA	1636	TTGGGATC A GCCTCCGC	2360
2547	AUGGCGGA CUGAUGAG X CGAA ICUGAUCC	1637	GGATCAGC C TCCGCCAT	2361
2548	AAUGGCGG CUGAUGAG X CGAA IGCUGAUC	1638	GATCAGCC T CCGCCATT	2362
2550	GGAAUGGC CUGAUGAG X CGAA IAGGCUGA	1639	TCAGCCTC C GCCATTCC	2363
2553	CUUGGAAU CUGAUGAG X CGAA ICGGAGGC	1640	GCCTCCGC C ATTCCAAG	2364
2554	ACUUGGAA CUGAUGAG X CGAA IGCGGAGG	1641	CCTCCGCC A TTCCAAGT	2365
2558	GUCGACUU CUGAUGAG X CGAA IAAUGGCG	1642	CGCCATTC C AAGTCGAC	2366
2559	UGUCGACU CUGAUGAG X CGAA IGAAUGGC	1643	GCCATTCC A AGTCGACA	2367
2567	AAGAAGAG CUGAUGAG X CGAA IUCGACUU	1644	AAGTCGAC A CTCTTCTT	2368
2569	UCAAGAAG CUGAUGAG X CGAA IUGUCGAC	1645	GTCGACAC T CTTCTTGA	2369
2571	GCUCAAGA CUGAUGAG X CGAA IAGUGUCG	1646	CGACACTC T TCTTGAGC	2370
2574	UCUGCUCA CUGAUGAG X CGAA IAAGAGUG	1647	CACTCTTC T TGAGCAGA	2371
2580	UCACGGUC CUGAUGAG X CGAA ICUCAAGA	1648	TCTTGAGC A GACCGTGA	2372
2584	CAAAUCAC CUGAUGAG X CGAA IUCUGCUC	1649	GAGCAGAC C GTGATTTG	2373
2603	CCAGCAGG CUGAUGAG X CGAA ICCUCUCU	1650	AGAGAGGC A CCTGCTGG	2374
2605	UUCCAGCA CUGAUGAG X CGAA IUGCCUCU	1651	AGAGGCAC C TGCTGGAA	2375
2606	UUUCCAGC CUGAUGAG X CGAA IGUGCCUC	1652	GAGGCACC T GCTGGAAA	2376
2609	UGGUUUCC CUGAUGAG X CGAA ICAGGUGC	1653	GCACCTGC T GGAAACCA	2377
2616	AGAAGUGU CUGAUGAG X CGAA IUUUCCAG	1654	CTGGAAAC C ACACTTCT	2378
2617	AAGAAGUG CUGAUGAG X CGAA IGUUUCCA	1655	TGGAAACC A CACTTCTT	2379
2619	UCAAGAAG CUGAUGAG X CGAA IUGGUUUC	1656	GAAACCAC A CTTCTTGA	2380
2621	UUUCAAGA CUGAUGAG X CGAA IUGUGGUU	1657	AACCACAC T TCTTGAAA	2381
2624	CUGUUUCA CUGAUGAG X CGAA IAAGUGUG	1658	CACACTIC T TGAAACAG	2382
2631	ACCCAGGC CUGAUGAG X CGAA IUUUCAAG	1659	CTTGAAAC A GCCTGGGT	2383
2634	GUCACCCA CUGAUGAG X CGAA ICUGUUUC	1660	GAAACAGC C TGGGTGAC	2384
2635	CGUCACCC CUGAUGAG X CGAA IGCUGUUU	1661	AAACAGCC T GGGTGACG	2385
2647	UGCCUAAA CUGAUGAG X CGAA TACCGUCA	1662	TGACGGTC C TTTAGGCA	2386
2648	CUGCCUAA CUGAUGAG X CGAA IGACCGUC	1663	GACGGTCC T TTAGGCAG	2387

Table 4

2655	CGGCAGGC CUGAUGAG X CGAA ICCUAAAG	1664	CTTTAGGC A GCCTGCCG	2388
2658	CGGCGGCA CUGAUGAG X CGAA ICUGCCUA	1665	TAGGCAGC C TGCCGCCG	2389
2659	ACGGCGGC CUGAUGAG X CGAA IGCUGCCU	1666	AGGCAGCC T GCCGCCGT	2390
2662	GAGACGGC CUGAUGAG X CGAA ICAGGCUG	1667	CAGCCTGC C GCCGTCTC	2391
2665	ACAGAGAC CUGAUGAG X CGAA ICGGCAGG	1668	CCTGCCGC C GTCTCTGT	2392
2669	CGGGACAG CUGAUGAG X CGAA IACGGCGG	1669	CCGCCGTC T CTGTCCCG	2393
2671	ACCGGGAC CUGAUGAG X CGAA IAGACGGC	1670	GCCGTCTC T GTCCCGGT	2394
2675	GUGAACCG CUGAUGAG X CGAA IACAGAGA	1671	TCTCTGTC C CGGTTCAC	2395
2676	GGUGAACC CUGAUGAG X CGAA IGACAGAG	1672	CTCTGTCC C GGTTCACC	2396
2682	CGGCAAGG CUGAUGAG X CGAA IAACCGGG	1673	CCOGGTTC A CCTTGCCG	2397
2684	CUCGGCAA CUGAUGAG X CGAA IUGAACCG	1674	CGGTTCAC C TTGCCGAG	2398
2685	UCUCGGCA CUGAUGAG X CGAA IGUGAACC	1675	GGTTCACC T TGCCGAGA	2399
2689	CCUCUCUC CUGAUGAG X CGAA ICAAGGUG	1676	CACCTTGC C GAGAGAGG	2400
2704	GGUGGGC CUGAUGAG X CGAA IACGCGCC	1677	GGCGCGTC T GCCCCACC	2401
2707	GAGGGUGG CUGAUGAG X CGAA ICAGACGC	1678	GCGTCTGC C CCACCCTC	2402
2708	UGAGGGUG CUGAUGAG X CGAA IGCAGACG	1679	CGTCTGCC C CACCCTCA	2403
2709	UUGAGGGU CUGAUGAG X CGAA IGGCAGAC	1680	GTCTGCCC C ACCCTCAA	2404
2710	UUUGAGGG CUGAUGAG X CGAA IGGGCAGA	1681	TCTGCCCC A CCCTCAAA	2405
2712	GGUUUGAG CUGAUGAG X CGAA IUGGGGCA	1682	TGCCCCAC C CTCAAACC	2406
2713	GGGUUUGA CUGAUGAG X CGAA IGUGGGGC	1683	GCCCCACC C TCAAACCC	2407
2714	AGGGUUUG CUGAUGAG X CGAA IGGUGGGG	1684	CCCCACCC T CAAACCCT	2408
2716	ACAGGGUU CUGAUGAG X CGAA IAGGGUGG	1685	CCACCCTC A AACCCTGT	2409
2720	CCCCACAG CUGAUGAG X CGAA IUUUGAGG	1686	CCTCAAAC C CTGTGGGG	2410
2721	GCCCCACA CUGAUGAG X CGAA IGUUUGAG	1687	CTCAAACC C TGTGGGGC	2411
2722	GGCCCCAC CUGAUGAG X CGAA IGGUUUGA	1688	TCAAACCC T GTGGGGCC	2412
2730	CACCAUCA CUGAUGAG X CGAA ICCCCACA	1689	TGTGGGGC C TGATGGTG	2413
2731	GCACCAUC CUGAUGAG X CGAA IGCCCCAC	1690	GTGGGGCC T GATGGTGC	2414
2740	GAGUCGUG CUGAUGAG X CGAA ICACCAUC	1691	GATGGTGC T CACGACTC	2415
2742	AAGAGUCG CUGAUGAG X CGAA IAGCACCA	1692	TGGTGCTC A CGACTCTT	2416
2747	GCAGGAAG CUGAUGAG X CGAA IUCGUGAG	1693	CTCACGAC T CTTCCTGC	2417
2749	UUGCAGGA CUGAUGAG X CGAA IAGUCGUG	1694	CACGACTC T TCCTGCAA	2418
2752	CCUUUGCA CUGAUGAG X CGAA IAAGAGUC	1695	GACTCTTC C TGCAAAGG	2419
2753	CCCUUUGC CUGAUGAG X CGAA IGAAGAGU	1696	ACTCTTCC T GCAAAGGG	2420
2756	GUUCCCUU CUGAUGAG X CGAA ICAGGAAG	1697	CTTCCTGC A AAGGGAAC	2421
2765	AGGUCUUC CUGAUGAG X CGAA IUUCCCUU	1698	AAGGGAAC T GAAGACCT	2422
2772	AAUGUGGA CUGAUGAG X CGAA IUCUUCAG	1699	CTGAAGAC C TCCACATT	2423
2773	UAAUGUGG CUGAUGAG X CGAA IGUCUUCA	1700	TGAAGACC T CCACATTA	2424
2775	CUUAAUGU CUGAUGAG X CGAA IAGGUCUU	1701	AAGACCTC C ACATTAAG	2425
2776	ACUUAAUG CUGAUGAG X CGAA IGAGGUCU	1702	AGACCTCC A CATTAAGT	2426
2778	CCACUUAA CUGAUGAG X CGAA IUGGAGGU	1703	ACCTCCAC A TTAAGTGG	2427
2788	UGUUAAAA CUGAUGAG X CGAA ICCACUUA	1704	TAAGTGGC T TITTAACA	2428
2796	GUUUUUCA CUGAUGAG X CGAA IUUAAAAA	1705	TTTTTAAC A TGAAAAAC	2429
2805	AGCUGCCG CUGAUGAG X CGAA IUUUUUCA	1706	TGAAAAAC A CGGCAGCT	2430
2810	GCUACAGC CUGAUGAG X CGAA ICCGUGUU	1707	AACACGGC A GCTGTAGC	2431
2813	GGAGCUAC CUGAUGAG X CGAA ICUGCCGU	1708	ACGGCAGC T GTAGCTCC	2432
2819	AGCUCGGG CUGAUGAG X CGAA ICUACAGC	1709	GCTGTAGC T CCCGAGCT	2433
2821	GUAGCUCG CUGAUGAG X CGAA IAGCUACA	1710	TGTAGCTC C CGAGCTAC	2434

2822	AGUAGCUC CUGAUGAG X CGAA IGAGCUAC	1711	GTAGCTCC C GAGCTACT	2435
2827	AAGAGAGU CUGAUGAG X CGAA ICUCGGGA	1712	TCCCGAGC T ACTCTCTT	2436
2830	GGCAAGAG CUGAUGAG X CGAA IUAGCUCG	1713	CGAGCTAC T CTCTTGCC	2437
2832	CUGGCAAG CUGAUGAG X CGAA IAGUAGCU	1714	AGCTACTC T CTTGCCAG	2438
2834	UGCUGGCA CUGAUGAG X CGAA IAGAGUAG	1715	CTACTCTC T TGCCAGCA	2439
2838	AAAAUGCU CUGAUGAG X CGAA ICAAGAGA	1716	TCTCTTGC C AGCATTTT	2440
2839	GAAAAUGC CUGAUGAG X CGAA IGCAAGAG	1717	CTCTTGCC A GCATTTTC	2441
2842	UGUGAAAA CUGAUGAG X CGAA ICUGGCAA	1718	TTGCCAGC A TTTTCACA	2442
2848	GCAAAAUG CUGAUGAG X CGAA IAAAAUGC	1719	GCATTTTC A CATTTTGC	2443
2850	AGGCAAAA CUGAUGAG X CGAA IUGAAAAU	1720	ATTTTCAC A TTTTGCCT	2444
2857	ACGAGAAA CUGAUGAG X CGAA ICAAAAUG	1721	CATTTTGC C TTTCTCGT	2445
2858	CACGAGAA CUGAUGAG X CGAA IGCAAAAU	1722	ATTTTGCC T TTCTCGTG	2446
2862	CUACCACG CUGAUGAG X CGAA IAAAGGCA	1723	TGCCTTTC T CGTGGTAG	2447
2875	UCUGUACU CUGAUGAG X CGAA ICUUCUAC	1724	GTAGAAGC C AGTACAGA	2448
2876	CUCUGUAC CUGAUGAG X CGAA IGCUUCUA	1725	TAGAAGCC A GTACAGAG	2449
2881	AAUUUCUC CUGAUGAG X CGAA IUACUGGC	1726	GCCAGTAC A GAGAAATT	2450
2891	CCCACCAC CUGAUGAG X CGAA IAAHIIICU	1727	AGAAATTC T GTGGTGGG	2451
2903	ACCUCGAA CUGAUGAG X CGAA IUUCCCAC	1728	GTGGGAAC A TTCGAGGT	2452
2915	CUGCAGGG CUGAUGAG X CGAA IACACCUC	1729	GAGGTGTC A CCCTGCAG	2453
2917	CUCUGCAG CUGAUGAG X CGAA IUGACACC	1730	GGTGTCAC C CTGCAGAG	2454
2918	GCUCUGCA CUGAUGAG X CGAA IGUGACAC	1731	GTGTCACC C TGCAGAGC	2455
2919	AGCUCUGC CUGAUGAG X CGAA IGGUGACA	1732	TGTCACCC T GCAGAGCT	2456
2922	CAUAGCUC CUGAUGAG X CGAA ICAGGGUG	1733	CACCCTGC A GAGCTATG	2457
2927	CUCACCAU CUGAUGAG X CGAA ICUCUGCA	1734	TGCAGAGC T ATGGTGAG	2458
2949	GGCACCUA CUGAUGAG X CGAA ICCUUAUC	1735	GATAAGGC T TAGGTGCC	2459
2957	UACAGCCU CUGAUGAG X CGAA ICACCUAA	1736	TTAGGTGC C AGGCTGTA	2460
2958	UUACAGCC CUGAUGAG X CGAA IGCACCUA	1737	TAGGTGCC A GGCTGTAA	2461
2962	AUGCUUAC CUGAUGAG X CGAA ICCUGGCA	1738	TGCCAGGC T GTAAGCAT	2462
2969	GCUCAGAA CUGAUGAG X CGAA ICUUACAG	1739	CTGTAAGC A TTCTGAGC	2463
2973	GCCAGCUC CUGAUGAG X CGAA IAAUGCUU	1740	AAGCATTC T GAGCTGGC	2464
2978	AACAAGCC CUGAUGAG X CGAA ICUCAGAA	1741	TTCTGAGC T GGCTTGTT	2465
2982	AAACAACA CUGAUGAG X CGAA ICCAGCUC	1742	GAGCTGGC T TGTTGTTT	2466
2998	CAUAUACA CUGAUGAG X CGAA IACUUAAA	1743	TTTAAGTC C TGTATATG	2467
2999	ACAUAUAC CUGAUGAG X CGAA IGACUUAA	1744	TTAAGTCC T GTATATGT	2468
3040	UUUUGAAA CUGAUGAG X CGAA ICUACUAU	1745	ATAGTAGC A TTTCAAAA	2469
3045	GUCCAUUU CUGAUGAG X CGAA IAAAUGCU	1746	AGCATTTC A AAATGGAC	2470
3058	GUUAAACC CUGAUGAG X CGAA IUACGUCC	1747	GGACGTAC T GGTTTAAC	2471
3067	GGAUAGGA CUGAUGAG X CGAA IUUAAACC	1748	GGTTTAAC C TCCTATCC	2472
3068	AGGAUAGG CUGAUGAG X CGAA IGUUAAAC	1749	GTTTAACC T CCTATCCT .	2473
3070	CAAGGAUA CUGAUGAG X CGAA IAGGUUAA	1750	TTAACCTC C TATCCTTG	2474
3071	CCAAGGAU CUGAUGAG X CGAA IGAGGUUA	1751	TAACCTCC T ATCCTTGG	2475
3075	CUCUCCAA CUGAUGAG X CGAA IAUAGGAG	1752	CTCCTATC C TTGGAGAG	2476
3076	GCUCUCCA CUGAUGAG X CGAA IGAUAGGA	1753	TCCTATCC T TGGAGAGC	2477
3085	GAGCCAGC CUGAUGAG X CGAA ICUCUCCA	1754	TGGAGAGC A GCTGGCTC	2478
3088	GGAGAGCC CUGAUGAG X CGAA ICUGCUCU	1755	AGAGCAGC T GGCTCTCC	2479
3092	AGGUGGAG CUGAUGAG X CGAA ICCAGCUG	1756	CAGCTGGC T CTCCACCT	2480
3094	CAAGGUGG CUGAUGAG X CGAA IAGCCAGC	1757	GCTGGCTC T CCACCTTG	2481

Table 4

3096	AACAAGGU CUGAUGAG X CGAA IAGAGCCA	1758	TGGCTCTC C ACCTTGTT	2482
3097	UAACAAGG CUGAUGAG X CGAA IGAGAGCC	1759	GGCTCTCC A CCTTGTTA	2483
3099	UGUAACAA CUGAUGAG X CGAA IUGGAGAG	1760	CTCTCCAC C TTGTTACA	2484
3100	GUGUAACA CUGAUGAG X CGAA IGUGGAGA	1761	TCTCCACC T TGTTACAC	2485
3107	ACAUAAUG CUGAUGAG X CGAA IUAACAAG	1762	CTTGTTAC A CATTATGT	2486
3109	UAACAUAA CUGAUGAG X CGAA IUGUAACA	1763	TGTTACAC A TTATGTTA	2487
3132	AGCAGAGC CUGAUGAG X CGAA ICUCGCUA .	1764	TAGCGAGC T GCTCTGCT	2488
3135	CAUAGCAG CUGAUGAG X CGAA ICAGCUCG	1765	CGAGCTGC T CTGCTATG	2489
3137	GACAUAGC CUGAUGAG X CGAA IAGCAGCU	1766	AGCTGCTC T GCTATGTC	2490
3140	AAGGACAU CUGAUGAG X CGAA ICAGAGCA	1767	TGCTCTGC T ATGTCCTT	2491
3146	UGGCUUAA CUGAUGAG X CGAA IACAUAGC	1768	GCTATGTC C TTAAGCCA	2492
3147	UUGGCUUA CUGAUGAG X CGAA IGACAUAG	1769	CTATGTCC T TAAGCCAA	2493
3153	UAAAUAUU CUGAUGAG X CGAA ICUUAAGG	1770	CCTTAAGC C AATATTTA	2494
3154	GUAAAUAU CUGAUGAG X CGAA IGCUUAAG	1771	CTTAAGCC A ATATTTAC	2495
3163	ACCUGAUG CUGAUGAG X CGAA IUAAAUAU	1772	ATATTTAC T CATCAGGT	2496
3165	UGACCUGA CUGAUGAG X CGAA IAGUAAAU	1773	ATTTACTC A TCAGGTCA	2497
3168	UAAUGACC CUGAUGAG X CGAA IAUGAGUA	1774	TACTCATC A GGTCATTA	2498
3173	AAAAAUAA CUGAUGAG X CGAA IACCUGAU	1775	ATCAGGTC A TTATTTTT	2499
3185	AUGGCCAU CUGAUGAG X CGAA IUAAAAAA	1776	TTTTTAC A ATGGCCAT	2500
3191	UAUUCCAU CUGAUGAG X CGAA ICCAUUGU	1777	ACAATGGC C ATGGAATA	2501
3192	UUNUUCCA CUGAUGAG X CGAA IGCCAUUG	1778	CAATGGCC A TGGAATAA	2502
3203	GUAAAAAU CUGAUGAG X CGAA IUUUAUUC	1779	GAATAAAC C ATTTTTAC	2503
3204	UGUAAAAA CUGAUGAG X CGAA IGUUUAUU	1780	AATAAACC A TTTTTACA	2504

Table 5: Human PTP-1B G-Cleaver Ribozyme and Target Sequence

Nt. position	Ribozyme Sequence	Seq. ID Nos.	Substrate Sequence	Seq. ID Nos.
25	CACUG UGAUG GCAUGCACUAUGC GCG GCCGUCUGCC	2505	GGCAGACGGC G CAGTG	2670
35	CUUCU UGAUG GCAUGCACUAUGC GCG GGCCCACUGC	2506	GCAGTGGGCC G AGAAG	2671
46	UGCUG UGAUG GCAUGCACUAUGC GCG GCCUCCUUCU	2507	AGAAGGAGGC G CAGCA	2672
55	CAGGG UGAUG GCAUGCACUAUGC GCG GGCUGCUGCG	2508	CGCAGCAGCC G CCCTG	2673
68	CUGCU UGAUG GCAUGCACUAUGC GCG GAACUCCUUU	2509	AAAGGAGITC G AGCAG	2674
86	CUUGU UGAUG GCAUGCACUAUGC GCG GAUCUGCUCG	2510	CGAGCAGATC G ACAAG	2675
138	CAUGU UGAUG GCAUGCACUAUGC GCG GGAUAUCCUG	2511	CAGGATATCC G ACATG	2676
143	GGCUU UGAUG GCAUGCACUAUGC GCG AUGUCGGAUA	2512	TATCCGACAT G AAGCC	2677
152	GAAGU UGAUG GCAUGCACUAUGC GCG ACUGGCUUCA	2513	TGAAGCCAGT G ACTTC	2678
195	UAUTU UGAUG GCAUGCACUAUGC GCG GGUUUTUGUU	2514	AACAAAACC G AAATA	2679
224	AUGGU UGAUG GCAUGCACUAUGC GCG AAAGGGACUG	2515	CAGTCCCTTT G ACCAT	2680
260	AUAGU UGAUG GCAUGCACUAUGC GCG AUUAUCUUCU	2516	AGAAGATAAT G ACTAT	2681
272	ACUAG UGAUG GCAUGCACUAUGC GCG GUUGAUAUAG	2517	CTATATCAAC G CTAGI	2682
280	UDUAU UGAUG GCAUGCACUAUGC GCG AAACUAGCGU	2518	ACCCTACTTT G ATAAA	2683
331	UUAGG UGAUG GCAUGCACUAUGC GCG AAAGGGCCCU	2519	AGGGCCTTT G CCTAA	2684
342	GACCG UGAUG GCAUGCACUAUGC GCG AUGUGUUAGG	2520	CCIAACACAI G CGGIC	2685
394	UUGAG UGAUG GCAUGCACUAUGC GCG AUGACGACAC	2521	GIGICGICAI G CICAA	2686
406	UCCAU UGAUG GCAUGCACUAUGC GCG ACUCUGUUGA	2522	TCAACAGAGT G ATGGA	2687
429	GUGCG UGAUG GCAUGCACUAUGC GCG AUUUUAACGA	2523	TCGTTAAAAT G CGCAC	2688
431	UUGUG UGAUG GCAUGCACUAUGC GCG GCAUUUUAAC	2524	GTTAAAATGC G CACAA	2689
466	AAGAU UGAUG GCAUGCACUAUGC GCG AUCUCUUUUU	2525	AAAAAGAGAT G ATCTT	2690
473	GUCUU UGAUG GCAUGCACUAUGC GCG AAAGAUCAUC	2526	GATGATCTTT G AAGAC	2691
487	AAUUU UGAUG GCAUGCACUAUGC GCG AAAUUUGUGU	2527	ACACAAATIT G AAATI	2692
499	GAGAU UGAUG GCAUGCACUAUGC GCG AAUGUUAAUU	2528	AATTAACATT G ATCTC	2693
905	AUCUU UGAUG GCAUGCACUAUGC GCG AGAGAUCAAU	2529	ATTGATCTCT G AAGAT	2694
532	UGUCG UGAUG GCAUGCACUAUGC GCG ACUGUAUAAU	2530	ATTATACAGT G CGACA	2695
534	GCUGU UGAUG GCAUGCACUAUGC GCG GCACUGUAUA	2531	TATACAGTGC G ACAGC	2696
573	HOTIOTI HEALIG GCALIGCACTIATICS GOG GAGTHICHING	2532	CAAGAAACT G AGAGA	2007

809	AAAGU UGAUG	AAAGU UGAUG GCAUGCACUAUGC GCG AGGCCAUGUG	AGGCCAUGUG	2533	CACATGGCCT G ACTTT	2698
623	UGAUU UGAUG	UGAUU UGAUG GCAUGCACUAUGC GCG AGGGACUCCA	AGGGACUCCA	2534	TGGAGTCCCT G AATCA	2699
643	AAGUU UGAUG	AAGUU UGAUG GCAUGCACUAUGC GCG AAGAAUGAGG	AAGAAUGAGG	2535	CCTCATTCTT G AACTT	2700
663	ACUCU UGAUG	ACUCU UGAUG GCAUGCACUAUGC GCG GGACUUUGAA	GGACUUUGAA	2536	TTCAAAGTCC G AGAGT	2701
902	CAGUG UGAUG	CAGUG UGAUG GCAUGCACUAUGC GCG ACCACAACGG	ACCACAACGG	2537	CCGTTGTGGT G CACTG	2702
711	CACUG UGAUG	CACUG UGAUG GCAUGCACUAUGC GCG AGUGCACCAC	AGUGCACCAC	2538	GIGGIGCACT G CAGTG	2703
716	GCCUG UGAUG	SCCUG UGAUG GCAUGCACUAUGC GCG ACUGCAGUGC	ACUGCAGUGC	2539	GCACTGCAGT G CAGGC	2704
752	GGUAU UGAUG	SGUAU UGAUG GCAUGCACUAUGC GCG AGCCAGACAG	AGCCAGACAG	2540	CTGTCTGGCT G ATACC	2705
759	AGAGG UGAUG	AGAGG UGAUG GCAUGCACUAUGC GCG AGGUAUCAGC	AGGUAUCAGC	2541	GCTGATACCT G CCTCT	2706
992	AUCAG UGAUG	AUCAG UGAUG GCAUGCACUAUGC GCG AAGAGGCAGG	AAGAGGCAGG	2542	CCTGCCTCTT G CTGAT	2707
169	UCCAU UGAUG	UCCAU UGAUG GCAUGCACUAUGC GCG AGCAAGAGGC	AGCAAGAGGC	2543	GCCTCTTGCT G ATGGA	2708
800	GAUAU UGAUG	GAUAU UGAUG GCAUGCACUAUGC GCG AACGGAAGAA	AACGGAAGAA	2544	TTCTTCCGTT G ATATC	2709
814	AACAG UGAUG	AACAG UGAUG GCAUGCACUAUGC GCG ACUUUCUUGA	ACUUUCUUGA	2545	TCAAGAAGT G CTGTT	2710
826	UUCCU UGAUG	UUCCU UGAUG GCAUGCACUAUGC GCG AUUUCUAÄCA	AUUUCUAACA	2546	TGTTAGAAAT G AGGAA	2711
847	UGGAU UGAUG	UGGAU UGAUG GCAUGCACUAUGC GCG AGCCCCAUCC	AGCCCCAUCC	2547	GGATGGGGCT G ATCCA	2712
960	CUGGU UGAUG	cueeu ueaus ecauscacuausc ece secueucues	GGCUGUCUGG	2548	CCAGACAGCC G ACCAG	2713
898	AAGCG UGAUG	AAGCG UGAUG GCAUGCACUAUGC GCG AGCUGGUCGG	AGCUGGUCGG	2549	COGACCAGCT G CGCTT	2714
870	AGAAG UGAUG	AGAAG UGAUG GCAUGCACUAUGC GCG GCAGCUGGUC	GCAGCUGGUC	2550	GACCAGCTGC G CTTCT	2715
889	UCGAU UGAUG	UCGAU UGAUG GCAUGCACUAUGC GCG ACAGCCAGGU	ACAGCCAGGU	2551	ACCTGGCTGT G ATCGA	2716
893	ACCUU UGAUG	ACCUU UGAUG GCAUGCACUAUGC GCG GAUCACAGCC	GAUCACAGCC	2552	GGCTGTGATC G AAGGT	2717
899	UUUGG UGAUG	UUUGG UGAUG GCAUGCACUAUGC GCG ACCUUCGAUC	ACCUUCGAUC	2553	GATCGAAGGT G CCAAA	2718
928	UCCUG UGAUG	UCCUG UGAUG GCAUGCACUAUGC GCG ACGGAAGAGU	ACGGAAGAGU	2554	ACTUTCOGT G CAGGA	2719
926	GUCCU UGAUG	GUCCU UGAUG GCAUGCACUAUGC GCG GUGGGAAAGC	GUGGGAAAGC	2555	GCTTTCCCAC G AGGAC	2720
71.6	AUGCU UGAUG	AUGCU UGAUG GCAUGCACUAUGC GCG GGGUGGGGGC	GGGUGGGGGC	2556	GCCCCCACCC G AGCAT	2721
1011	GGAUU UGAUG	GGAUT UGAUG GCAUGCACUAUGC GCG GUTUGGGUGG	GUUUGGGUGG	2557	CCACCCAAAC G AATCC	2722
1038	CCCUG UGAUG	CCCUG UGAUG GCAUGCACUAUGC GCG AUUUCCCAUU	AUTUCCCAUT	2558	AATGGGAAAT G CAGGG	2723
1069	UCCUU UGAUG	UCCUU UGAUG GCAUGCACUAUGC GCG ACCCACUGGU	ACCCACUGGU	2559	ACCAGTGGGT G AAGGA	2724
1098	DGGGG DGAUG	UGGGG UGAUG GCAUGCACUAUGC GCG AGUCUUUAUC	AGUCUUUAUC	2560	GATAAAGACT G CCCCA	2725
1133	UGCGG UGAUG	DOCGG UGAUG GCAUGCACUAUGC GCG AUUUAAGGGG	AUUUAAGGGG	2561	CCCCTTAAAT G CCGCA	2726
1136	GGGUG UGAUG	GGGUG UGAUG GCAUGCACUAUGC GCG GGCAUUUAAG	GGCAUUUAAG	2562	CITABATGCC G CACCC	2727
1151	GCUUU UGAUG	GCUUU UGAUG GCAUGCACUAUGC GCG GAUGCCGUAG	GAUGCCGUAG	2563	CTACGGCATC G AAAGC	2728

UGACU UGAUG GCAUGCACUAUGC GCG AUGCUUUCGA
AACUU UGAUG GCAUGCACUAUGC GCG AGUGUCUUGA
CACCU UGAUG GCAUGCACUAUGC GCG GAAGACUUCC
cuada udana acaudeacanande dea aceucaaada
GGAGG UGAUG GCAUGCACUAUGC GCG AGCCUGGGCA
UCGGG UGAUG GCAUGCACUAUGC GCG AGUGACGGCU
CUUCU UGAUG GCAUGCACUAUGC GCG GGGCAGUGAC
GUCCU UGAUG GCAUGCACUAUGC GCG GUCCUUCUCG
CAGUG UGAUG GCAUGCACUAUGC GCG AUGGUCCUCG
UAACU UGAUG GCAUGCACUAUGC GCG AGUGCAUGGU
CCACG UGAUG GCAUGCACUAUGC GCG ACAUGUUGAC
GUAAG UGAUG GCAUGCACUAUGC GCG GCCGGCCGUG
UGUAG UGAUG GCAUGCACUAUGC GCG AGAGGUAAGC
AGGGU UGAUG GCAUGCACUAUGC GCG AGGCUAUGUG
AGAGG UGAUG GCAUGCACUAUGC GCG GGACAGUGGG
GCGGG UGAUG GCAUGCACUAUGC GCG AGAGGCGGAC
CUCUG UGAUG GCAUGCACUAUGC GCG GGGCAGAGGC
UCGGG UGAUG GCAUGCACUAUGC GCG GUGGGCUCUG
CUAGU UGAUG GCAUGCACUAUGC GCG GGGCGUGGGC
SECSE UGAUG GCAUGCACUAUGC GCS AUGCCUGCUA
UACCG UGAUG GCAUGCACUAUGC GCG GGCAUGCCUG
UCCGG UGAUG GCAUGCACUAUGC GCG GGCCCUUACC
CUACG UGAUG GCAUGCACUAUGC GCG GGUCCGGCGG
UAGUG UGAUG GCAUGCACUAUGC GCG AGAACCAACG
AGGGG UGAUG GCAUGCACUAUGC GCG AAAAAGUAAA
GUAÇU UGAUG GCAUGCACUAUGC GCG AAAGUGGAAG
CUCCU UGAUG GCAUGCACUAUGC GCG AAAAAAUGGC
UCUUU UGAUG GCAUGCACUAUGC GCG ACUCUCCUCA
GCCAG UGAUG GCAUGCACUAUGC GCG AUGGUACUCU
CUCUG UGAUG GCAUGCACUAUGC GCG GCCGCCAGCA
UGGGG UGAUG GCAUGCACUAUGC GCG GAGCCCCAAG

1723	UCUGG UGAUG GCAUGCACUAUGC GCG GUGCCGCCCG	2595	CGGGCGGCAC G CCAGA	2760
1742	AGAUU, UGAUG GCAUGCACUAUGC GCG AAGGGGGGGG	2596	CCCCCCCTT G AATCT	2761
1748	CCCUG UGAUG GCAUGCACUAUGC GCG AGAUUCAAGG	2597	CCTTGAATCT G CAGGG	2762
1811	UAGUG UGAUG GCAUGCACUAUGC GCG ACUAUGGAUG	2598	CATCCATAGT G CACTA	2763
1827	UGGUU UGAUG GCAUGCACUAUGC GCG AAGAAAUGC	2599	GCATTTTCTT G AACCA	2764
1853	GACAU UGAUG GCAUGCACUAUGC GCG AAAAAUUUU	2600	AAAATTTTT G ATGTC	2765
1865	UGAUG UGAUG GCAUGCACUAUGC GCG AAGGCUGACA	2601	TGTCAGCCTT G CATCA	2766
1931	CAUGG UGAUG GCAUGCACUAUGC GCG AAAGCCUUCC	2602	GGAAGCCITI G CCATG	2767
1942	CGCAG UGAUG GCAUGCACUAUGC GCG AGGCCCAUGG	2603	CCATGGGCCT G CTGCG	2768
1945	UGACG UGAUG GCAUGCACUAUGC GCG AGCAGGCCCA	2604	TGGGCCTGCT G CGTCA	2769
1997	AAUAU UGAUG GCAUGCACUAUGC GCG ACUAAAUAAC	2605	GTTATTAGT G ATATT	2770
2014	CUUCU UGAUG GCAUGCACUAUGC GCG ACGUUACCCA	5606	TGGGTAACGT G AGAG	2771
2030	UAUAG UGAUG GCAUGCACUAUGC GCG AUUGUUCUAU	2607	ATAGAACAAT G CTATA	2772
2045	GUGUU UGAUG GCAUGCACUAUGC GCG AUUAUAUAUU	2608	AATATATAT G AACAC	2773
2073	CACAU UGADG GCAUGCACUAUGC GCG AUGUIUCUUA	2609	TAAGAACAT G ATGTG	2774
2078	AAUCU UGAUG GCAUGCACUAUGC GCG ACAUCAUGUU	2610	AACATGATGT G AGATT	2775
2094	AUAAG UGAUG GCAUGCACUAUGC GCG GGGACAAAGU	2611	ACTITGICCC G CITAI	2776
2103	GGGAG UGAUG GCAUGCACUAUGC GCG AGAAUAAGCG	2612	CGCTTATTCT G CTCCC	2777
2117	UCUAG UGAUG GCAUGCACUAUGC GCG AGAUAACAGG	2613	CCTGTTATCT G CTAGA	2778
2140	GGGAG UGAUG GCAUGCACUAUGC GCG AGUGAUUGAG	2614	CTCAATCACT G CTCCC	2779
2162	ACAUG UGAUG GCAUGCACUAUGC GCG AUUCUAAUAC	2615	GTATTAGAAT G CATGT	2780
2186	UUCAU UGAUG GCAUGCACUAUGC GCG AGGACACAAG	2616	CTTGTGTCCT G ATGAA	2781
2189	UNDUU UGAUG GCAUGCACUAUGC GCG AUCAGGACAC	2617	GTGTCCTGAT G AAAA	2782
2200	UCAAG UGAUG GCAUGCACUAUGC GCG ACAUAUUUUU	2618	AAAAATATGT G CTTGA	2783
2204	CAUTU UGADG GCAUGCACUAUGC GCG AAGCACAUAU	2619	ATATGTGCTT G AAATG	2784
5209	UUUCU UGAUG GCAUGCACUAUGC GCG AUUUCAAGCA	2620	TGCTTGAAAT G AGAAA	2785
2219	GAGAU UGAUG GCAUGCACUAUGC GCG AAAGUUUCUC	2621	GAGAACTTT G ATCTC	2786
2226	GUAAG UGAUG GCAUGCACUAUGC GCG AGAGAUCAAA	2622	TTTGATCTCT G CTTAC	2787
2238	UGGGG UGAUG GCAUGCACUAUGC GCG ACAUUAGUAA	2623	TTACTAATGT G CCCCA	2788
2260	ACAGG UGAUG GCAUGCACUAUGC GCG AGGUUGGACU	2624	AGTCCAACCT G CCTGT	2789
2266	UCAUG UGAUG GCAUGCACUAUGC GCG ACAGGCAGGU	2625	ACCIGCTGI G CAIGA	2790

2791	2792	2793	2794	2795	2796	2797	2798	2799	2800	2801	2802	2803	2804	2805	2806	2807	2808	2809	2810	2811	2812	2813	2814	2815	2816	2817	2818	2819	2820	
GCCTGTGCAT G ACCTG	TGCATGACCT G ATCAT	TAAGCCIGIT G CIGAA	GCCTGTTGCT G AAGTC	AGTCATTGTC G CTCAG	GCAATAGGGT G CAGIT	ATAGGCATTT G CCTAA	TICCIGGCAT G ACACT	ACACTCTAGT G ACTTC	ACTICCIGGI G AGGCC	GCAGGGTCTT G CTGTA	CACACCTCAC G CTCTG	CTCTGGACAT G ATTTA	GACACCCCC G CCCCC	ATCAGCCTCC G CCATT	ATTCCAAGIC G ACACT	CACTCTTCTT G AGCAG	AGCAGACCGT G ATTTG	AGAGGCACCT G CTGGA	CACACTTCTT G AAACA	CAGCCTGGGT G ACGGT	TAGGCAGCCT G CCGCC	GCAGCCTGCC G CCGTC	GGTTCACCTT G CCGAG	TCACCTTGCC G AGAGA	CGAGAGAGC G CGTCT	AGGCGCGTCT G CCCCA	TGTGGGCCT G ATGGT	GCCTGATGGT G CTCAC	TGGTGCTCAC G ACTCT	
2626	2627	2628	2629	2630	2631	2632	2633	2634	2635	2636	2637	2638	2639	2640	2641	2642	2643	2644	2645	2646	2647	2648	2649	2650	2651	2652	2653	2654	2655	
CAGGU UGAUG GCAUGCACUAUGC GCG AUGCACAGGC	AUGAU UGAUG GCAUGCACUAUGC GCG AGGUCAUGCA	UUCAG UGAUG GCAUGCACUAUGC GCG AACAGGCUUA	GACUU UGAUG GCAUGCACUAUGC GCG AGCAACAGGC	CUGAG UGAUG GCAUGCACUAUGC GCG GACAAUGACU	AACUG UGAUG GCAUGCACUAUGC GCG ACCCUAUUGC	UUAGG UGAUG GCAUGCACUAUGC GCG AAAUGCCUAU	AGUGU UGAUG GCAUGCACUAUGC GCG AUGCCAGGAA	GAAGU UGAUG GCAUGCACUAUGC GCG ACUAGAGUGU	GGCCU UGAUG GCAUGCACUAUGC GCG ACCAGGAAGU	UACAG UGAUG GCAUGCACUAUGC GCG AAGACCCUGC	CAGAG UGAUG GCAUGCACUAUGC GCG GUGAGGUGUG	UNANU UGAUG GCAUGCACUAUGC GCG AUGUCCAGAG	GGGGG UGAUG GCAUGCACUAUGC GCG GGGGGUGUC	AAUGG UGAUG GCAUGCACUAUGC GCG GGAGGCUGAU	AGUGU UGAUG GCAUGCACUAUGC GCG GACUUGGAAU	CUGCU UGAUG GCAUGCACUAUGC GCG AAGAAGAGUG	CAAAU UGAUG GCAUGCACUAUGC GCG ACGGUCUGCU	UCCAG UGAUG GCAUGCACUAUGC GCG AGGUGCCUCU	UGUUU UGAUG GCAUGCACUAUGC GCG AAGAAGUGUG	ACCGU UGAUG GCAUGCACUAUGC GCG ACCCAGGCUG	GGCGG UGAUG GCAUGCACUAUGC GCG AGGCUGCCUA	GACGG UGAUG GCAUGCACUAUGC GCG GGCAGGCUGC	CUCGG UGAUG GCAUGCACUAUGC GCG AAGGUGAACC	UCUCU UGAUG GCAUGCACUAUGC GCG GGCAAGGUGA	AGACG UGAUG GCAUGCACUAUGC GCG GCCUCUCUCG	UGGGG UGAUG GCAUGCACUAUGC GCG AGACGCGCCU	ACCAU UGAUG GCAUGCACUAUGC GCG AGGCCCCACA	GUGAG UGAUG GCAUGCACUAUGC GCG ACCAUCAGGC	AGAGU UGAUG GCAUGCACUAUGC GCG GUGAGCACCA	- Compression of the Compression
2270	2275	2308	2311	2323	2338	2362	2378	2389	2400	2433	2483	2494	2520	2546	2559	2571	2582	2602	2621	2635	2655	2658	2682	2685	2694	2700	2727	2733	2739	

2761	GUCUU UGAUG GCAUGCACUAUGC GCG AGUUCCCUUU	2657	AAAGGGAACT G AAGAC	2822
2793	UUUUU UGAUG GCAUGCACUAUGC GCG AUGUUAAAAA	2658	TITITAACAT G AAAAA	2823
2818	UAGCU UGAUG GCAUGCACUAUGC GCG GGGAGCUACA	2659	TGTAGCTCCC G AGCTA	2824
2831	GCUGG UGAUG GCAUGCACUAUGC GCG AAGAGAGUAG	2660	CTACTCTCTT G CCAGC	2825
2850	AAAGG UGAUG GCAUGCACUAUGC GCG AAAAUGUGAA	2661	TTCACATTTT G CCTTT	2826
2902	CACCU UGAUG GCAUGCACUAUGC GCG GAAUGUUCCC	2662	GGGAACATTC G AGGTG	2827
2915	CUCUG UGAUG GCAUGCACUAUGC GCG AGGGUGACAC	2663	GIGICACCCI G CAGAG	2828
2928	CACCU UGAUG GCAUGCACUAUGC GCG ACCAUAGCUC	2664	GAGCTATGGT G AGGTG	2829
2950	CCUGG UGAUG GCAUGCACUAUGC GCG ACCUAAGCCU	2665	AGGCTTAGGT G CCAGG	2830
2969	CAGCU UGAUG GCAUGCACUAUGC GCG AGAAUGCUUA	2666	TAAGCATTCT G AGCTG	2831
3123	CAGCU UGAUG GCAUGCACUAUGC GCG GCUACCUCUC	2667	GAGAGGTAGC G AGCTG	2832
3128	CAGAG UGAUG GCAUGCACUAUGC GCG AGCUCGCUAC	2668	GTAGCGAGCT G CTCTG	2833
3133	CAUAG UGAUG GCAUGCACUAUGC GCG AGAGCAGCUC	2669	GAGCTGCTCT G CTATG	2834

Table 6: Human PTP-1B DNAzyme and Target Sequence

Nt. Position	DNAzyme Sequence	Seq. ID Nos.	Substrate Sequence	Nos.
11	GCTCTAGG GGCTAGCTACAACGA CGCGTCGC	2835	GCGACGCG G CCUAGAGC	3545
18	GTCTGCCG GGCTAGCTACAACGA TCTAGGCC	2836	GGCCUAGA G CGGCAGAC	3546
21	GCCGTCTG GGCTAGCTACAACGA CGCTCTAG	2837	CUAGAGCG G CAGACGGC	3547
25	CTGCGCCG GGCTAGCTACAACGA CTGCCGCT	2838	AGCGGCAG A CGGCGCAG	3548
28	CCACTGCG GGCTAGCTACAACGA CGTCTGCC	2839	GGCAGACG G CGCAGUGG	3549
30	GCCCACTG GGCTAGCTACAACGA GCCGTCTG	2840	CAGACGGC G CAGUGGGC	3550
33	TCGGCCCA GGCTAGCTACAACGA TGCGCCGT	2841	ACGGCGCA G UGGGCCGA	3551
37	CTICICGG GGCTAGCTACAACGA CCACTGCG	2842	CGCAGUGG G CCGAGAAG	3552
4.9	CTGCTGCG GGCTAGCTACAACGA CTCCTTCT	2843	AGAAGGAG G CGCAGCAG	3553
51	GGCTGCTG GGCTAGCTACAACGA GCCTCCTT	2844	AAGGAGGC G CAGCAGCC	3554
54	GGCGCCTG GGCTAGCTACAACGA TGCGCCTC	2845	GAGGCGCA G CAGCCGCC	3555
57	CAGGGCGG GGCTAGCTACAACGA TGCTGCGC	2846	GOGCAGCA G COGCCCUG	3556
0.9	GGCCAGGG GCCTACCTACGA GGCTGCTG	2847	CAGCAGCC G CCCUGGCC	3557
99	ATGACGGG GGCTAGCTACAACGA CAGGGCGG	2848	ccgcccug g cccgucau	3558
70	CICCATGA GGCTAGCTACAACGA GGGCCAGG	2849	CCUGGCCC G UCAUGGAG	3559
73	CATCTCCA GGCTAGCTACAACGA GACGGGCC	2850	GGCCCGUC A UGGAGAUG	3560
79	CITITICCA GGCTAGCTACAACGA CICCAIGA	2851	UCAUGGAG A UGGAAAAG	3561
90	TGCTCGAA GGCTAGCTACAACGA TCCTTTTC	2852	GAAAAGGA G UUCGAGCA	3562
96	TCGATCTG GGCTAGCTACAACGA TCGAACTC	2853	GAGUICGA G CAGAUCGA	3563
100	CTIGICGA GGCTAGCTACAACGA CTGCTCGA	2854	UCGAGCAG A UCGACAAG	3564
104	CGGACTIG GGCTAGCTACAACGA CGATCTGC	2855	GCAGAUCG A CAAGUCCG	3565
108	CICCCGGA GGCTAGCTACAACGA TIGICGAI	2856	AUCGACAA G UCCGGGAG	3566
116	CCGCCCAG GGCTAGCTACAACGA TCCCGGAC	2857	GUCCGGGA G CUGGGCGG	3567
121	AATGGCCG GGCTAGCTACAACGA CCAGCTCC	2858	GGAGCUGG G CGGCCAUU	3568
124	GTAAATGG GGCTAGCTACAACGA CGCCCAGC	2859	GCUGGGCG G CCAUUNAC	3569
127	CTGGTAAA GGCTAGCTACAACGA GGCCGCCC	2860	GGGCGGCC A UUUACCAG	3570
131	TATCCTGG GGCTAGCTACAACGA AAATGGCC	2861	GGCCAUUU A CCAGGAUA	3571
137	GTCGGATA GGCTAGCTACAACGA CCTGGTAA	2862	UDACCAGG A UNUCCGAC	3572

200	CATABLE AND ASSESSMENT OF THE PARTY OF THE P	2004	CHAITAINS & OCCURGIN	3604
272	AACIAGCG GGCIAGCIACAACGA IGAIAIAG	2034	CONTROL A CONTROL	
277	CAAACTAG GGCTAGCTACAACGA GTTGATAT	2895	AUAUCAAC G CUAGUUUG	3605
281	TIATCAAA GGCTAGCTACAACGA TAGCGTTG	2896	CAACGCUA G UJUGAUAA	3606
286	CATITITA GGCTAGCTACAACGA CAAACTAG	2897	CUAGUUUG A UAAAAUG	3607
292	TICITICA GCTAGCTACAACGA TITIATCA	2898	UGAUAAAA A UGGAAGAA	3608
301	CCTTTGGG GGCTAGCTACAACGA TTCTTCCA	2899	UGGAAGAA G CCCAAAGG	3609
311	GAATGTAA GGCTAGCTACAACGA TCCTTTGG	2900	CCAAAGGA G UUACAUUC	3610
314	TAAGAATG GGCTAGCTACAACGA AACTCCTT	2901	AAGGAGUU A CAUUCUUA	3611
316	GGTAAGAA GGCTAGCTACAACGA GTAACTCC	2902	GGAGUUAC A UUCUUACC	3612
322	GCCCTGGG GGCTAGCTACAACGA AAGAATGT	2903	ACAUUCUU A CCCAGGGC	3613
329	GCAAAGGG GGCTAGCTACAACGA CCTGGGTA	2904	UACCCAGG G CCCUTUGC	3614
336	GIGITAGG GGCTAGCTACAACGA AAAGGGCC	2905	GGCCCUUU G CCURACAC	3615
341	CGCATGTG GGCTAGCTACAACGA TAGGCAAA	2906	UUUGCCUA A CACAUGCG	3616
343	ACCCCATG GGCTAGCTACAACGA GTTAGGCA	2907	UGCCUAAC A CAUGCGGU	3617
345	TGACCGCA GGCTAGCTACAACGA GTGTTAGG	2908	CCUAACAC A UGCGGUCA	3618
347	AGTGACCG GGCTAGCTACAACGA ATGTGTTA	5062	UNACACAU G CGGUCACU	3619
350	AAAAGTGA GGCTAGCTACAACGA CGCATGTG	2910	CACAUGCG G UCACUUUU	3620
353	CCCAAAAG GGCTAGCTACAACGA GACCGCAT	2911	AUGCGGUC A CUUTUGGG	3621
364	CCACACCA GGCTAGCTACAACGA CTCCCAAA	2912	UUUGGGAG A UGGUGUGG	3622
367	CTCCCACA GGCTAGCTACAACGA CATCTCCC	2913	GGGAGAUG G UGUGGGAG	3623
369	TGCTCCCA GGCTAGCTACAACGA ACCATCTC	2914	GAGAUGGU G UGGGAGCA	3624
375	CITITICIG GGCIAGCIACAAGGA TCCCACAC	2915	GUGUGGGA G CAGAAAAG	3625
383	CACCCCTG GGCTAGCTACAACGA TTTTCTGC	2916	GCAGAAAA G CAGGGGUG	3626
389	TGACGACA GGCTAGCTACAACGA CCCTGCTT	2917	AAGCAGGG G UGUCGUCA	3627
391	CATGACGA GGCTAGCTACAACGA ACCCCTGC	2918	GCAGGGGU G UCGUCAUG	3628
394	GAGCATGA GGCTACCAACGA GACACCCC	2919	GGGGUGUC G UCAUGCUC	3629
397	GITGAGCA GGCTAGCTACAACGA GACGACAC	2920	GUGUCGUC A UGCUCAAC	3630
399	CIGITIGAG GGCTAGCTACGA AIGACGAC	2921	GUCGUCAU G CUCAACAG	3631
404	TCACTCTG GGCTAGCTACAACGA TGAGCATG	2922	CAUGCUCA A CAGAGUGA	3632
409	CTCCATCA GGCTAGCTACAACGA TCTGTTGA	2923	UCAACAGA G UGAUGGAG	3633
412	TITITICE GGCTAGCTACAACGA CACTCTGT	2924	ACAGAGUG A UGGAGAAA	3634

422	TTAACGAA GGCTAGCTACAACGA CTTTCTCC	2925	GGAGAAAG G UUCGUUAA	3635
426	CATTTTAA GGCTAGCTACAACGA GAACCTTT	2926	AAAGGUUC G UUAAAAUG	3636
432	TGTGCGCA GGCTAGCTACAACGA TTTAACGA	2927	UCGUDAAA A UGCGCACA	3637
434	ATTGTGCG GGCTAGCTACGA ATTTTAAC	2928	GUUAAAAU G CGCACAAU	3638
436	GTATTGTG GGCTAGCTACAACGA GCATTTTA	2929	UNANAUGC G CACAAUAC	3639
438	CAGTATTG GGCTAGCTACAACGA GCGCATTT	2930	AAAUGCGC A CAAUACUG	3640
441	GCCCAGTA GCCTACCAACGA TGTGCGCA	2931	UGCGCACA A UACUGGCC	3641
443	GTGGCCAG GGCTAGCTACAACGA ATTGTGCG	2932	CGCACAAU A CUGGCCAC	3642
447	TTTTGTGG GGCTAGCTACAACGA CAGTATTG	2933	CAAUACUG G CCACAAAA	3643
450	TCTTTTTG GGCTAGCTACAACGA GGCCAGTA	2934	UACUGGCC A CAAAAGA	3644
469	AAAGATCA GGCTAGCTACAACGA CTCTTTTT	2935	AAAAAGAG A UGAUCUUU	3645
472	TTCAAAGA GGCTAGCTACAACGA CATCTCTT	2936	AAGAGAUG A UCUUUGAA	3646
482	AATTTGTG GGCTAGCTACAACGA CTTCAAAG	2937	CUUUGAAG A CACAAAUU	3647
484	CAAATTIG GGCTAGCTACAACGA GTCTTCAA	2938	UUGAAGAC A CAAAUUUG	3648
488	ATTICAAA GGCTAGCTACAACGA TIGIGICI	2939	AGACACAA A UUUGAAAU	3649
495	AATGTTAA GGCTAGCTACAACGA TTCAAATT	2940	AAUUUGAA A UUAACAUU	3650
499	GATCAATG GGCTAGCTACAACGA TAATTTCA	2941	UGRANUNA A CAUUSAUC	3651
501	GAGATCAA GGCTAGCTACAACGA GTTAATTT	2942	AAAUUAAC A UUGAUCUC	3652
505	TTCAGAGA GGCTAGCTACAACGA CAATGTTA	2943	UAACAUUG A UCUCUGAA	3653
515	ACTIGATA GGCTAGCTACAACGA CTICAGAG	2944	CUCUGAAG A UAUCAAGU	3654
517	TGACTTGA GGCTAGCTACAACGA ATCTTCAG	2945	CUGAAGAU A UCAAGUCA	3655
522	TAATATGA GGCTAGCTACAACGA TTGATATC	2946	GAUAUCAA G UCAUAUUA	3656
525	GTATAATA GGCTAGCTACAACGA GACTTGAT	2947	AUCAAGUC A UAUUAUAC	3657
527	CTGTATAA GGCTAGCTACAACGA ATGACTTG	2948	CAAGUCAU A UUAUACAG	3658
530	GCACTGTA GGCTAGCTACAACGA AATATGAC	2949	GUCAUAUU A UACAGUGC	3659
532	TCGCACTG GGCTAGCTACAACGA ATAATATG	2950	CAUAUUAU A CAGUGGA	3660
535	CTGTCGCA GGCTAGCTACAACGA TGTATAAT	2951	AUUAUACA G UGCGACAG	3661
537	AGCTGTCG GGCTAGCTACAACGA ACTGTATA	2952	UAUACAGU G CGACAGCU	3662
540	TCTAGCTG GGCTAGCTACAACGA CGCACTGT	2953	ACAGUGCG A CAGCUAGA	3663
543	AATTCTAG GGCTAGCTACAACGA TGTCGCAC	2954	GUGCGACA G CUAGAAUU	3664
549	TTTTCCAA GGCTAGCTACAACGA TCTAGCTG	2955	CAGCUAGA A UUGGAAAA	3665

562	THEGGTING GGCTAGCTACAACGA AAGGITTT		AAAACCUU A CAACCCAA	7667
		7327		
565	TICTIGGG GGCTAGCTACAACGA IGTAAGGT	2958	ACCUUACA A CCCAAGAA	3668
574	CTCTCGAG GGCTAGCTACAACGA TTCTTGGG	2959	CCCAAGAA A CUCGAGAG	3669
583	ATGTAAGA GGCTAGCTACAACGA CTCTCGAG	2960	CUCGAGAG A UCUUACAU	3670
588	TGGAAATG GGCTAGCTACAACGA AAGATCTC	2961	GAGAUCUU A CAUUUCCA	3671
290	AGTGGAAA GGCTAGCTACAACGA GTAAGATC	2962	GAUCUUAC A UUUCCACU	3672
596	TGGTATAG GGCTAGCTACAACGA GGAAATGT	2963	ACAUUUCC A CUAUACCA	3673
599	ATGTGGTA GGCTAGCTACAACGA AGTGGAAA	2964	UUUCCACU A UACCACAU	3674
601	CCATGTGG GGCTAGCTACAACGA ATAGTGGA	2965	UCCACUAU A CCACAUGG	3675
604	AGGCCATG GGCTAGCTACAACGA GGTATAGT	2966	ACUAUACC A CAUGGCCU	3676
909	TCAGGCCA GGCTAGCTACAACGA GTGGTATA	2967	UNUACCAC A UGGCCUGA	3677
609	AAGTCAGG GGCTAGCTACAACGA CATGTGGT	2968	ACCACAUG G CCUGACUU	3678
614	CTCCAAAG GGCTAGCTACAACGA CAGGCCAT	2969	AUGGCCUG A CUUUGGAG	3679
622	TTCAGGGA GGCTAGCTACAACGA TCCAAAGT	2970	ACUUJGGA G UCCCUGAA	3680
630	GCTGGTGA GGCTAGCTACAACGA TCAGGGAC	2971	GUCCCUGA A UCACCAGC	3681
633	GAGGCTGG GGCTAGCTACAACGA GATTCAGG	2972	CCUGAAUC A CCAGCCUC	3682
637	GAATGAGG GGCTAGCTACAACGA TGGTGATT	2973	AAUCACCA G CCUCAUUC	3683
642	TTCAAGAA GGCTAGCTACAACGA GAGGCTGG	2974	CCAGCCUC A UNCUUGAA	3684
650	AAAGAAAG GGCTAGCTACAACGA TCAAGAAT	2975	AUUCUUGA A CUUUCUUU	3685
664	CICTCGGA GGCTAGCTACAACGA TITGAAAA	2976	UUUUCAAA G UCCGAGAG	3686
672	GACCCIGA GGCTACTACAACGA TCTCGGAC	2977	GUCCGAGA G UCAGGGUC	3687
678	CTGAGTGA GGCTAGCTACAACGA CCTGACTC	2978	GAGUCAGG G UCACUCAG	3688
681	GGGCTGAG GGCTAGCTACAACGA GACCCTGA	2979	UCAGGGUC A CUCAGCCC	3689
989	GCTCCGGG GGCTAGCTACAACGA TGAGTGAC	2980	GUCACUCA G CCCGGAGC	3690
693	GGCCCGTG GGCTAGCTACAACGA TCCGGGCT	2981	AGCCCGGA G CACGGGCC	3691
695	CGGGCCCG GGCTAGCTACAACGA GCTCCGGG	2982	CCCGGAGC A CGGGCCCG	3692
669	ACAACGGG GGCTAGCTACAACGA CCGTGCTC	2983	GAGCACGG G CCCGUUGU	3693
703	CACCACAA GGCTAGCTACAACGA GGGCCCGT	2984	ACGGGCC G UNGUGGUG	3694
206	GIGCACCA GGCTAGCTACAACGA AACGGGCC	2985	GGCCCGUU G UGGUGCAC	3695
709	GCAGTGCA GGCTAGCTACAACGA CACAACGG	2986	CCGUUGUG G UGCACUGC	3696

	CACTGCAG GGCTAGCTACAACGA GCACCACA	2988	UGUGGUGC A CUGCAGUG	3698
	CTGCACTG GGCTAGCTACAACGA AGTGCACC	2989	GGUGCACU G CAGUGCAG	3699
	TGCCTGCA GGCTAGCTACAACGA TGCAGTGC	2990	GCACUGCA G UGCAGGCA	3700
	GATGCCTG GGCTAGCTACAACGA ACTGCAGT	2991	ACUGCAGU G CAGGCAUC	3701
	IGCCGATG GGCTAGCTACAACGA CTGCACTG	2992	CAGUGCAG G CAUCGGCA	3702
	CCTGCCGA GGCTAGCTACAACGA GCCTGCAC	2993	GUGCAGGC A UCGGCAGG	3703
	CAGACCTG GGCTAGCTACAACGA CGATGCCT	2994	AGGCAUCG G CAGGUCUG	3704
	GTTCCAGA GGCTAGCTACAACGA CTGCCGAT	2995	AUCGGCAG G UCUGGAAC	3705
	ACAGAAGG GGCTAGCTACAACGA TCCAGACC	2996	gencussa a councusu	3706
	CAGCCAGA GGCTAGCTACAACGA AGAAGGTT	2997	AACCUNCU G UCUGGCUG	3707
	GGTATCAG GGCTAGCTACAACGA CAGACAGA	2998	UCUGUCUG G CUGAUACC	3708
	GGCAGGTA GGCTAGCTACAACGA CAGCCAGA	2999	ucuggcug a vaccugcc	3709
	GAGGCAGG GGCTAGCTACAACGA ATCAGCCA	3000	UGGCUGAU A CCUGCCUC	3710
	GCAAGAGG GGCTAGCTACAACGA AGGTATCA	3001	UGAUACCU G CCUCUUGC	3711
	TCCATCAG GGCTAGCTACAACGA AAGAGGCA	3002	ueccucun e cuenuesa	3712
	CTTGTCCA GGCTAGCTACAACGA CAGCAAGA	3003	UCUUGCUG A UGGACAAG	3713
	TCCTCTIG GGCTAGCTACAACGA CCATCAGC	3004	GCUGAUGG A CAAGAGGA	3714
	AAGAAGGG GGCTAGCTACAACGA CTTTCCTC	3008	GAGGAAAG A CCCUUCUU	3715
	SATATCAA GGCTAGCTACAACGA GGAAGAAG	3006	CUICUICC G UUGAUAUC	3716
	TCTTGATA GGCTAGCTACAACGA CAACGGAA	3007	UUCCGUUG A UAUCAAGA	3717
	TTTCTTGA GGCTAGCTACAACGA ATCAACGG	3008	CCGUUGAU A UCAAGAAA	3718
	TAACAGCA GGCTAGCTACAACGA TTTCTTGA	3009	UCAAGAAA G UGCUGUUA	3719
819 TCTAACAG G	TCTAACAG GGCTAGCTACAACGA ACTTTCTT	3010	AAGAAAGU G CUGUUAGA	3720
822 ATTICIAN G	ATTICIAA GGCIAGCIACAACGA AGCACITI	3011	AAAGUGCU G UUAGAAAU	3721
829 CTTCCTCA G	CTICCICA GGCTAGCTACAACGA TICTAACA	3012	UGUUAGAA A UGAGGAAG	3722
837 ATCCGAAA G	ATCCGAAA GGCTAGCTACAAGGA TTCCTCAT	3013	AUGAGGAA G UUUCGGAU	3723
844 CAGCCCCA G	CAGCCCCA GGCTAGCTACAACGA CCGAAACT	3014	AGUUUCGG A UGGGGCUG	3724
849 TGGATCAG C	TGGATCAG GGCTAGCTACAACGA CCCATCCG	3015	CGGAUGGG G CUGAUCCA	3725
853 TGTCTGGA G	TOTCTGGA GGCTAGCTACAACGA CAGCCCCA	3016	UGGGGCUG A UCCAGACA	3726
859 GTCGGCTG G	GTCGGCTG GGCTAGCTACAACGA CTGGATCA	3017	UGAUCCAG A CAGCCGAC	3727

862	CTOGICGG GGCTAGCTACAACGA TGTCTGGA	3018	UCCAGACA G CCGACCAG	3728
998	GCAGCTGG GGCTAGCTACAACGA CGGCTGTC	3019	GACAGCCG A CCAGCUGC	3729
870	AAGCGCAG GGCTAGCTACAACGA TGGTCGGC	3020	GCCGACCA G CUGCGCUU	3730
873	GAGAAGCG GGCTAGCTACAACGA AGCTGGTC	3021	GACCAGCU G CGCUUCUC	3731
875	AGGAGAAG GGCTAGCTACAACGA GCAGCTGG	3022	CCAGCUGC G CUUCUCCU	3732
884	CAGCCAGG GGCTAGCTACAACGA AGGAGAAG	3023	CUICUCCU A CCUGGCUG	3733
688	GATCACAG GGCTAGCTACAACGA CAGGTAGG	3024	CCUACCUG G CUGUGAUC	3734
892	TTCGATCA GGCTAGCTACAACGA AGCCAGGT	3025	ACCUBBEU B UGAUCBAA	3735
895	ACCTTCGA GGCTAGCTACAACGA CACAGCCA	3026	UGGCUGUG A UCGAAGGU	3736
902	ATTIGGCA GGCTAGCTACAACGA CTTCGATC	3027	GAUCGAAG G UGCCAAAU	3737
904	GAATTIGG GGCTAGCTACAACGA ACCTICGA	3028	UCGAAGGU G CCAAAUUC	3738
606	ATGATGAA GGCTAGCTACAACGA TTGGCACC	3029	GGUGCCAA A UUCAUCAU	3739
913	CCCCATGA GGCTAGCTACAACGA GAATTTGG	3030	CCAAAUUC A UCAUGGGG	3740
916	GTCCCCCA GGCTAGCTACAACGA GATGAATT	3031	AAUUCAUC A UGGGGGAC	3741
923	CGGAAGAG GGCTAGCTACAACGA CCCCCATG	3032	CAUGGGG A CUCUUCCG	3742
931	ATCCTGCA GGCTAGCTACAACGA GGAAGAGT	3033	ACUCUUCC G UGCAGGAU	3743
933	TGATCCTG GGCTAGCTACAACGA ACGGAAGA	3034	UCUUCCGU G CAGGAUCA	3744
938	TCCACTGA GGCTAGCTACGACGA CCTGCACG	3035	CGUGCAGG A UCAGUGGA	3745
942	TCCTTCCA GGCTAGCTACAACGA TGATCCTG	3036	CAGGAUCA G UGGAAGGA	3746
951	TGGGAAAG GGCTAGCTACAACGA TCCTTCCA	3037	UGGAAGGA G CUUUCCCA	3747
959	GGTCCTCG GGCTAGCTACAACGA GGGAAAGC	3038	GCUUUCCC A CGAGGACC	3748
965	GCTCCAGG GGCTAGCTACAACGA CCTCGTGG	3039	CCACGAGG A CCUGGAGC	3749
972	GGTGGGGG GGCTAGCTACAACGA TCCAGGTC	3040	GACCUGGA G CCCCCACC	3750
978	TGCTCGGG GGCTAGCTACAACGA GGGGGCTC	3041	GAGCCCC A CCCGAGCA	3751
984	GGGATATG GGCTAGCTACAACGA TCGGGTGG	3042	CCACCCGA G CAUAUCCC	3752
986	GGGGGATA GGCTAGCTACAACGA GCTCGGGT	3043	ACCCGAGC A UAUCCCCC	3753
988	TGGGGGGA GGCTAGCTACAACGA ATGCTCGG	3044	CCGAGCAU A UCCCCCCA	3754
966	CGGGGAGG GGCTAGCTACAACGA GGGGGGAT	3045	AUCCOCCC A CCUCCCCG	3755
1005	TTGGGTGG GGCTAGCTACAACGA CGGGGAGG	3046	ccucces s ccaccean	3756
1008	CGTTTGGG GGCTAGCTACAACGA GGCCGGGG	3047	CCCGGCC A CCCAAACG	3757
1014	AGGATTCG GGCTAGCTACAACGA TTGGGTGG	3048	CCACCCAA A CGAAUCCU	3758

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1018	201100100000000000000000000000000000000			
1026	TIGIGIGG GGCIAGCIACAACGA TCCAGGAI	3050	AUCCUGGA G CCACACAA	3760
1029	CCATTGTG GGCTAGCTACAACGA GGCTCCAG	3051	CUGGAGCC A CACAAUGG	3761
1031	TCCCATTG GGCTAGCTACAACGA GTGGCTCC	3052	GGAGCCAC A CAAUGGGA	3762
1034	ATTICCCA GGCTAGCTACAACGA TGTGTGGC	3053	GCCACACA A UGGGAAAU	3763
1041	TCCCTGCA GGCTAGCTACAACGA TTCCCATT	3054	AAUGGGAA A UGCAGGGA	3764
1043	ACTCCCTG GGCTAGCTACAACGA ATTTCCCA	3055	UGGGAAAU G CAGGGAGU	3765
1050	GGGAAGAA GGCTAGCTACAACGA TCCCTGCA	3056	UGCAGGGA G UUCUUCCC	3766
1901	ACTGGTGA GGCTAGCTACAACGA TTGGGBAG	3057	CUUCCCAA A UCACCAGU	3767
1064	CCCACTGG GGCTACCAACGA GATTTGGG	3058	CCCAAAUC A CCAGUGGG	3768
1068	TTCACCCA GGCTAGCTACAACGA TGGTGATT	3059	AAUCACCA G UGGGUGAA	3769
1072	TICCITCA GGCIAGCIACAACGA CCACIGGI	3060	ACCAGUGG G UGAAGGAA	3770
1084	CICCIGGG GGCTAGCTACGA CICTICCI	3061	AGGAAGAG A CCCAGGAG	3771
1094	AGTCTTTA GGCTAGCTACAACGA CCTCCTGG	3062	CCAGGAGG A UAAAGACU	3772
1100	TGGGGCAG GGCTAGCTACAACGA CTTTATCC	3063	GGAUAAAG A CUGCCCCA	3773
1103	TGATGGGG GGCTAGCTACAACGA AGTCTTTA	3064	UAAAGACU G CCCCAUCA	3774
1108	TTCCTTGA GGCTAGCTACAACGA GGGGCAGT	3065	ACUGCCCC A UCAAGGAA	3775
1127	TTAAGGGG GGCTAGCTACAACGA TTCCTTTT	3066	AAAAGGAA G CCCCUUAA	3776
1136	GTGCGGCA GGCTAGCTACAACGA TTAAGGGG	3067	CCCCUUAA A UGCCGCAC	3777
1138	GGGTGCGG GGCTAGCTACGA ATTTAAGG	3068	CCUUAAAU G CCGCACCC	3778
1141	GIAGGGIG GCCTAGCIACAACGA GGCATITA	3069	UNANUGCC G CACCCUAC	3779
1143	CCGTAGGG GGCTAGCTACAACGA GCGGCATT	30.70	AAUGCOGC A CCCUACGG	3780
1148	CGATGCCG GGCTAGCTACAACGA AGGGTGCG	3071	CGCACCCU A CGGCAUCG	3781
1151	TITICGAIG GGCTAGCTACGACGA CGTAGGGT	3072	ACCCUACG G CAUCGNAA	3782
1153	GCTTTCGA GGCTAGCTACAACGA GCCGTAGG	3073	CCUACGGC A UCGARAGC	3783
1160	GACTCATG GGCTAGCTACAACGA TITCGATG	3074	CAUCGAAA G CAUGAGUC	3784
1162	TTGACTCA GGCTAGCTACAACGA GCTTTCGA	3075	UCGAAAGC A UGAGUCAA	3785
1166	TGTCTTGA GGCTAGCTACAAGGA TCATGCTT	3076	AAGCAUGA G UCAAGACA	3786
1172	CITCAGIG GGCIAGCIACAACGA CITGACIC	3077	GAGUCAAG A CACUGAAG	3787
1174	AACTICAG GGCIAGCIACAACGA GICTIGAC	3078	GUCAAGAC A CUGAAGUU	3788
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1205	TCCCCCCA GGCIAGCIACAACGA GACCCGAC	3082	ducadon a coccosio	3792
1214	CTCSAAGA GGCTAGCTACAACGA TTCCCCCC	3083	GGGGGGAA G UCUUCGAG	3793
	CCTGGGCA GGCTAGCTACAACGA CTCGAAGA	3084	UCUUCGAG G UGCCCAGG	3794
1216	AGCCTGGG GGCTAGCTACAACGA ACCTCGAA	3085	UNCGAGGU G CCCAGGCU	3795
1222	GGAGGCAG GGCTAGCTACAACGA CTGGGCAC	3086	GUGCCCAG G CUGCCUCC	3796
1225	TGGGGAGG GGCTAGCTACAACGA AGCCTGGG	3087	CCCAGGCU G CCUCCCCA	3797
1234	CCCTTTGG GGCTAGCTACAACGA TGGGGAGG	3088	CCUCCCCA G CCAAAGGG	3798
1245	AGTISACGG GGCTAGCTACAACGA TCCCCTTT	3089	AAAGGGA G CCGUCACU	3799
1248	GGCAGTGA GGCTAGCTACAACGA GGCTCCCC	3090	GGGGAGCC G UCACUSCC	3800
1251	TCGGGCAG GGCTAGCTACAACGA GACGGCTC	3091	GAGCOGUC A CUGCCCGA	3801
1254	TTCTCGGG GGCTAGATACAACGA AGTGACGG	3092	CCGUCACU G CCCGAGAA	3802
1265	GGTCCTCG GGCTAGCTACAACGA CCTTCTCG	3093	CGAGAAGG A CGAGGACC	3803
1271	GTGCATGG GGCTAGCTACAACGA CCTCGTCC	3094	GGACGAGG A CCAUGCAC	3804
1274	TCAGTGCA GGCTAGCTACAACGA GGTCCTCG	3095	CGAGGACC A UGCACUGA	3805
1276	ACTCAGTG GGCTAGCTACAACGA ATGGTCCT	3096	AGGACCAU G CACUGAGU	3806
1278	TAACTCAG GGCTAGCTACAACGA GCATGGTC	3097	GACCAUGC A CUGAGUUA	3807
1283	TCCAGTAA GGCTAGCTACAACGA TCAGTGCA	3098	UGCACUGA G UUACUGGA	3808
1286	GCTTCCAG GGCTAGCTACAACGA AACTCAGT	3099	ACUGAGUU A CUGGAAGC	3809
1293	AGGAAGG GGCTAGCTACAACGA TICCAGTA	3100	UACUGGAA G CCCUUCCU	3810
1303	CATGITGA GGCTACTACAACGA CAGGAAGG	3101	CCUUCCUG G UCAACAUG	3811
1307	CGCACATG GGCTAGCTACAACGA TGACCAGG	3102	CCUGGUCA A CAUGUGCG	3812
1309	CACGCACA GGCTAGCTACAACGA GTTGACCA	3103	UGGUCAAC A UGUGCGUG	3813
1311	GCCACGCA GGCTAGCTACAACGA ATGTTGAC	3104	GUCAACAU G UGCGUGGC	3814
1313	TAGCCACG GGCTAGCTACAACGA ACATGTTG	3105	CAACAUGU G CGUGGCUA	3815
1315	CGINGCCA GGCIAGCIACAACGA GCACAIGI	3106	ACAUGUGC G UGGCUACG	3816
1318	GACCGTAG GGCTACTACAACGA CACGCACA	3107	UGUGCGUG G CUACGGUC	3817
1321	GAGGACCG GGCTAGCTACAACGA AGCCACGC	3108	GCGUGGCU A CGGUCCUC	3818
1324	CGTGAGGA GGCTAGCTACAACGA CGTAGCCA	3109	UBGCUACG G UCCUCACG	3819
1330	GCCGGCCG GGCTAGCTACAACGA GAGGACCG	3110	COGUCCUC A COOCCOOC	3820

CT	CTTACCTA GGCTAGCTACAACGA CGCGGCAT	3143	AUGCCGCG G UAGGUAAG	3853
GG	GGCCCTTA GGCTAGCTACAACGA CTACCGCG	3144	CGCGGUAG G UAAGGGCC	3854
TC	TCCGGCGG GGCTAGCTACAACGA CCTTACCT	3145	AGGUAAGG G CCGCCGGA	3855
Ő	CGGTCCGG GGCTAGCTACAACGA GGCCCTTA	3146	UAAGGGCC G CCGGACCG	3856
E.	CTACGCGG GGCTAGCTACAACGA CCGGCGGC	3147	GCCGCCGG A CCGCGUAG	3857
TC	TCTCTACG GGCTAGCTACAACGA GGTCCGGC	3148	GCCGGACC G CGUAGAGA	3858
ပ္ပ	GCTCTCTA GGCTAGCTACAACGA GCGGTCCG	3149	CGGACCGC G UAGAGAGC	3859
Ś	GGGCCCGG GGCTAGCTACAACGA TCTCTACG	3150	CGUAGAGA G CCGGGCCC	3860
Œ	GTCCGGGG GGCTAGCTACAACGA CCGGCTCT	3151	AGAGCCGG G CCCCGGAC	3861
AA	AACGTCCG GGCTAGCTACAACGA CCGGGGCC	3152	GGCCCCGG A CGGACGUU	3862
AA	AACCAACG GGCTAGCTACAACGA CCGTCCGG	3153	CCGGACGG A CGUUGGUU	3863
AG	AGAACCAA GGCTAGCTACAACGA GTCCGTCC	3154	GGACGGAC G UNGGUUCU	3864
GD	GTGCAGAA GGCTAGCTACAACGA CAACGTCC	3155	GGACGUUG G UUCUGCAC	3865
TL	TTTTAGTG GGCTAGCTACAACGA AGAACCAA	3156	UUGGUUCU G CACUAAAA	3866
98	SGTTTTAG GGCTAGCTACAACGA GCAGAACC	3157	GGUUCUGC A CUAAAACC	3867
AA	AAGATGGG GGCTAGCTACAACGA TTTAGTGC	3158	GCACUAAA A CCCAUCUU	3868
1530 - GG	GGGGAAGA GGCTACTACAACGA GGGTTTTA	3159	UNANACCC A UCUUCCCC	3869
GA	GACACACA GGCTAGCTACAACGA CCGGGGAA	3160	UUCCCCGG A UGUGUGUC	3870
ď.	GAGACACA GGCTAGCTACAACGA ATCCGGGG	3161	CCCCGGAU G UGUGUCUC	3871
£	GTGAGACA GGCTAGCTACAACGA ACATCCGG	3162	CCGGAUGU G UGUCUCAC	3872
9	GGGTGAGA GGCTACTACAACGA ACACATCC	3163	GGAUGUGU G UCUCACCC	3873
AŢ	ATGAGGG GGCTACTACAACGA GAGACACA	3164	UGUGUCUC A CCCCUCAU	3874
TA	TAAAAGGA GGCTAGCTACAACGA GAGGGGTG	3165	CACCCCUC A UCCUNUA	3875
8	GCAAAAAG GGCTAGCTACAACGA AAAAGGAT	3166	AUCCUUUU A CUUUUUGC	3876
98	GGAAGGGG GGCTAGCTACAACGA AAAAAGTA	3167	UACUUUUU G CCCCUUCC	3877
AC	ACTCAAAG GGCTAGCTACAACGA GGAAGGGG	3168	CCCCUUCC A CUUUGAGU	3878
AT	ATTTGGTA GGCTAGCTACAACGA TCAAAGTG	3169	CACUUUGA G UACCAAAU	3879
99	GGATTIGG GGCTAGCTACAACGA ACTCAAAG	3170	CUUUGAGU A CCAAAUCC	3880
ម	CTTGTGGA GGCTAGCTACAACGA TTGGTACT	3171	AGUACCAA A UCCACAAG	3881
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1770	ATATGGAG GGCTAGCTACAACGA GGAGAGIT	3204	AACOCOCC A COCCAOAO	2374
1775	AATAAATA GGCTAGCTACAACGA GGAGTGGA	3205	UCCACUCC A UAUTUAUU	3915
1777	TAAATAAA GGCTAGCTACAACGA ATGGAGTG	3206	CACUCCAU A UUUAUUUA	3916
1781	TGTTTAAA GGCTAGCTACAACGA AAATATGG	3207	CCAUAUUU A UUUAAACA	3917
1787	AAAAATTG GGCTAGCTACAACGA TTAAATAA	3208	UNAUTURA A CARITUTU	3918
1790	GGAAAAAA GGCTAGCTACAACGA TGTTTAAA	3209	UUUAAACA A UUUUUUCC	3919
1805	TAIGGAIG GGCTAGCTACAACGA CTTIGGGG	3210	CCCCAAAG G CAUCCAUA	3920
1807	ACTATGGA GGCTAGCTACAACGA GCCTTTGG	3211	CCAAAGGC A UCCAUAGU	3921
1811	GTGCACTA GGCTAGCTACAACGA GGATGCCT	3212	AGGCAUCC A UAGUGCAC	3922
1814	CTAGTGCA GGCTAGCTACAACGA TATGGATG	3213	CAUCCAUA G UGCACUAG	3923
1816	TGCTAGTG GGCTAGCTACAACGA ACTATGGA	3214	UCCAUAGU G CACUAGCA	3924
1818	AATGCTAG GGCTAGCTACAACGA GCACTATG	3215	CAUAGUGC A CUAGCAUU	3925
1822	AGAAAATG GGCTAGCTACAACGA TAGTGCAC	3216	GUGCACUA G CAUUUCU	3926
1824	CAAGAAAA GGCTAGCTACAACGA GCTAGTGC	3217	GCACUAGC A UNUUCUUG	3927
1834	ATTATIGG GGCTAGCTACAACGA TCAAGAAA	3218	UUUCUUGA A CCAAUAAU	3928
1838	ATACATTA GGCTAGCTACAACGA TGGTTCAA	3219	UUGAACCA A UAAUGUAU	3929
1841	TIAATACA GGCTAGCTACAACGA TATIGGIT	3220	AACCAAUA A UGUAUUAA	3930
1843	TITIAATA GGCTAGCTACAACGA ATTATTGG	3221	CCAAUAAU G UAUUAAAA	3931
1845	AATTTTAA GGCTAGCTACAACGA ACATTATT	3222	AAUAAUGU A UUAAAAUU	3932
1821	TCAAAAAA GGCTAGCTACAACGA TTTAATAC	3223	GUAUUAAA A UUUUUUGA	3933
1859	GGCTGACA GGCTAGCTACAACGA CAAAAAAT	3224	AUTUUTUG A UGUCAGCC	3934
1861	AAGGCTGA GGCTAGCTACAACGA ATCAAAAA	3225	UUUUUGAU G UCAGCCUU	3935
1865	ATGCAAGG GGCTAGCTACAACGA TGACATCA	3226	UGAUGUCA G CCUUGCAU	3936
1870	CCTTGATG GGCTAGCTACAACGA AAGGCTGA	3227	UCAGCCUU G CAUCAAGG	3937
1872	GCCCTTGA GGCTAGCTACAACGA GCAAGGCT	3228	AGCCUUGC A UCAAGGGC	3938
1879	TGATAAAG GGCTAGCTACAACGA CCTTGATG	3229	CAUCAAGG G CUUUAUCA	3939
1884	CTTTTTGA GGCTAGCTACAACGA AAAGCCCT	3230	AGGCUUU A UCAAAAG	3940
1892	TTATTGTA GGCTAGCTACAACGA TTTTTGAT	3231	AUCAAAAA G UACAAUAA	3941
1894	TATTATTG GGCTAGCTACAACGA ACTITITG	3232	CAAAAAGU A CAAUAAUA	3942
1897	ATTTATTA GGCTAGCTACAACGA TGTACTTT	3233	AAAGUACA A UAAUAAAU	3943
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Trecchin described-backs Nationals 3337	1912	CAGTACTA GGCTAGCTACAACGA CTGAGGAT	3236	AUCCUCAG G DAGDACUG	3946
ATTICCHE GESTINGTHORANCE NUTWORTER 3139	1915	TCCCAGTA GGCTAGCTACAACGA TACCTGAG	3237	CUCAGGUA G UACUGGGA	3947
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GCCCATOG GGCTHOCTICANCIA MAGCUTT 3341	1931	TGGCAAAG GGCTAGCTACAACGA CTTCCATT	3240	AAUGGAAG G CUUUGCCA	3950
COMBACTION GETTHACTHORNERS REGNAMED	1936	GCCCATGG GGCTACTACTACGA AAAGCCTT	3241	AAGGCUUU G CCAUGGGC	3951
GOOGGOAG GETCHOORDOR AGENCEAT 3343 1 1 1 1 1 1 1 1 1	1939	CAGGCCCA GGCTAGCTACAACGA GGCAAAGC	3242	GCUUUGCC A UGGGCCUG	3952
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GCTTICADA GGCTAGCTACAACCA CETUCICCC 3351	1976	TACAACCG GGCTAGCTACAACGA CCTCCTTC	3250	GAAGGAGG A CGGUUGUA	3960
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CONTRACTOR CONTRACTOR CONTRACTOR	2000	CAATATCA GGCTAGCTACAACGA TAAATAAC	3257	GUUAUUN G UGAUAUUG	3967
ACCRADA GGTINGTICANGUS ATTOCTICAS GTINGCES GGTINGTICANGUS ANTINCIC TCAGGTIN GGTINGTICANGUS CONCART TTCTCICG GGCTINGTICANGUS TROCCAS TTCTTCICA GGTINGTICANGUS TROCCAS TTCTTCICA GGTINGTICANGUS TRUCCAS TTGTTCICA GGTINGTICANGUS TRUCCAS TTGTTCICANGUS TRU	2003	CCACAATA GGCTAGCTACAACGA CACTAAAT	3258	AUTUAGUG A UAUTGUGG	3968
TETLACCOA GESTRACTIVO-DACIOA MATATCAC 3260 TECLACITIA GESTRACTIVO-DACIOA MATATCACA 3261 TECTLACICA GESTRACTIVO-DACIOA TITACCOACA 3363 TECTLACICA GESTRACTIVO-DACIOA STITACCOA 3363 TEGTLACITICA GESTRACTIVO-DACIOA CITTACIOC	2002	ACCCACAA GGCTAGCTACAACGA ATCACTAA	3259	UNAGUGAU A UNGUGGGU	3969
TCAGGTIA GGCTAGCTACAACGA CCACAGTA 3261 TTCTCAG GGCTAGCTACAACGA TACCCACA 3362 TTGTTCTCA GGCTAGCTACAACGA GTTACCACA 3263 TTGTTCTA GGCTAGCTACAACGA GTTACCAC 3364 TAGCATTG GGCTAGCTACAACGA TCTATCTAC 3265	2008	GTTACCCA GGCTAGCTACAACGA AATATCAC	3260	GUGAUAUU G UGGGUAAC	3970
TICTORIO GGICIACTINOANCIA TIACCONOA 3363 TICTORIO GGICIACATONIOANOA GITACOCA 3363 TICTORIA GGICIACATONIOANOA CITATORIO 3364 PAGNITICI GGICIACATONIOANO ILCUNICTIC 3265	2012	TCACGITA GGCTAGCTACAACGA CCACAATA	3261	UAUUGUGG G UAACGUGA	3971
TCTTCTCA GGCTAGCTACAACAA GTTACCCA 3263 TTGTTCTA GGCTAGCTACAACAA CTTCTCAC 3264 TAGCATTG GGCTAGCTACAACAA TCTATCTT 3265	2015	TTCTCACG GGCTAGCTACAACGA TACCCACA	3262	UGUGGGUA A CGUGAGAA	3972
TIGITCIA GGCIAGCIACAACAA CITCICAC 3264 TAGCAITG GGCIAGCIACAACAA TCIAICTI 3265	2017	TCTTCTCA GGCTAGCTACAACGA GTTACCCA	3263	UGGGUNAC G UGAGAAGA	3973
TAGCATTG GGCTAGCTACACGA TCTATCTT 3265	2025	TIGITCIA GGCTAGCTACAACGA CITCTCAC	3264	GUGAGAAG A UAGAACAA	3974
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TOCKTIVE GETRACTIA-ACCEA MITTATION	2041	ATTATATA GGCTAGCTACAACGA TATAGCAT	3269	AUGCUAUA A UAUAUAAU	3979
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CCCCCCTG GENERACTO-ACCES TO-ATTIVOTOR 1273 UNIVERSA N. COCCUBBOR	2048	CGTGTTCA GGCTAGCTACAACGA TATATAT	3272	AAUAUAUA A UGAACACG	3982
PACCOCC GEOTIGETICALAND GITTOTT 2274 Unividan's A GUIDSUIA	2052	CCCACGTG GGCTAGCTACAACGA TCATTATA	3273	UAUAAUGA A CACGUGGG	3983
ANTACCA GGTNGCTACAACA GTGTTCOM	2054	TACCCACG GGCTAGCTACAACGA GTTCATTA	3274	UNAUGANC A CGUGGGUA	3984
APTITANA GEORGETICALAGIA COLOGIST 1276 ACCUEDED AUGUSTA	2056	AATACCCA GGCTAGCTACAACGA GTGTTCAT	3275	AUGAACAC G UGGGUAUU	3985
TRATTAMA GOCTHOCTHOLANGEN ACCOLOGY 2277 ANGEROBUR N. UNUMAUMA	2060	ATTANATA GGCTAGCTACAACGA CCACGTGT	3276	ACACGUGG G UAUTURAU	3986
	2062	TTAITAAA GGCTAGCTACAACGA ACCCACGT	3277	ACGUGGGU A UUUAAUAA	3987
ACAPUENTE GEOTRACTICALACIA TECTYTYTY	2067	GITICITA GGCIAGCIACAACGA TAAATACC	3278	GGUAUTUA A UAAGAAAC	3988
TORONTO, GETRACTIONAGIA OTTICTTA 1280	2074	ACATCATG GGCTAGCTACAACGA TTCTTATT	3279	AAUAAGAA A CAUGAUGU	3989
APCTO-CO. GESTIGATICADARGA CATTITE 2281 GAMACURA O HOUSEAU	2076	TCACATCA GGCTAGCTACAACGA GTTTCTTA	3280	UNAGNANC A UGAUGUGA	3990
TAATCTC GETAGCTACAAGA AFOOTOT	2079	ATCTCACA GGCTAGCTACAACGA CATGTTTC	3281	GAAACAUG A UGUGAGAU	3991
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ADDROCKA GOTHOCTOLANCIA MAGGOOM 2226 UUUUUUU CUCODUUL UUUUUUU UUGUAN GOTHOCTICAACIA AAGGOOM 2225 UUCOCODUU A UUUUUUU UUGUAN GOTHOCTICAACIA AAGANANA 2389 UUCOCODUU A UUUUUU UUGUAN GOTHOCTICAACIA AAGANANA 2389 UUCOCODUU A UUUUUUU UUGUANA COOLOGOOM UUCOCODUU AAGANANA GOTHOCTICAACIA AAGANANA 2390 UUCOCUUU A UUUUUUU UUGUANA GOTHOCTICAACIA AAGANAA 2390 UUCOCUUU A UUUUUUU AAGANAA GOTHOCTICAACIA AAGANAA 2391 UUUUUU AAGANAA AAGANAA 2391 UUUUUU AAGANAA AAGANAA 2391 UUUUU AAGANAA AAGANAAA AAGANAAAA AAGANAAAAA AAGANAAAAAA AAGANAAAAA AAGANAAAAAA AAGANAAAAAAA AAGANAAAAAAAA	2094	AAGCGGGA GGCTAGCTACAACGA AAAGTAAT	3285	AUJACUUU G UCCCGCUU	3995
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GHACTMGN GECTROCTARCHAGGA CTAGGAGA 1392 UCUVCUDA A UCUMBUUC ATTGAGAA GECTROCTARCHAGGA TAGANCTA 2293 UGBAUCHAG UGUCANU AGGAGAGA GETRAGAGAA TSAGAATTAGAA 13294 AGAUCHAGA CGGAGGAG GETRAGARCHAGAAGAA ASTTRAGA 13295 UCUCAAUC CGGAGGAGAGAACAAAAAAAAAAAAAAAAAAAAAAAAA	2122	AGATCTAG GGCTAGCTACAACGA AGATAACA	3291	UGUNAUCU G CUAGAUCU	4001
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	2145	CGGGGGAG GGCTAGCTACAACGA AGTGATTG	3296	CAAUCACU G CUCCCCCG	4006

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2153	AATACACA GGCTAGCTACAACGA GGGGGAGC	3537	TOCOCCELL C HENALITAG	4008
2155	CTANTACA GGCTAGCTACAACGA ACGGGGGA	3298	OCCUCAGO & OCCUCAGO	4009
2157	TTCTAATA GGCTAGCTACAACGA ACACGGGG	3299	CCCCGUGO G DADOASAA	0104
2159	CATTCTAA GGCTAGCTACAACGA ACACACGG	3300.	CCGUGUGU A UUAGAAUG	4010
27.65	TACATGCA GGCTAGCTACAACGA TCTAATAC	3301	GUAUUAGA A UGCAUGUA	101
23757	CTTACATE GGCTAGCTACACGA ATTCTAAT	3302	AUUAGAAU G CAUGUAAG	4012
7160	ACCUTAGE GGCTAGCTACAACGA GCATTCTA	3303	UAGAAUGC A UGUAAGGU	4013
2123	ACACCITIA GGCTAGCTACAACGA ATGCATTC	3304	GAAUGCAU G UAAGGUCU	4014
21.12	CRAGAGG GGCTAGCTACAAGGA CTTACATG	3305	CAUGUAAG G UCUUCUUG	4015
2184	TCAGGACA GGCTAGCTACAACGA AAGAAGAC	3306	GUCUNCUU G UGUCCUGA	4016
2186	CATCAGGA GGCTAGCTACAACGA ACAAGAAG	3307	CUUCUUGU G UCCUGAUG	401/
2192	ATTITICA GCCTACCTACGA CAGGACAC	3308	GUGUCCUG A UGAAAAAU	4018
2199	AGCACATA GGCTAGCTACAACGA TITTCATC	3309	GAUGNAAA A UAUGUGCU	400V
2201	CAAGCACA GGCTAGCTACAACGA ATTITICA	3310	UGARAGAU A UGUGCUUG	200
2203	TICAAGCA GGCIAGCIACAACGA ATATITII	3311	AAAAUAU G UGCUUGAA	1204
2205	ATTICAAG GGCTAGCTACAACGA ACATATIT	3312	AAAUAUGU G CUUGAAAU	4022
2212	GITICICA GGCTAGCTACAACGA TICAAGCA	3313	UGCUUGAA A UGAGAAAC	4004
2219	GATCAAAG GGCTAGCTACAACGA TTCTCATT	3314	AAUGAGAA A CUUUGAUC	2001
2225	AGCAGAGA GGCTAGCTACAACGA CAAAGTTT	3315	AAACUUUG A UCUCUGCU	4025
2231	TTAGTAAG GGCTAGCTACAACGA AGAGATCA	3316	UGAUCUCU G CUUACUAA	4026
2000	CACATTAG GGCTAGCTACAACGA AAGCAGAG	3317	CUCUGCUU A CUAAUGUG	405/
6622	COCCORD GOTTACTACTACTA TAGTAAGC	3318	GCUUACUA A UGUGCCCC	4028
2223	ATTGGGGA GGCTAGCTACAACGA ATTAGTAA	3319	UNACUAAU G UGCCCAU	4029
2243	ACATGGGG GGCTACCTACAACGA ACATTAGT	3320	ACUAAUGU G CCCCAUGU	4030
0,00	CTTCCACA GGCTACTACTACGA GGGGCACA	3321	UGUGCCCC A UGUCCAAG	4031
8577	CITICACA COCTAGCTACAACGA ATGGGGCA	3322	UGCCCCAU G UCCAAGUC	4032
7520	THEORY OF THE CANADA CANADA THEORY	3323	AUGUCCAA G UCCAACCU	4033
2256	AGGI IGGA GGCIMOCIACABOGA TGGACITIG	3324	CAAGUCCA A CCUGCCUG	4034
2261	CAGGCAGG GOCTAGGTACAACGA AGGTTGGA	3325	UCCAACCU G CCUGUGCA	4035
2265	TGCACAGG GGCIAGCIACAGCGA AGGCAGGI	3326	ACCUGCCU G UGCAUGAC	4036
2269	GICATOCA GOLDOCANOSISCOS		TOURDILL O CHICAGOTTO	4037

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-		3358	GCCUGUGC A DGACCUGA	4038
TGATCAGG GGCTAC	TGATCAGG GGCTAGCTACAACGA CATGCACA	3329	UGUSCAUG A CCUGANCA	0000
TGTAATGA GGCTAG	TGTAATGA GGCTAGCTACAACGA CAGGTCAT	3330	AUGACCUG A UCAMMACA	4040
CCATGTAA GGCTAC	CCATGTAA GGCTAGCTACAACGA GATCAGGT	3331	ACCUGAUC A UNACAUGG	4041
CAGCCATG GGCTAG	CAGCCATG GGCTAGCTACAACGA AATGATCA	3332	UGAUCAUU A CAUGGCIIG	4042
CACAGCCA GGCTAC	CACAGCCA GGCTAGCTACAACGA GTAATGAT	3333	AUCAUUAC A UGGCUGUG	4043
AACCACAG GGCTAC	AACCACAG GGCTAGCTACAACGA CATGTAAT	3334	AUUACAUG G CUGUGGUU	4044
AGGAACCA GGCTAC	AGGAACCA GGCTAGCTACAACGA AGCCATGT	3335	ACAUGGCU G UGGUUCCU	4045
CTTAGGAA GGCTAG	CTTAGGAA GGCTAGCTACAACGA CACAGCCA	3336	UGGCUGUG G UUCCUAAG	4046
GCAACAGG GGCTAG	GCAACAGG GGCTAGCTACAACGA TTAGGAAC	3337	GUUCCUAA G CCUGUUGC	4047
TTCAGCAA GGCTAG	TTCAGCAA GGCTAGCTACAACGA AGGCTTAG	3338	CUAAGCCU G UUGCUGAA	4048
GACTICAG GOCTAG	GACTICAG GGCIAGCIACAACGA AACAGGCI	3339	AGCCUGUU G CUGAAGUC	4049
GACAATGA GGCTAG	GACAATGA GGCTAGCTACAACGA TTCAGCAA	3340	UUGCUGAA G UCAUUGUC	4050
AGCGACAA GGCTAG	AGCGACAA GGCTAGCTACAACGA GACTTCAG	3341	CUGAAGUC A UNGUCACU	4051
CTGAGCGA GGCTAG	CTGAGCGA GGCTAGCTACAACGA AATGACTT	3342	AAGUCAUU G UCGCUCAG	4052
TIGCIGAG GGCTAG	TIGCIGAG GGCTAGCTACAACGA GACAATGA	3343	UCAUUGUC G CUCAGCAA	4053
CCCTATTG GGCTAG	CCCTAITG GGCIAGCTACAACGA TGAGCGAC	3344	GUCGCUCA G CAAUAGGG	4054
GCACCCTA GGCTAG	GCACCCTA GGCTAGCTACAACGA TGCTGAGC	3345	GCUCAGCA A UAGGGUGC	4055
AAACTGCA GGCTAG	AAACTGCA GGCTAGCTACAACGA CCTATTGC	3346	GCAAUAGG G UGCAGUUU	4056
GAAAACTG GGCTAG	GAAAACTG GGCTAGCTACAACGA ACCCTATT	3347	AAUAGGGU G CAGUUUC	4057
CTGGARAA GGCTAG	CTGGAAAA GGCTAGCTACAACGA TGCACCCT	3348	AGGGUGCA G UUUUCCAG	4058
AATGCCTA GGCTAG	AATGCCTA GGCTAGCTACAACGA TCCTGGAA	3349	UUCCAGGA A UAGGCAUU	4059
GGCAAATG GGCTAG	GGCAAATG GGCTAGCTACAACGA CTATTCCT	3350	AGGAAUAG G CAIRIIGCC	4060
TAGGCAAA GGCTAG	TAGGCAAA GGCTAGCTACAACGA GCCTATTC	3351	GAAUAGGC A UUUGCCUA	4061
GAATTAGG GGCTAG	GAATTAGG GGCTAGCTACAACGA AAATGCCT	3352	AGGCAUTU G CCUAAUUC	4062
GCCAGGAA GGCTAG	GCCAGGAA GGCTAGCTACAACGA TAGGCAAA	3353	UNUGCCUA A UNCCUGGC	4063
GTGTCATG GGCTAG	GTGTCATG GGCTAGCTACAACGA CAGGAATT	3354	AAUUCCUG G CAUGACAC	4004
GAGTGTCA GGCTAGG	GAGTGTCA GGCTAGCTACAACGA GCCAGGAA	3355	UUCCUGGC A UGACACTIC	4065
CTAGAGTG GGCTAGG	CTAGAGIG GGCTAGCTACAACGA CATGCCAG	3356	CUGGCAUG A CACUCUAG	4066
CACTAGAG GGCTAGG	CACTAGAG GGCTAGCTACAACGA GTCATGCC	3357	GGCAUGAC A CUCUAGUG	4067
SGAAGTCA GGCTAGG	SGAAGTCA GGCTAGCTACAACGA TAGAGTGT	3358	ACACUCUA G DGACTITIC	4060

2333	CCAGGAAG GGCIAGCIACAACGA CACINGAG	2000	coconoca w coorcoca	1
2403	GGGCCTCA GGCTAGCTACAACGA CAGGAAGT	T 3360	ACTUCCUG G UGAGGCCC	4070
2408	AGGCTGGG GGCTAGCTACAACGA CTCACCAG	3361	CUGGUGAG G CCCAGCCU	4071
2413	AGGACAGG GGCTAGCTACAACGA TGGGCCTC	C 3362	GAGGCCCA G CCUGUCCU	4072
2417	TACCAGGA GGCTAGCTACAACGA AGGCTGGG	3363	CCCAGCCU G UCCUGGUA	4073
2423	CTGCTGTA GGCTAGCTACAACGA CAGGACAG	3364	CUGUCCUG G DACAGCAG	4074
2425	CCCTGCTG GGCTAGCTACAACGA ACCAGGAC	3365	GUCCUGGU A CAGCAGGG	4075
2428	AGACCCTG GGCTAGCTACAACGA TGTACCAG	3366	CUGGUACA G CAGGGUCU	4076
2433	CAGCAAGA GGCTAGCTACAACGA CCTGCTGT	T 3367	ACAGCAGG G UCUUGCUG	4077
2438	AGTTACAG GGCTAGCTACAACGA AAGACCCT	T 3368	AGGUCUU G CUGUAACU	4078
2441	CTGAGTTA GGCTAGCTACAACGA AGCAAGAC	3369	GUCUUGCU G UAACUCAG	4079
2444	TGTCTGAG GGCTAGCTACAACGA TACAGCAA	A 3370	UUGCUGUA A CUCAGACA	4080
2450	TTGGAATG GGCTAGCTACAACGA CTGAGTTA	A 3371	UAACUCAG A CAUUCCAA	4081
2452	CCTTGGAA GGCTAGCTACAACGA GTCTGAGT	T 3372	ACUCAGAC A UUCCAAGG	4082
2461	TTCCCATA GGCTAGCTACAACGA CCTTGGAA	A 3373	UUCCAAGG G UAUGGGAA	4083
2463	GCTTCCCA GGCTAGCTACAACGA ACCCTTGG	G 3374	CCAAGGGU A UGGGAAGC	4084
2470	GAATATGG GGCTAGCTACAACGA TTCCCATA	A 3375	UAUGGGAA G CCAUAUUC	4085
2473	TGTGAATA GGCTAGCTACAACGA GGCTTCCC	C 3376	GGGAAGCC A UAUUCACA	4086
2475	GGTGTGAA GGCTAGCTACAACGA ATGGCTTC	C 3377	GAAGCCAU A UUCACACC	4087
2479	GTGAGGTG GGCTAGCTACAACGA GAATATGG	G 3378	CCAUAUUC A CACCUCAC	4088
2481	GCGTGAGG GGCTAGCTACAACGA GTGAATAT	T 3379	AUAUUCAC A CCUCACGC	4089
2486	CCAGAGCG GGCTAGCTACAACGA GAGGTGTG	3380	CACACCUC A CGCUCUGG	4090
2488	GTCCAGAG GGCTAGCTACAACGA GTGAGGTG	3381	CACCUCAC G CUCUGGAC	4091
2495	AAATCATG GGCTAGCTACAACGA CCAGAGCG	3382	CGCUCUGG A CAUGAUTU	4092
2497	CTAAATCA GGCTAGCTACAACGA GTCCAGAG	3383	CUCUGGAC A UGAUUUAG	4093
2500	TCCCTAAA GGCTAGCTACAACGA CATGTCCA	A 3384	UGGACAUG A UUUAGGGA	4094
2510	TGTCCCTG GGCTAGCTACAACGA TTCCCTAA	A 3385	UUAGGGAA G CAGGGACA	4095
2516	GGGGGGTG GGCTAGCTACAACGA CCCTGCTT	T 3386	AAGCAGGG A CACCCCC	960%
2518	GCGGGGG GGCTAGCTACAACGA GTCCCTGC	3387	GCAGGGAC A CCCCCGC	4097
2525	GTGGGGG GGCTAGCTACAACGA GGGGGGTG	3388	CACCCCC G CCCCCCAC	4098
2530	DODDOOD TOOKSOKEDOKEDOD DOKKEDOO	0000	000000000000000000000000000000000000000	

2541	GAGGCTGA GGCTAGCTACGA CCCAAAGG	3390	CCUUUGGG A UCAGCCUC	4100
2545	GGCGGAGG GGCTAGCTACAACGA TGATCCCA	3391	UGGGAUCA G CCUCCGCC	4101
2551	TGGAATGG GGCTAGCTACAACGA GGAGGCTG	3392	CAGCCUCC G CCAUUCCA	4102
2554	ACTIGGAA GGCIAGCIACAACGA GGCGGAGG	3393	CCUCCGCC A UUCCAAGU	4103
2561	AGTOTOGA GGCTAGCTACAACGA TTGGAATG	3394	CAUUCCAA G UCGACACU	4104
2565	GAAGAGTG GGCTAGCTACAACGA CGACTTGG	3395	CCAAGUCG A CACUCUUC	4105
2567	AAGAAGAG GGCTAGCTACAACGA GTCGACTT	3396	AAGUCGAC A CUCUUCUU	4106
2578	ACGGTCTG GGCTAGCTACGACGA TCAAGAAG	3397	CUUCUUGA G CAGACCGU	4107
2582	AATCACGG GGCTAGCTACAACGA CTGCTCAA	3398	UUGAGCAG A CCGUGAUU	4108
2585	CCAAATCA GGCTAGCTACAACGA GGTCTGCT	3399	AGCAGACC G UGAUUUGG	4109
2588	CTTOCAAA GGCTAGCTACAACGA CACGGTCT	3400	AGACCGUG A UUUGGAAG	4110
2601	AGCAGGIG GGCTAGCTACAACGA CICICIIC	3401	GAAGAGAG G CACCUGCU	4111
2603	CCAGCAGG GGCTAGCTACAACGA GCCTCTCT	3402	AGAGAGGC A CCUGCUGG	4112
2607	GITTCCAG GGCTAGCTACAACGA AGGTGCCT	3403	AGGCACCU G CUGGAAAC	4113
2614	AAGTGTGG GGCTAGCTACAACGA TTCCAGCA	3404	UGCUGGAA A CCACACUU	4114
2617	AAGAAGTG GGCTAGCTACAACGA GGTTTCCA	3405	UGGAAACC A CACUUCUU	4115
2619	TCAAGAAG GGCTAGCTACAACGA GTGGTTTC	3406	GANACCAC A CUICUUGA	4116
2629	CCAGGCTG GGCTAGCTACAACGA TTCAAGAA	3407	UUCUUGAA A CAGCCUGG	4117
2632	CACCCAGG GGCTAGCTACGA TGTTTCAA	3408	UUGAAACA G CCUGGGUG	4118
2638	GACCGTCA GGCTAGCTACAACGA CCAGGCTG	3409	CAGCCUGG G UGACGGUC	4119
2641	AAGGACCG GGCTAGCTACAACGA CACCCAGG	3410	CCUGGGUG A CGGUCCUU	4120
2644	CIAAAGGA GGCTAGCTACAACGA CGTCACCC	3411	GGGUGACG G UCCUUUAG	4121
2653	GCAGGCTG GGCTAGCTACAACGA CTAAAGGA	3412	UCCUUNAG G CAGCCUGC	4122
2656	GCGGCAGG GSCTAGCTACAACGA TGCCTANA	3413	UUDAGGCA G CCUGCCGC	4123
2660	GACGGCGG GGCTAGCTACAACGA AGGCTGCC	3414	GGCAGCCU G CCGCCGUC	4124
2663	AGAGACGG GGCTAGCTACAACGA GGCAGGCT	3415	AGCCUGCC G CCGUCUCU	4125
2666	GACAGAGA GGCTAGCTACAACGA GGCGGCAG	3416	cueccece e nenenene	4126
2672	AACCGGGA GGCTAGCTACAACGA AGAGACGG	3417	ccencoco e occessoo	4127
2678	AAGGTGAA GGCTAGCTACAACGA CGGGACAG	3418	CUGUCCCG G UUCACCUU	4128
2682	CGGCAAGG GGCTAGCTACAACGA GAACCGGG	3419	cccaunc a ccuusccs	4129
2687	TCTCTCGG GGCTAGCTACGA AAGGTGAA	3420	UUCACCUU G CCGAGAGA	4130

2607	Change Gernagenachanga CTCTCGG	3421	CGAGAGAG G CGCGUCUG	4131
1000	HOHOMOTO SOCIAL SERVICE STREET	2477	DESIGNATION OF THE PROPERTY.	4132
5699	GGCAGACG GGCTAGCTACAACGA GCCTCTCT	3422	Achedeer o concorr	
2701	GGGGCAGA GGCTAGCTACAACGA GCGCCTCT	3423	AGAGGCGC G UCUGCCCC	4133
2705	GGGTGGGG GGCTAGCTACAACGA AGACGCGC	3424	GCGCGUCU G CCCCACCC	4134
2710	TTTGAGGG GGCTAGCTACAACGA GGGGCAGA	3425	UCUGOCCC A CCCUCAAA	4135
2718	CCACAGGG GGCTAGCTACAACGA TTGAGGGT	3426	ACCCUCAA A CCCUGUGG	4136
2723	AGGCCCCA GGCTAGCTACAACGA AGGGTTTG	3427	CAAACCCU G UGGGGCCU	4137
2728	CCATCAGG GGCTAGCTACAACGA CCCACAGG	3428	CCUGUGGG G CCUGAUGG	4138
2733	GAGCACCA GGCTAGCTACAACGA CAGGCCCC	3429	GGGGCCUG A UGGUGCUC	4139
2736	CGTGAGCA GGCTAGCTACAACGA CATCAGGC	3430	GCCUGAUG G UGCUCACG	4140
2738	GTCGTGAG GGCTAGCTACAACGA ACCATCAG	3431	CUGAUGGU G CUCACGAC	4141
2742	AAGAGTCG GGCTAGCTACAACGA GAGCACCA	3432	UGGUGCUC A CGACUCUU	4142
2745	AGGAAGAG GGCTAGCTACAACGA CGTGAGCA	3433	UGCUCACG A CUCUUCCU	4143
2754	TCCCTTTG GGCTAGCTACAACGA AGGAAGAG	3434	CUCUUCCU G CAAAGGGA	4144
2763	GTCTTCAG GGCTAGCTACAACGA TCCCTTTG	3435	CAAAGGGA A CUGAAGAC	4145
2770	TGTGGAGG GGCTAGCTACAACGA CTTCAGTT	3436	AACUGAAG A CCUCCACA	4146
2776	ACTIVATE GECTACTACAACGA GGAGGTCT	3437	AGACCUCC A CAUUAAGU	4147
2778	CCACTTAA GGCTAGCTACAACGA GTGGAGGT	3438	ACCUCCAC A UNAAGUGG	4148
2783	AAAAGCCA GGCTAGCTACAACGA TTAATGTG	3439	CACAUDAA G UGGCUUUU	4149
2786	TTAAAAAG GGCTAGCTACAACGA CACTTAAT	3440	AUUNAGUG G CUUTUUNA	4150
2794	TITICATG GGCTAGCTACAACGA TAAAAAGC	3441	GCUUUUUA A CAUGAAAA	4151
2796	GITITICA GGCIAGCIACAACGA GITAAAAA	3442	UUUUUAAC A UGAAAAC	4152
2803	CTGCCGTG GGCTAGCTACAACGA TTTTCATG	3443	CAUGAAAA A CACGGCAG	4153
2805	AGCTGCCG GGCTAGCTACAACGA GTTTTTCA	3444	UGAAAAC A CGGCAGCU	4154
2808	TACAGCTG GGCTAGCTACAACGA CGTGTTTT	3445	AAAACACG G CAGCUGUA	4155
2811	AGCTACAG GGCTAGCTACAACGA TGCCGTGT	3446	ACACGGCA G CUGUAGCU	4156
2814	GGGAGCTA GGCTAGCTACAACGA AGCTGCCG	3447	CGGCAGCU G UAGCUCCC	4157
2817	CTCGGGAG GGCTAGCTACGA TACAGCTG	3448	CAGCUGUA G CUCCCGAG	4158
2825	GAGAGTAG GGCTAGCTACAACGA TCGGGAGC	3449	GCUCCOGA G CUACUCUC	4159
2828	CAAGAGAG GGCTAGCTACAACGA AGCTCGGG	3450	CCCGAGCU A CUCUCUUG	4160
2836	AATGCTGG GGCTAGCTACAACGA AAGAGAGT	3451	ACUCUCUU G CCAGCAUU	4161

			The state of the s	4160
2840	TGAAAATG GGCTAGCTACAACGA TGGCAAGA	3452	UCUUGCCA & CAUGUUCA	7075
2842	TGTGAAAA GGCTAGCTACAACGA GCTGGCAA	3453	UUGCCAGC A UUUUCACA	4163
2848	GCAAAATG GGCTAGCTACAACGA GAAAATGC	3454	GCAUTUUC A CAUUTUGC	4164
2850	AGGCAAAA GGCTAGCTACAACGA GTGAAAAT	3455	AUUUUCAC A UUUUGCCU	4165
2855	GAGNAAGG GGCTAGCTACAACGA AAAATGTG	3456	CACAUUJU G CCUUUCUC	4166
2864	TTCTACCA GGCTAGCTACAACGA GAGAAAGG	3457	CCUUICUC G UGGUAGAA	4167
2867	GGCTTCTA GGCTAGCTACAACGA CACGAGAA	3458	UNCUCADA G DAGAAGCC	4168
2873	TGTACTGG GGCTAGCTACAACGA TTCTACCA	3459	UGGUAGAA G CCAGUACA	4169
2877	TCTCTGTA GGCTAGCTACAACGA TGGCTTCT	3460	AGAAGCCA G UACAGAGA	4170
2879	TITCICIG GGCTAGCTACGA ACTGGCTT	3461	AAGCCAGU A CAGAGAAA	4171
2887	CCACAGAA GGCTAGCTACAACGA TTCTCTGT	3462	ACAGAGAA A UUCUGUGG	4172
2892	TCCCACCA GGCTAGCTACAACGA AGAATTTC	3463	GAAAUUCU G UGGUGGGA	4173
2895	TGTTCCCA GGCTAGCTACAACGA CACAGAAT	3464	AUUCUGUG G UGGGAACA	4174
2901	CTCGAATG GGCTAGCTACAACGA TCCCACCA	3465	UGGUGGGA A CAUUCGAG	4175
2903	ACCTCGAA GGCTAGCTACAACGA GTTCCCAC	3466	GUGGGAAC A UUCGAGGU	4176
2910	GGGTGACA GGCTAGCTACAACGA CTCGAATG	3467	CAUUCGAG G UGUCACCC	4177
2912	CAGGGTGA GGCTAGCTACAACGA ACCTCGAA	3468	UUCGAGGU G UCACCCUG	4178
2915	CTGCAGGG GGCTAGCTACAACGA GACACCTC	3469	GAGGUGUC A CCCUGCAG	4179
2920	TAGCICIG GGCTAGCTACAACGA AGGGTGAC	3470	GUCACCCU G CAGAGCUA	4180
2925	CACCATAG GGCTAGCTACAACGA TCTGCAGG	3471	CCUGCAGA G CUAUGGUG	4181
2928	CCTCACCA GGCTAGCTACAACGA AGCTCTGC	3472	GCAGAGCU A UGGUGAGG	4182
2931	ACACCTCA GGCTAGCTACAACGA CATAGCTC	3473	GAGCUAUG G UGAGGUGU	4183
2936	TATCCACA GGCTAGCTACAACGA CTCACCAT	3474	AUGGUGAG G UGUGGAUA	4184
2938	CTIATCCA GGCTAGCTACAACGA ACCTCACC	3475	GGUGAGGU G UGGAUAAG	4185
2942	AAGCCTTA GGCTAGCTACAACGA CCACACCT	3476	AGGUGUGG A UAAGGCUU	4186
2947	CACCTAAG GGCTAGCTACAACGA CTTATCCA	3477	UGGAUAAG G CUUAGGUG	4187
2953	GCCTGGCA GGCTAGCTACAACGA CTAAGCCT	3478	AGGCUUNG G UGCCAGGC	4188
2955	CAGCCTOG GGCTAGCTACAACGA ACCTAAGC	3479	GCUUNGGU G CCAGGCUG	4189
2960	GCTTACAG GGCTAGCTACAACGA CTGGCACC	3480	GGUGCCAG G CUGUAAGC	4190
2963	AATGCTTA GGCTAGCTACAACGA AGCCTGGC	3481	GCCAGGCU G DAAGCAUU	4191
2967	TOAGAATG GGCTAGCTACAAGGA TTACAGCC	3482	GGCUGUAA G CAUUCUGA	4192

4193	4194	4195	4196	4197	4198	4199	4200	4201	4202	4203	4204	4205	4206	4207	4208	4209	4210	4211	4212	4213	4214	5167	0.00	4216	4216	4217 4217 4217	4217 4217 4218 4219	4216 4217 4218 4219 4219 4220	4216 4217 4218 4219 4220 4221	4216 4217 4218 4219 4219 4220 4221
CUGUAAGC A DUCUGAGC	CAUUCUGA G CUGGCUUG	CUCAGCUG G CUUGUUGU	GCUGGCUU G UUGUUUUU	GGCUUGUU G UUUUUAAG	GUUUUUAA G UCCUGUAU	UAAGUCCU G UAUAUGUA	AGUCCUGU A UAUGUAUG	UCCUGUAU A UGUAUGUA	CUGUAUAU G UAUGUAGU	GUAUAUGU A UGUAGUAG	AUAUGUAU G UAGUAGUU	UGUAUGUA G UAGUUUGG	AUGUAGUA G UUUGGGUG	UAGUUUGG G UGUGUAUA	GUUUGGGU G UGUAUAUA	UUGGGUGU G UAUAUAUA	GGGUGUGU A UAUAUAGU	GUGUGUAU A UAUAGUAG	GUGUAUAU A UAGUAGCA	UNDADADA G DAGCAUDU	AUAUAGUA G CAUUUCAA	AUAGUAGC A UUUCAAAA		AUUCAAA A UGGACGUA	AUUUCAAA A UGGACGUA CAAAAUGG A CGUACUGG	AUUUCAAA A UGGACGUA CAAAAUGG A CGUACUGG AAAUGGAC G UACUGGUU	AUUUCAAA A UGGACGUA CAAAAUGG A CGUACUGG AAAUGGAC G UACUGGUU AUGGACGU A CUGGUUUA	AUDUCAAA A UGGACGUA CAAAAUGG A CGUACUGG AAAUGGACGU A CUGGUUUA AUGGACGU A CUGGUUUA ACGUACUG G UUUAACCU	AUTUCAAA A UGGACGUA CAAAMUGA A CGUACUGG AAAUGAAC G UACUGGUU AGGACGU A CUGGUUAA ACGUACUA A CCUCCUAU	AUTUCAAA A UGGACGUA CAAAAUGA A CURCUGUU AAAUGAAC G UUCUGGUU AUGGACGU A CUGGUUUA AGGUACUG A UUGACCU CUGGUUA ACCUCUAU AACCUCCU A UCCUTGGAA AACCUCCU A UCCUTGGAA
3483	3484	3485	3486	3487	3488	3489	3490	3491	3492	3493	3494	3495	3496	3497	3498	3499	3500	3501	3502	3503	3504	3505		3506	3506	3506	3506 3507 3508	3506 3507 3508 3509 3510	3506 3507 3508 3509 3510	3506 3507 3508 3509 3510 3512
CONTRACTOR COUNTRACTOR COUNTRACTOR	CANGCCAG GGCTAGCTACAACGA TCAGAATG	ACAACAAG GGCTAGCTACAACGA CAGCTCAG	AAAAACAA GGCTAGCTACAACGA AAGCCAGC	CTTARAAA GGCTAGCTACAACGA AACAAGCC	ATACAGGA GGCTAGCTACAACGA TTAAAAAC	TACATATA GGCTAGCTACAACGA AGGACTTA	CATACATA GGCTAGCTACAACGA ACAGGACT	TACATACA GGCTAGCTACAACGA ATACAGGA	ACTACATA GGCTAGCTACAACGA ATATACAG	CTACTACA GGCTAGCTACAACGA ACATATAC	AACTACTA GGCTAGCTACAACGA ATACATAT	CCAAACTA GGCTAGCTACAACGA TACATACA	CACCCAAA GGCTAGCTACAACGA TACTACAT	TATACACA GGCTAGCTACAACGA CCAAACTA	TATATACA GGCTAGCTACAACGA ACCCAAAC	TATATATA GGCTAGCTACAACGA ACACCCAA	ACTATATA GGCTAGCTACAACGA ACACACCC	CTACTATA GGCTAGCTACAACGA ATACACAC	TGCTACTA GGCTAGCTACAACGA ATATACAC	AAATGCTA GGCTAGCTACAACGA TATATATA	TTGAAATG GGCTAGCTACAACGA TACTATAT	TITIGAAA GGCIAGCIACAACGA GCIACTAI	THE COURT OF THE PROPERTY OF T	THE STATE OF THE S	CCAGTACG GGCTAGCTACAACGA CCATTITG	CCAGTACG GGCTAGCTACAACGA CCATTTTG AACCAGTA GGCTAGCTACAACGA GTCCATTT	CACATAGO GOCTAGOTACAGOA COATITIO AACCAGTA GOCTAGOTACAGOA GOCCATITI TAAACAG GOCTAGOTAGAACAA ACGTCCATI	TANATICA GGETAGCIACANGO CONTITTO ACCAGIA GGCTAGCIACANGO CONTITTO TANACCAG GGCTAGCTACANGO ACGTCCATT NAGITIANA GGCTAGCTACANGO ACGTCCAT AGGTTANA GGCTAGCTACANGO ACGTCCAT	TAGGELAR GENERAL PROPERTY TO THE ACCORDING GETTAGCTACANGEA CONTITUTE AACCORD GECTAGCTACANGEA CONTITUTE TAAACCAG GECTAGCTACANGEA ACGTCOAT NGGTTAAA GECTAGCTACANGAA CAGTAGCTACANGAA CAGTAGCTACANGAA CAGTAGCTACANGAA CAGTAGCTACANGAACAA TAAGAAG GECTAGCTACANGAACAA TAAGAAG GECTAGCTACANGAACAA TAAGAAG GECTAGCTACANGAACAA TAAGAAG GECTAGCTACANGAACAA TAAGAAG GECTAGCTACANGAACAA TAAGAAG GECTAGCTACANGAACAA TAAGAAGAA TAAGAAA TAAGAAGAA TAAGAAA TAAGAAAA TAAGAAA TAAGAAAA TAAGAAAA TAAGAAAA TAAGAAAAAAAA	тичного из сигностительного из продукти обетилети
0000	2976	2980	2984	2987	2995	3000	3002	3004	3006	3008	3010	3013	3016	3022	3024	3026	3028	3030	3032	3035	3038	3040	3048		3052	3052	3052	3052 3054 3056 3060	3052 3054 3056 3060	3052 3054 3056 3060 3065 3065

3086	AGAGCCAG GGCTAGCTACAACGA TGCTCTCC	3514	GGAGAGCA G CUGGCUCU	4224
3090	GIGGAGAG GGCTAGCTACAACGA CAGCTGCT	3515	AGCAGCUG G CUCUCCAC	4225
3097	TAACAAGG GGCTAGCTACAACGA GGAGAGCC.	3516	GGCUCUCC A CCUUGUUA	4226
3102	ATGTGTAA GGCTAGCTACAACGA AAGGTGGA	3517	UCCACCUU G UUACACAU	4227
3105	ATAATGIG GGCIAGCIACAACGA AACAAGGI	3518	ACCUUGUU A CACAUUAU	4228
3107	ACATAATG GGCTAGCTACAACGA GTAACAAG	3519	CUNGUNAC A CAUNAUGU	4229
3109	TAACATAA GGCTAGCTACAACGA GTGTAACA	3520	UGUUACAC A UUAUGUUA	4230
3112	CTCTAACA GGCTAGCTACAACGA AATGTGTA	3521	UACACAUU A UGUUAGAG	4231
3114	CTCTCTAA GGCTAGCTACAACGA ATAATGTG	3522	CACAUUAU G UUAGAGAG	4232
3123	GCTCGCTA GGCTAGCTACAAGGA CTCTCTAA	3523	UNAGAGAG G UAGCGAGC	4233
3126	GCAGCTCG GGCTAGCTACAACGA TACCTCTC	3524	GAGAGGUA G CGAGCUGC	4234
3130	CAGAGCAG GGCTAGCTACAACGA TCGCTACC	3525	GGUNGCGN G CUGCUCUG	4235
3133	TAGCAGAG GGCTAGCTACAACGA AGCTCGCT	3526	AGCGAGCU G CUCUGCUA	4236
3138	GGACATAG GGCTAGCTACAACGA AGAGCAGC	3527	GCUGCUCU G CUAUGUCC	4237
3141	TAAGGACA GGCTAGCTACAACGA AGCAGAGC	3528	GCUCUGCU A UGUCCUUA	4238
3143	CTTAAGGA GGCTAGCTACAACGA ATAGCAGA	3529	UCUGCUAU G UCCUUAAG	4239
3151	AATATTGG GGCTAGCTACAACGA TTAAGGAC	3530	GUCCUUAA G CCAAUAUU	4240
3155	AGTABATA GGCTAGCTACAACGA TGGCTTAA	3531	UNAAGCCA A UAUUUACU	4241
3157	TGAGTAAA GGCTAGCTACAACGA ATTGGCTT	3532	AAGCCAAU A UUUACUCA	4242
3161	CTGATGAG GGCTAGCTACAACGA AAATATTG	3533	CAAUAUUU A CUCAUCAG	4243
3165	TGACCTGA GGCTAGCTACAACGA GAGTAAAT	3534	AUTUACUC A UCAGGUCA	4244
3170	AATAATGA GGCTAGCTACAACGA CTGATGAG	3535	CUCAUCAG G UCAUUAUU	4245
3173	AAAAATAA GGCTAGCTACAACGA GACCTGAT	3536	AUCAGGUC A UNAUTUTU	4246
3176	GTANAMA GGCTAGCTACAACGA AATGACCT	3537	AGGUCAUU A UUJUUUAC	4247
3183	GGCCATTG GGCTAGCTACAACGA AAANATA	3538	UAUTUUTU A CAAUGGCC	4248
3186	CATGGCCA GGCTAGCTACAACGA TGTAAAAA	3539	UUUUUACA A UGGCCAUG	4249
3189	TTCCATGG GGCTAGCTACAACGA CATTGTAA	3540	UUACAAUG G CCAUGGAA	4250
3192	TTAITCCA GGCTAGCTACAACGA GGCCATTG	3541	CAAUGGCC A UGGAAUAA	4251
3197	ATGGITIA GGCIAGCIACAACGA ICCAIGGC	3542	GCCAUGGA A UAAACCAU	4252
3201	AAAAATGG GGCTAGCTACAACGA TTATTCCA	3543	UGGAAUAA A CCAUUUUU	4253
3204	TGTAAAAA GGCTAGCTACAACGA GGTTTATT	3544	AAUAAACC A UUUUUACA	4254

Table 7: Human PTP-1B Hairpin Ribozyme and Target Sequence

Nt.	Ribozyme sequence	Seq. ID Nos.	Substrate Sequence	Seq. ID
10	GCUCUA AGAA GCGU ACCAGAGAAACA X GUACAUUACCUGGUA	4255	ACGC GGCC TAGAGC	4331
23	UGCGCC AGNA GCCG ACCAGAGAACA X GUACAUUACCUGGUA	4256	CGGC AGAC GGCGCA	4332
2,6	CAGGGC AGAA GCUG ACCAGAGAAACA X GUACAUUACCUGGUA	4257	CAGC AGCC GCCCTG	4333
29	GGCCAG AGAA GCUG ACCAGAGAACA X GUACAUUACCUGGUA	4258	CAGC CGCC CTGGCC	4334
86	UUGUCG AGAA GCUC ACCAGAGAAACA X GUACAUUACCUGGUA	4259	GAGC AGAT CGACAA	4335
220	CANAGG AGAA GACG ACCAGAGAAACA X GUACAUUACCUGGUA	4260	CGTC AGTC CCTTTG	4336
239	AGUUDA AGAA GACU ACCAGAGAAACA X GUACAUUACCUGGUA	4261	AGTC GGAT TAAACT	4337
612	UCCAAA AGAA GGCC ACCAGAGAAACA X GUACAUUACCUGGUA	4262	GGCC TGAC TITGGA	4338
636	GAAUGA AGAA GGUG ACCAGAGAAACA X GUACAUUACCUGGUA	4263	CACC AGCC TCATTC	4339
685	GCUCCG AGAA GAGU ACCAGAGAAACA X GUACAUUACCUGGUA	4264	ACTC AGCC CGGAGC	4340
702	CACCAC AGAA GGCC ACCAGAGAACA X GUACAUUACCUGGUA	4265	GGCC CGTT GTGGTG	4341
748	CAGCCA AGAA GAAG ACCAGAGAAACA X GUACAUUACCUGGUA	4266	CITC TGIC TGGCTG	4342
763	GCAAGA AGAA GGUA ACCAGAGAAACA X GUACAUUACCUGGUA	4267	TACC TGCC TCTTGC	4343
773	UUGUCC AGAA GCAA ACCAGAGAAACA X GUACAUUACCUGGUA	4268	TIGC IGAT GGACAA	4344
801	GADAUC AGAA GAAG ACCAGAGAAACA X GUACAUUACCUGGUA	4269	CITC CGIT GATAIC	4345
842	AGCCCC AGAA GAAA ACCAGAGAAACA X GUACAUUACCUGGUA	4270	TTTC GGAT GGGGCT	4346
851	GUCUGG AGAA GCCC ACCAGAGAACA X GUACAUUACCUGGUA	4271	GGGC TGAT CCAGAC	4347
861	CUGGUC AGAA GUCU ACCAGAGAAACA X GUACAUUACCUGGUA	4272	AGAC AGCC GACCAG	4348
864	CAGCUG AGNA GCUG ACCAGAGAACA X GUACAUUACCUGGUA	4273	CAGC CGAC CAGCTG	4349
869	AAGCGC AGAA GGUC ACCAGAGAACA X GUACAUUACCUGGUA	4274	GACC AGCT GCGCTT	4350
1102	UGAUGG AGAA GUCU ACCAGAGAAACA X GUACAUUACCUGGUA	4275	AGAC TGCC CCATCA	4351
1224	UGGGGA AGAA GCCU ACCAGAGAAACA X GUACAUUACCUGGUA	4276	AGGC TGCC TCCCCA	4352
1253	UUCUCG AGNA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	4277	TCAC TGCC CGAGAA	4353
1323	CGUGAG AGNA GUAG ACCAGAGAAACA X GUACAUUACCUGGUA	4278	CTAC GGTC CTCACG	4354
1332	AGCGCC AGAA GUGA ACCAGAGAAACA X GUACAUUACCUGGUA	4279	TCAC GGCC GGCGCT	4355
1361	CUGUUG AGAA GGAA ACCAGAGAAACA X GUACAUUACCUGGUA	4280	TTCC TGTT CAACAG	4356
1383	AGGAGG AGAA GGCU ACCAGAGAACA X GUACAUUACCUGGUA	4281	AGCC TGAC CCTCCT	4357
1	Allocation of the control of the con	4282	CCAC TGTC CGCCTC	4358

	STOCKED & CONTROLLED	4283	TOTC COCC TCTGCC	4359
1416	t	4284		4360
1422	t	4285	TAGCAG	4361
1441	CUGCUA AGAA GGCG ACCAGAGAAACA A SOACACOACCGGGGG	4286	CCGC GGTA GGTAAG	4362
1460	CUUACC AGAA GCGG ACCAGAGAACA A GGACAGAGCGGGGA	4287	GGGC CGCC GGACCG	4363
1473	COGUCC AGAA GUCC ACCAGAGAGACA & COMMISSION OF THE COGUCA	4288	CGCC GGAC CGCGTA	4364
1477	NACGUE AGAM GOOG ACCAGGAGAGAAACA X GUACAUUACCUGGUA	4289		4365
1501	ACCOUNT AGES GILC ACCAGAGAACA X GUACAUACCUGGUA	4290		4366
1505	ACCANO AGAS GOOD ACCADAGAGAACA X GUACAUUACCUGGUA	4291		4367
1539	ACACAC ASAN GGIIG ACCAGAGAACA X GUACAUUACCUGGUA	4292		4368
16/0	CCCAR ASER CICI ACCAGAGAACA X GUACAUVACCUGGUA	4293		4369
1/35	SESSES AGAS GACA ACCAGAGAAACA X GUACAUUACCUGGUA	4294	TGTC AGCC TIGCAT	4370
74RT	TOTAL TOTAL GOOD ACTARGABARDA X GUACAUUACCUGGUA	4295	GGCC TGCT GCGTCA	4371
1946	USACCE AGAIN GACG ACCAGAGAAGCA X GUACAUUACCUGGUA	4296	CGTC AGAC CAGTAC	4372
1955	GUACUS AGAS CHILL ACCAGAGAACA X GUACAUUACCUGGUA	4297	GACC AGTA CTGGGA	4373
1000	GCHING AGAA GUCC ACCAGAGAAACA X GUACAUUACCUGGUA	4298	GGAC GGTI GTAAGC	4374
2000	ANIMAC AGAA GCITT ACCACAGAAACA X GUACAUUACCUGGUA	4299	AAGC AGTT GTTATT	4375
1988	ARCHUN AGAA GGAC ACCAGAGAAACA X GUACAUUACCUGGUA	4300	GTCC CGCT TAITCT	4376
2038	ACCESS AGES GESTI ACCACACAAACA X GUACAUUACCUGGUA	4301	ATTC TGCT CCCTGT	4377
2101	CREGGG AGAA GUGA ACCAGAGAACA X GUACAUUACCUGGUA	4302	TCAC TGCT CCCCCG	4378
1177	THE THE POST OF A CONTRACT X GUACAUUACCUGGUA	4303	GTCC TGAT GAMAA	4379
2190	THINGIS AGAS GAGS ACCAGAGAAGA X GUACAUUACCUGGUA	4304	TCTC TGCT TACTAA	4380
2230	HIGGACA AGAA GGUU ACCAGAGAAACA X GUACAUUACCUGGUA	4305	AACC TGCC TGTGCA	4381
2022	GITANTIG AGAA GGUC ACCAGAGAAACA X GUACAUUACCUGGUA	4306	GACC TGAT CATTAC	4382
6177	THICKOL BOAD GCCH ACCAGAGAACA X GUACAUUACCUGGUA	4307	AGCC TGTT GCTGAA	4383
2309	CHOCAR AGAS COSC SCCREGGGGGGGGGC X GUACAUUACCUGGUA	4308	GTGC AGIT TTCCAG	4384
2345	COSSIGN ACRE CELES ACCAGAGAGAACA X GUACAUUACCUGGUA	4309	GCCC AGCC TGTCCT	4385
2412	HAGGACA AGAA GGCTI ACCAGAGAAACA X GUACAUUACCUGGUA	4310	AGCC TGTC CTGGTA	- 4386
2410	CHOCKER ACAN COOR ACCAGRAACA X GUACAUUACCUGGUA	4311	CCCC CGCC CCCCAC	4387
2524	GUGGGG AGAN GAILG ACCAGAGAAGA X GUACAUNACCUGGUA	4312	GATC AGCC TCCGCC	4388
2544	GGGGGA ASAN GANG ACCAGAGAAACA X GIACAUUACCUGGUA	4313	GAGC AGAC CGTGAT	4389
2580	AUCACE AGAS GCOC ACCRECATE OF THE STATE OF T			

4390	100	4331	4392	4393	4394	4395	4396	4397	4398	4399		4400	4401	4402	4403	4404	4405	50,	4406
Casa noon casas	Curc 1901 Course	AAAC AGCC TGGGTG	TGAC GGTC CTTIAG	AGGC AGCC TGCCGC	AGCC TGCC GCCGTC	CTGC CGCC GTCTCT	ccdc cgrc rergrc	TCTC TGTC CCGGTT	TCCC GGIT CACCIT	CONTROL COOK CHOO	הפור ופרר הרשההה	GGCC TGAT GGTGCT	CGGC AGCT GTAGCT	CAGC TGTA GCTCCC	AGCC AGTA CAGAGA	GTCC TGTA TATGTA	BORDOO BOOK BOOK	GAGC AGCT GGCTC1	GAGC TGCT CTGCTA
	4314	4315	4316	4317	4318	4319	4320	4321	4322		4323	4324	4325	4326	4327	4328	2002	4329	4330
	GUUUCC AGAA GGUG ACCAGAGAACA X GUACAUUACCUGGUA	CACCURA AGAA GUUU ACCAGAGAACA X GUACAUUACCUGGUA	CHARLES AGAIN GILLS ACCAGAGAACA X GUACAUUACCUGGUA	COMPANY ACCESSAGES A CHACALIFACCUGGUA	GUGGUCH AGAM GULU ANCHORORORANA X GIRCAINIACCUGGUA	GACGGC BOARD SOCIOCACOARDA V GIRCAINIACCUGGUA	AUAGAC AGAG ACCACAGAGAACA X CHACANITACCUGGUA	GACAGA AGAA GCGG ACCAGAGAGACA X GIACAITIACCUGGUA	AACCUG MONA GNOW ACCUSAGEMENT IN CONTROLLING	AAGGUG AGAA GGGA ALCAGNGAAACA A GGACAGGGGG	GGGUGG AGAA GACG ACCAGAGAACA X GUACAUUACCUGGUA	ACCAUTAGES GROCE ACCAGAGARCE X GUACAUTACCUGGUA	ASCALL MAIN COCC ACCACAGAACA X GUACAUDACCUGGUA	AGCUAL AGAS COLO ACCAGADAGA X GUACAUDACCUGGUA	GGGMGC MOMA GCGG MCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	UCUCUG AGAA GGCU ACCAGAGAGAGA	UACAUA AGAA GGAC ACCAGAGAACA X GUACAUGACCOGGON	AGAGCC AGAA GCUC ACCAGAGAACA X GUACAUUACCUGGUA	TIACCAG AGAA GCUC ACCAGAGAACA X GUACAUUACCUGGUA
	2606	2631	1007	2643	2655	2659	2992	2665	2671	2677	2704		16/2	2810	2813	2876	2999	2085	2133

Table

Table 8: Anti Human PTP-1B HH, NCH, and G Cleaver Ribozymes

Alias	Ribozyme Sequence	Seq. ID Nos	Substrate Seq.	Seq. ID Nos.
нн				
PTP1B-599	UGUGGUA CUGADGAGGCCGUDAGGCCGAA AGUGGAA	4407	UUCCACU A UACCACA	4425
PTP1B-879	GGUAGGA CUGAUGAGGCCGUUAGGCCGAA AAGCGCA	4408	UGCGCUU C UCCUACC	4426
PTP1B-1393	UGGAGUG CUGAUGAGGCCGUUAGGCCGAA AGGAGGG	4409	cccuccu c cacucca	4427
PTP1B-1398	GGAGGUG CUGAUGAGGCCGUUAGGCCGAA AGUGGAG	4410	CUCCACU C CACCUCC	4428
PTF1B-1404	GUGGGUG CUGAUGAGCCGUUAGGCCGAA AGGUGGA	4411	UCCACCU C CACCCAC	4429
PTP1B-2118	UAGCAGA CUGAUGAGGCCGUUAGGCCGAA AACAGGG	4412	CCCUGUU A UCUGCUA	4430
PTP1B-2181	GACACAA CUGAUGAGGCCGUUAGGCCGAA AAGACCU	4413	AGGUCUU C UUGUGUC	4431
PTP1B-2183	AGGACAC CUGAUGAGGCCGUUAGGCCGAA AGAAGAC	4414	enconco o engocco.	4432
PTP1B-2238	GCCACAU CUGAUGAGGCCGUUAGGCCGAA AGUAAGC	4415	GCUUACU A AUGUGCC	4433
PTP1B-2252	GGACUUG CUGAUGAGGCCGUUAGGCCGAA ACAUGGG	4416	CCCAUGU C CAAGUCC	4434
NCH				
PTP1B-1395	GGUGGAG CUGAUGAGGCCGUUAGGCCGAA IGAGGAG	4417	CUCCUCC A CUCCACC	4435
PTF1B-1408	GACAGUG CUGAUGAGGCCGUUAGGCCGAA IUGGAGG	4418	ccuccac c cacugue	4436
PTP1B-1555	GGAUGAG CUGAUGAGGCCGUUAGGCCGAA IGUGAGA	4419	UCUCACC C CUCAUCC	4437
PTP1B-1578	AGUGGAA CUGAUGAGGCCGUUAGGCCGAA IGGCAAA	4420	UNUGCCC C UNCCACU	4438
PTP1B-2113	GAUAACA CUGAUGAGGCCGUUAGGCCGAA IGAGCAG	4421	CUGCUCC C UGUDAUC	4439
G-Cleaver				
PTP1B-1267	GUCCU UGAUGGCAUGCACUAUGCGCG GUCCUUCUCG	4422	CGAGAAGGAC G AGGAC	4440
PTP1B-2184	GGACA UGAUGGCAUGCACUAUGCGCG AAGAAGACCU	4423	AGGUCUUCUU G UGUCC	4441
PTP1B-2241	GGGCA UGAUGGCAUGCACUAUGCGCG AUUAGUAAGC	4424	GCUUACUAAU G UGCCC	4442

Table 9

Table 9: Human methionine aminopeptidase type 2 (Met AP-2) Hammerhead Ribozyme and Target Sequence

Nt. position	Ribozyme Sequence	Seq ID nos.	Substrate Sequence	Seq ID nos.
9	CCGAGAGA CUGAUGAG X CGAA ACGAGGGA	1	TCCCTCGT C TCTCTCGG	413
11	GCCCGAGA CUGAUGAG X CGAA AGACGAGG	2	CCTCGTCT C TCTCGGGC	414
13	UUGCCCGA CUGAUGAG X CGAA AGAGACGA	3	TCGTCTCT C TCGGGCAA	415
15	UGUUGCCC CUGAUGAG X CGAA AGAGAGAC	4	GTCTCTCT C GGGCAACA	416
43	GAGGCCGC CUGAUGAG X CGAA ACCUCCUC	5	GAGGAGGT A GCGGCCTC	417
51	GGCUCCCG CUGAUGAG X CGAA AGGCCGCU	6	AGCGGCCT C CGGGAGCC	418
80	GUCGUCUG CUGAUGAG X CGAA AUCCAGGU	7	ACCTGGAT C CAGACGAC	419
108	CAGCCGUA CUGAUGAG X CGAA AGGCAGCU	8	AGCTGCCT C TACGGCTG	420
110	CUCAGCCG CUGAUGAG X CGAA AGAGGCAG	9	CTGCCTCT A CGGCTGAG	421
167	UGCUGCAG CUGAUGAG X CGAA AGGCCCUU	10	AAGGGCCT T CTGCAGCA	422
168	CUGCUGCA CUGAUGAG X CGAA AAGGCCCU	11	AGGGCCTT C TGCAGCAG	423
194	UGAUUCUU CUGAUGAG X CGAA AUCAGGUU	12	AACCTGAT A AAGAATCA	424
201	AGGCUCCU CUGAUGAG X CGAA AUUCUUUA	13	TAAAGAAT C AGGAGCCT	425
210	CAUCCACU CUGAUGAG X CGAA AGGCUCCU	14	AGGAGCCT C AGTGGATG	426
223	UGUCUUGC CUGAUGAG X CGAA ACUUCAUC	15	GATGAAGT A GCAAGACA	427
234	AUCUUUCC CUGAUGAG X CGAA ACUGUCUU	16	AAGACAGT T GGAAAGAT	428
243	CCAAUGCU CUGAUGAG X CGAA AUCUUUCC	17	GGAAAGAT C AGCATTGG	429
249	UAUCUUCC CUGAUGAG X CGAA AUGCUGAU	18	ATCAGCAT T GGAAGATA	430
257	UCUUUCUU CUGAUGAG X CGAA AUCUUCCA	19	TGGAAGAT A AAGAAAGA	431
355	UCUGUUUG CUGAUGAG X CGAA ACUUUUGG	20	CCAAAAGT T CAAACAGA	432
356	GUCUGUUU CUGAUGAG X CGAA AACUUUUG	21	CAAAAGTT C AAACAGAC	4 3 3
368	AACUGAGG CUGAUGAG X CGAA AGGGUCUG	22	CAGACCCT C CCTCAGTT	434
372	UUGGAACU CUGAUGAG X CGAA AGGGAGGG	23	CCCTCCCT C AGTTCCAA	435
376	CAUAUUGG CUGAUGAG X CGAA ACUGAGGG	24	CCCTCAGT T CCAATATG	436
377	ACAUAUUG CUGAUGAG X CGAA AACUGAGG	25	CCTCAGTT C CAATATGT	437
382	AGGUCACA CUGAUGAG X CGAA AUUGGAAC	26	GTTCCAAT A TGTGACCT	438
393	CAUUAGGA CUGAUGAG X CGAA ACAGGUCA.	27	TGACCTGT A TCCTAATG	439
395	ACCAUUAG CUGAUGAG X CGAA AUACAGGU	28	ACCTGTAT C CTAATGGT	440
398	UACACCAU CUGAUGAG X CGAA AGGAUACA	29	TGTATCCT A ATGGTGTA	441
406	UUGGGAAA CUGAUGAG X CGAA ACACCAUU	30	AATGGTGT A TTTCCCAA	442
408	CUUUGGGA CUGAUGAG X CGAA AUACACCA	31	TGGTGTAT T TCCCAAAG	443
409	CCUUUGGG CUGAUGAG X CGAA AAUACACC	32	GGTGTATT T CCCAAAGG	444
410	UCCUUUGG CUGAUGAG X CGAA AAAUACAC	33	GTGTATTT C CCAAAGGA	445
432	UGGGUGGG CUGAUGAG X CGAA AUUCGCAU	34	ATGCGAAT A CCCACCCA	446
464	AGUUCUCC CUGAUGAG X CGAA AGCAGCUG	35	CAGCTGCT T GGAGAACT	447
473	UUCACUUG CUGAUGAG X CGAA AGUUCUCC	36	GGAGAACT A CAAGTGAA	448
495	CCUGAUCU CUGAUGAG X CGAA AUGCUUUC	37	GAAAGCAT T AGATCAGG	449
496	GCCUGAUC CUGAUGAG X CGAA AAUGCUUU	38	AAAGCATT A GATCAGGC	450
500	ACUUGCCU CUGAUGAG X CGAA AUCUAAUG	39	CATTAGAT C AGGCAAGT	451
517	UCAUUCCA CUGAUGAG X CGAA AUCUCUUC	40	GAAGAGAT T TGGAATGA	452
518	AUCAUUCC CUGAUGAG X CGAA AAUCUCUU	41	AAGAGATT T GGAATGAT	453
527	UUCUCGAA CUGAUGAG X CGAA AUCAUUCC	42	GGAATGAT T TTCGAGAA	454
		1	L	1

Table 9

528	CUUCUCGA CUGAUGAG X CGAA AAUCAUUC	43	GAATGATT T TCGAGAAG	455
529	GCUUCUCG CUGAUGAG X CGAA AAAUCAUU	44	AATGATTT T CGAGAAGC	456
530	AGCUUCUC CUGAUGAG X CGAA AAAAUCAU	45	ATGATTTT C GAGAAGCT	457
551	AACUUGUC CUGAUGAG X CGAA AUGUGCUU	46	AAGCACAT C GACAAGTT	458
559	UAUUUUCU CUGAUGAG X CGAA ACUUGUCG	47	CGACAAGT T AGAAAATA	459
560	GUAUUUUC CUGAUGAG X CGAA AACUUGUC	48	GACAAGTT A GAAAATAC	460
567	UCAUUACG CUGAUGAG X CGAA AUUUUCUA	49	TAGAAAAT A CGTAATGA	461
571	CAGCUCAU CUGAUGAG X CGAA ACGUAUUU	50	AAATACGT A ATGAGCTG	462
583	CCAGGCUU CUGAUGAG X CGAA AUCCAGCU	51	AGCTGGAT C AAGCCTGG	463
604	· CAGAUUUC CUGAUGAG X CGAA AUCAUUGU	52	ACAATGAT A GAAATCTG	464
610	UUUUCACA CUGAUGAG X CGAA AUUUCUAU	53	ATAGAAAT C TGTGAAAA	465
621	AGUCUUCC CUGAUGAG X CGAA ACUUUUCA	54	TGAAAAGT T GGAAGACT	466
632	CUUGCGUG CUGAUGAG X CGAA ACAGUCUU	55	AAGACTGT T CACGCAAG	467
633	ACUUGCGU CUGAUGAG X CGAA AACAGUCU	56	AGACTGTT C ACGCAAGT	468
642	CUUUUAUU CUGAUGAG X CGAA ACUUGCGU	57	ACGCAAGT T AATAAAAG	469
643	UCUUUUAU CUGAUGAG X CGAA AACUUGCG	58	CGCAAGTT A ATAAAAGA	470
646	UUCUCUUU CUGAUGAG X CGAA AUUAACUU	59	AAGTTAAT A AAAGAGAA	471
660	CUGCAUUU CUGAUGAG X CGAA AUCCAUUC	60	GAATGGAT T AAATGCAG	472
661	CCUGCAUU CUGAUGAG X CGAA AAUCCAUU	61	AATGGATT A AATGCAGG	473
678	CAGUAGGA CUGAUGAG X CGAA AUGCCAGG	62	CCTGGCAT T TCCTACTG	474
679	CCAGUAGG CUGAUGAG X CGAA AAUGCCAG	63	CTGGCATT T CCTACTGG	475
680	UCCAGUAG CUGAUGAG X CGAA AAAUGCCA	64	TGGCATTT C CTACTGGA	476
683	ACAUCCAG CUGAUGAG X CGAA AGGAAAUG	65	CATTTCCT A CTGGATGT	477
692	AUUGAGAG CUGAUGAG X CGAA ACAUCCAG	66	CTGGATGT T CTCTCAAT	478
693	UAUUGAGA CUGAUGAG X CGAA AACAUCCA	67	TGGATGTT C TCTCAATA	479 480
695	AUUAUUGA CUGAUGAG X CGAA AGAACAUC	68	GATGTTCT C TCAATAAT	480
697	CAAUUAUU CUGAUGAG X CGAA AGAGAACA	69	TGTTCTCT C AATAATTG	482
701	AGCACAAU CUGAUGAG X CGAA AUUGAGAG	70	CTCTCAAT A ATTGTGCT TCAATAAT T GTGCTGCC	482
704	GGCAGCAC CUGAUGAG X CGAA AUUAUUGA	71		484
716	GGGAGUAU CUGAUGAG X CGAA AUGGGCAG	72	CTGCCCAT T ATACTCCC	484
717	UGGGAGUA CUGAUGAG X CGAA AAUGGGCA	73	TGCCCATT A TACTCCCA CCCATTAT A CTCCCAAT	486
719	AUUGGGAG CUGAUGAG X CGAA AUAAUGGG	74	ATTATACT C CCAATGCC	487
722	GGCAUUGG CUGAUGAG X CGAA AGUAUAAU	75	ACAACAGT A TTACAGTA	488
745	UACUGUAA CUGAUGAG X CGAA ACUGUUGU	76	ACAGCAGT A TTACAGTA AACAGTAT T ACAGTATG	489
747	CAUACUGU CUGAUGAG X CGAA AUACUGUU		ACAGTAT T ACAGTATGA	490
748	UCAUACUG CUGAUGAG X CGAA AAUACUGU	78	ACAGTATT A CAGTATGA ATTACAGT A TGATGACA	491
753	UGUCAUCA CUGAUGAG X CGAA ACUGUAAU	79	GATGACAT C TGTAAAAT	492
763	AUUUUACA CUGAUGAG X CGAA AUGUCAUC	80	ACATCTGT A AAATAGAC	492
767	GUCUAUUU CUGAUGAG X CGAA ACAGAUGU	81	TGTAAAAT A GACTTTGG	493
772	CCAAAGUC CUGAUGAG X CGAA AUUUUACA	82		494
777	GUGUUCCA CUGAUGAG X CGAA AGUCUAUU	83	AATAGACT T TGGAACAC ATAGACTT T GGAACACA	495
778	UGUGUUCC CUGAUGAG X CGAA AAGUCUAU	84		496
788	ACCACUUA CUGAUGAG X CGAA AUGUGUUC	85	GAACACAT A TAAGTGGT	497
790	CUACCACU CUGAUGAG X CGAA AUAUGUGU	86	ACACATAT A AGTGGTAG	498
797	AAUAAUCC CUGAUGAG X CGAA ACCACUUA	87	TAAGTGGT A GGATTATT	500
802	CAGUCAAU CUGAUGAG X CGAA AUCCUACC	88	GGTAGGAT T ATTGACTG	.501
803	ACAGUCAA CUGAUGAG X CGAA AAUCCUAC	89	GTAGGATT A TTGACTGT	- 501

Table 9

	14010			
805	GCACAGUC CUGAUGAG X CGAA AUAAUCCU	90	AGGATTAT T GACTGTGC	502
815	GACAGUAA CUGAUGAG X CGAA AGCACAGU	91	ACTGTGCT T TTACTGTC	503
816	UGACAGUA CUGAUGAG X CGAA AAGCACAG	92	CTGTGCTT T TACTGTCA	504
817	GUGACAGU CUGAUGAG X CGAA AAAGCACA	93	TGTGCTTT T ACTGTCAC	505
818	AGUGACAG CUGAUGAG X CGAA AAAAGCAC	94	GTGCTTTT A CTGTCACT	506
823	UUAAAAGU CUGAUGAG X CGAA ACAGUAAA	95	TTTACTGT C ACTTTTAA	507
827	GGGAUUAA CUGAUGAG X CGAA AGUGACAG	96	CTGTCACT T TTAATCCC	508
828	UGGGAUUA CUGAUGAG X CGAA-AAGUGACA	97	TGTCACTT T TAATCCCA	509
829	UUGGGAUU CUGAUGAG X CGAA AAAGUGAC	98	GTCACTTT T AATCCCAA	510
830	UUUGGGAU CUGAUGAG X CGAA AAAAGUGA	99	TCACTTTT A ATCCCAAA	511
833	AUAUUUGG CUGAUGAG X CGAA AUUAAAAG	100	CTTTTAAT C CCAAATAT	512
840	ACGUAUCA CUGAUGAG X CGAA AUUUGGGA	101	TCCCAAAT A TGATACGT	513
845	UAAUAACG CUGAUGAG X CGAA AUCAUAUU	102	AATATGAT A CGTTATTA	514
849	CUUUUAAU CUGAUGAG X CGAA ACGUAUCA	103	TGATACGT T ATTAAAAG	515
850	GCUUUUAA CUGAUGAG X CGAA AACGUAUC	104	GATACGTT A TTAAAAGC	516
852	CAGCUUUU CUGAUGAG X CGAA AUAACGUA	105	TACGTTAT T AAAAGCTG	517
853	ACAGCUUU CUGAUGAG X CGAA AAUAACGU	106	ACGTTATT A AAAGCTGT	518
862	GCAUCUUU CUGAUGAG X CGAA ACAGCUUU	107	AAAGCTGT A AAAGATGC	519
872	AGUGUUAG CUGAUGAG X CGAA AGCAUCUU	108	AAGATGCT A CTAACACT	520
875	UCCAGUGU CUGAUGAG X CGAA AGUAGCAU	109	ATGCTACT A ACACTGGA	521
886	GCACACUU CUGAUGAG X CGAA AUUCCAGU	110	ACTGGAAT A AAGTGTGC	522
901	CGAACAUC CUGAUGAG X CGAA AUUCCAGC	111	GCTGGAAT T GATGTTCG	523
907	CACAGACG CUGAUGAG X CGAA ACAUCAAU	112	ATTGATGT T CGTCTGTG	524
908	ACACAGAC CUGAUGAG X CGAA AACAUCAA	113	TTGATGTT C GTCTGTGT	525
911	AUCACACA CUGAUGAG X CGAA ACGAACAU	114	ATGTTCGT C TGTGTGAT	526
922	GCCUCACC CUGAUGAG X CGAA ACAUCACA	115	TGTGATGT T GGTGAGGC	527
934	ACUUCUUG CUGAUGAG X CGAA AUGGCCUC	116	GAGGCCAT C CAAGAAGT	528
943	GACUCCAU CUGAUGAG X CGAA ACUUCUUG	117	CAAGAAGT T ATGGAGTC	529
944	GGACUCCA CUGAUGAG X CGAA AACUUCUU	118	AAGAAGTT A TGGAGTCC	530 531
951	CUUCAUAG CUGAUGAG X CGAA ACUCCAUA	119	TATGGAGT C CTATGAAG	531
954	CAACUUCA CUGAUGAG X CGAA AGGACUCC	120	GGAGTCCT A TGAAGTTG	532
961	UCUAUUUC CUGAUGAG X CGAA ACUUCAUA	121	TATGAAGT T GAAATAGA	533
967	UUCCCAUC CUGAUGAG X CGAA AUUUCAAC	122	GTTGAAAT A GATGGGAA	535
981	UCACUUGA CUGAUGAG X CGAA AUGUCUUC	123	GAAGACAT A TCAAGTGA AGACATAT C AAGTGAAA	536
983	UUUCACUU CUGAUGAG X CGAA AUAUGUCU	124	AGACCATAT C CAGTGATCT	537
997	AGAUUACG CUGAUGAG X CGAA AUUGGUUU	125	CAATCCGT A ATCTAAAT	538
1001	AUUUAGAU CUGAUGAG X CGAA ACGGAUUG	126	TCCGTAAT C TAAATGGA	539
1004	UCCAUUUA CUGAUGAG X CGAA AUUACGGA	127	CGTAATCT A AATGGACA	540
1006	UGUCCAUU CUGAUGAG X CGAA AGAUUACG	128	ATGGACAT T CAATTGGG	541
1016	CCCAAUUG CUGAUGAG X CGAA AUGUCCAU	130	TGGACATT C AATTGGGC	542
1017	GCCCAAUU CUGAUGAG X CGAA AAUGUCCA	131	CATTCAAT T GGGCAATA	543
1021	UAUUGCCC CUGAUGAG X CGAA AUUGAAUG	132	TGGGCAAT A TAGAATAC	544
1029	GUAUUCUA CUGAUGAG X CGAA AUUGCCCA	133	GGCAATAT A GAATACAT	545
1031	AUGUAUUC CUGAUGAG X CGAA AUAUUGCC	134	TATAGAAT A CATGCTGG	546
1036	CCAGCAUG CUGAUGAG X CGAA AUUCUAUA	134	GTGCCGAT T GTGAAAGG	547
1060	CCUUUCAC CUGAUGAG X CGAA AUCGGCAC	135	GGAGAAGT A TATGCAAT	548
1102	AUUGCAUA CUGAUGAG X CGAA ACUUCUCC	136	GGAGAAGI A TATGCAAT	540

Table 9

	Table			
1104	CANUUGCA CUGAUGAG X CGAA AUACUUCU	137	AGAAGTAT A TGCAATTG	549
1111	AAGGUUUC CUGAUGAG X CGAA AUUGCAUA	138	TATGCAAT T GAAACCTT	550
1119	UACUACCA CUGAUGAG X CGAA AGGUUUCA	139	TGAAACCT T TGGTAGTA	551
1120	GUACUACC CUGAUGAG X CGAA AAGGUUUC	140	GAAACCTT T GGTAGTAC	552
1124	UCCUGUAC CUGAUGAG X CGAA ACCAAAGG	141	CCTTTGGT A GTACAGGA	553
1127	UUUUCCUG CUGAUGAG X CGAA ACUACCAA	142	TTGGTAGT A CAGGAAAA	554
1141	UCAUGAAC CUGAUGAG X CGAA ACACCUUU	143	AAAGGTGT T GTTCATGA	555
1144	UCAUCAUG CUGAUGAG X CGAA ACAACACC	144	GGTGTTGT T CATGATGA	556
1145	AUCAUCAU CUGAUGAG X CGAA AACAACAC	145	GTGTTGTT C ATGATGAT	557
1154	ACAUUCCA CUGAUGAG X CGAA AUCAUCAU	146	ATGATGAT A TGGAATGT	558
1163	GUAAUGUG CUGAUGAG X CGAA ACAUUCCA	147	TGGAATGT T CACATTAC	559
1164	UGUAAUGU CUGAUGAG X CGAA AACAUUCC	148	GGAATGTT C ACATTACA	560
1169	UUUCAUGU CUGAUGAG X CGAA AUGUGAAC	149	GTTCACAT T ACATGAAA	561
1170	UUUUCAUG CUGAUGAG X CGAA AAUGUGAA	150	TTCACATT A CATGAAAA	562
1181	AACAUCAA CUGAUGAG X CGAA AUUUUUCA	151	TGAAAAAT T TTGATGTT	563
1182	CAACAUCA CUGAUGAG X CGAA AAUUUUUC	152	GAAAATT T TGATGTTG	564
1183	CCAACAUC CUGAUGAG X CGAA AAAUUUUU	153	AAAAATTT T GATGTTGG	565
1189	ACAUGUCC CUGAUGAG X CGAA ACAUCAAA	154	TTTGATGT T GGACATGT	566
1204	GGAAGCCU CUGAUGAG X CGAA AUUGGCAC	155	GTGCCAAT A AGGCTTCC	567
1210	GUUCUUGG CUGAUGAG X CGAA AGCCUUAU	156	ATAAGGCT T CCAAGAAC	568
1211	UGUUCUUG CUGAUGAG X CGAA AAGCCUUA	157	TAAGGCTT C CAAGAACA	569
1227	CAUUUAAC CUGAUGAG X CGAA AGUGUUUU	158	AAAACACT T GTTAAATG	570
1230	UGACAUUU CUGAUGAG X CGAA ACAAGUGU	159	ACACTTGT T AAATGTCA	571
1231	AUGACAUU CUGAUGAG X CGAA AACAAGUG	160	CACTTGTT A AATGTCAT	572
1237	UCAUUGAU CUGAUGAG X CGAA ACAUUUAA	161	TTAAATGT C ATCAATGA	573
1240	UUUUCAUU CUGAUGAG X CGAA AUGACAUU	162	AATGTCAT C AATGAAAA	574 575
1251	GGGUUCCA CUGAUGAG X CGAA AGUUUUCA	163	TGAAAACT T TGGAACCC	575
1252	AGGGUUCC CUGAUGAG X CGAA AAGUUUUC	164	GAAAACTT T GGAACCCT	
1261	CAGAAGGC CUGAUGAG X CGAA AGGGUUCC	165	GGAACCCT T GCCTTCTG	577
1266	UGCGGCAG CUGAUGAG X CGAA AGGCAAGG	166	CCTTGCCT T CTGCCGCA	578 579
1267	CUGCGGCA CUGAUGAG X CGAA AAGGCAAG	167	CTTGCCTT C TGCCGCAG	579
1286	UCCCAAGC CUGAUGAG X CGAA AUCCAGCC	168	GGCTGGAT C GCTTGGGA	580
1290	UUUCUCCC CUGAUGAG X CGAA AGCGAUCC	169	GGATCGCT T GGGAGAAA	
1301	CAAGUAUU CUGAUGAG X CGAA ACUUUCUC	170	GAGAAAGT A AATACTTG	582 583
1305	CCAUCAAG CUGAUGAG X CGAA AUUUACUU	171	AAGTAAAT A CTTGATGG	584
1308	GAGCCAUC CUGAUGAG X CGAA AGUAUUUA	172	TAAATACT T GATGGCTC	
1316	AUUCUUCA CUGAUGAG X CGAA AGCCAUCA	173	TGATGGCT C TGAAGAAT	585 586
1325	GUCACACA CUGAUGAG X CGAA AUUCUUCA	174	TGAAGAAT C TGTGTGAC	587
1335	CAAUGCCC CUGAUGAG X CGAA AGUCACAC	175	GTGTGACT T GGGCATTG	587
1342	GGAUCUAC CUGAUGAG X CGAA AUGCCCAA	176	TTGGGCAT T GTAGATCC	588
1345	UAUGGAUC CUGAUGAG X CGAA ACAAUGCC	177	GGCATTGT A GATCCATA	599
1349	UGGAUAUG CUGAUGAG X CGAA AUCUACAA	178	TTGTAGAT C CATATCCA	590
1353	AUGGUGGA CUGAUGAG X CGAA AUGGAUCU	179	AGATCCAT A TCCACCAT	591
1355	UAAUGGUG CUGAUGAG X CGAA AUAUGGAU	180	ATCCATAT C CACCATTA	592
1362	UGUCACAU CUGAUGAG X CGAA AUGGUGGA	181	TCCACCAT T ATGTGACA	593
1363	AUGUCACA CUGAUGAG X CGAA AAUGGUGG	182	CCACCATT A TGTGACAT	594
1372	GAUCCUUU CUGAUGAG X CGAA AUGUCACA	183	TGTGACAT T AAAGGATC	595

Table 9

1373	UGAUCCUU CUGAUGAG X CGAA AAUGUCAC	184	GTGACATT A AAGGATCA	596
1380	CUGUAUAU CUGAUGAG X CGAA AUCCUUUA	185	TAAAGGAT C ATATACAG	597
1383	GCGCUGUA CUGAUGAG X CGAA AUGAUCCU	186	AGGATCAT A TACAGCGC	598
1385	UUGCGCUG CUGAUGAG X CGAA AUAUGAUC	187	GATCATAT A CAGCGCAA	599
1395	UAUGUUCA CUGAUGAG X CGAA AUUGCGCU	188	AGCGCAAT T TGAACATA	600
1396	GUAUGUUC CUGAUGAG X CGAA AAUUGCGC	189	GCGCAATT T GAACATAC	601
1403	CAGGAUGG CUGAUGAG X CGAA AUGUUCAA	190	TTGAACAT A CCATCCTG	602
1408	CGCAACAG CUGAUGAG X CGAA AUGGUAUG	191	CATACCAT C CTGTTGCG	603
1413	UUGGACGC CUGAUGAG X CGAA ACAGGAUG	192	CATCCTGT T GCGTCCAA	604
1418	ACAUGUUG CUGAUGAG X CGAA ACGCAACA	193	TGTTGCGT C CAACATGT	605
1427	AACUUCUU CUGAUGAG X CGAA ACAUGUUG	194	CAACATGT A AAGAAGTT	606
1435	CUGCUGAC CUGAUGAG X CGAA ACUUCUUU	195	AAAGAAGT T GTCAGCAG	607
1438	CCUCUGCU CUGAUGAG X CGAA ACAACUUC	196	GAAGTTGT C AGCAGAGG	608
1455	AAGUUUAA CUGAUGAG X CGAA AGUCAUCU	197	AGATGACT A TTAAACTT	609
1457	CUAAGUUU CUGAUGAG X CGAA AUAGUCAU	198	ATGACTAT T AAACTTAG	610
1458	ACUAAGUU CUGAUGAG X CGAA AAUAGUCA	199	TGACTATT A AACTTAGT	611
1463	UUUGGACU CUGAUGAG X CGAA AGUUUAAU	200	ATTAAACT T AGTCCAAA	612
1464	CUUUGGAC CUGAUGAG X CGAA AAGUUUAA	201	TTAAACTT A GTCCAAAG	613
1467	UGGCUUUG CUGAUGAG X CGAA ACUAAGUU	202	AACTTAGT C CAAAGCCA	614
1479	AAGGUGUU CUGAUGAG X CGAA AGGUGGCU	203	AGCCACCT C AACACCTT	- 615
1487	AGAAAAUA CUGAUGAG X CGAA AGGUGUUG	204	CAACACCT T TATTTTCT	616
1488	CAGAAAAU CUGAUGAG X CGAA AAGGUGUU	205	AACACCTT T ATTTTCTG	617
1489	UCAGAAAA CUGAUGAG X CGAA AAAGGUGU	206	ACACCTTT A TTTTCTGA	618
1491	GCUCAGAA CUGAUGAG X CGAA AUAAAGGU	207	ACCTITAT T TTCTGAGC	619
1492	AGCUCAGA CUGAUGAG X CGAA AAUAAAGG	208	CCTTTATT T TCTGAGCT	620
1493	AAGCUCAG CUGAUGAG X CGAA AAAUAAAG	209	CTTFAFFT T CTGAGCTT	621
1494	AAAGCUCA CUGAUGAG X CGAA AAAAUAAA	210	TTTATTTT C TGAGCTTF	622
1501	UUCCAACA CUGAUGAG X CGAA AGCUCAGA	211	TCTGAGCT T TGTTGGAA	623
1502	UUUCCAAC CUGAUGAG X CGAA AAGCUCAG	212	CTGAGCTF T GTTGGAAA	624
1505	UGUUUUCC CUGAUGAG X CGAA ACAAAGCU	213	AGCTTTGT T GGAAAACA	625
1518	AAUUCUGG CUGAUGAG X CGAA AUCAUGUU	214	AACATGAT A CCAGAATT	626
1526	GGCAAAUU CUGAUGAG X CGAA AUUCUGGU	215	ACCAGAAT T AATTTGCC	627
1527	UGGCAAAU CUGAUGAG X CGAA AAUUCUGG	216	CCAGAATT A ATTTGCCA	628
1530	AUGUGGCA CUGAUGAG X CGAA AUUAAUUC	217	GAATTAAT T TGCCACAT	629
1531	CAUGUGGC CUGAUGAG X CGAA AAUUAAUU	218	AATTAATT T GCCACATG	630
1541	AAACAGAC CUGAUGAG X CGAA ACAUGUGG	219.	CCACATGT T GTCTGTTT	631
1544	UUAAAACA CUGAUGAG X CGAA ACAACAUG	220	CATGTTGT C TGTTTTAA	632
1548	ACUGUUAA CUGAUGAG X CGAA ACAGACAA	221	TTGTCTGT T TTAACAGT	633
1549	CACUGUUA CUGAUGAG X CGAA AACAGACA	222	TGTCTGTT T TAACAGTG	634
1550	CCACUGUU CUGAUGAG X CGAA AAACAGAC	223	GTCTGTTT T AACAGTGG	635
1551	UCCACUGU CUGAUGAG X CGAA AAAACAGA	224	TCTGTTTT A ACAGTGGA	636
1567	AAAAGUAU CUGAUGAG X CGAA ACAUGGGU	225	ACCCATGT A ATACTTTT	637
1570	GAUAAAAG CUGAUGAG X CGAA AUUACAUG	226	CATGTAAT A CTTTTATC	638
1573	AUGGAUAA CUGAUGAG X CGAA AGUAUUAC	227	GTAATACT T TTATCCAT	639
1574	CAUGGAUA CUGAUGAG X CGAA AAGUAUUA	228	TAATACTT T TATCCATG	640
1575	ACAUGGAU CUGAUGAG X CGAA AAAGUAUU	229	AATACTIT T ATCCATGT	641
1576	AACAUGGA CUGAUGAG X CGAA AAAAGUAU	230	ATACTTTT A TCCATGTT	642

Table 9

1578	UAAACAUG CUGAUGAG X CGAA AUAAAAGU	231	ACTITIAT C CATGITTA	643
1584	CUUUUUUA CUGAUGAG X CGAA ACAUGGAU	232	ATCCATGT T TAAAAAAG	644
1585	UCUUUUUU CUGAUGAG X CGAA AACAUGGA	233	TCCATGTT T AAAAAAGA	645
1586	UUCUUUUU CUGAUGAG X CGAA AAACAUGG	234	CCATGTTT A AAAAAGAA	646
1600	UUUGUCCA CUGAUGAG X CGAA AUUCCUUC	235	GAAGGAAT T TGGACAAA	647
1601	CUUUGUCC CUGAUGAG X CGAA AAUUCCUU	236	AAGGAATT T GGACAAAG	648
1619	UUACAUUA CUGAUGAG X CGAA ACGGUUUG	237	CAAACCGT C TAATGTAA	549
1621	AAUUACAU CUGAUGAG X CGAA AGACGGUU	238	AACCGTCT A ATGTAATT	650
1626	UGGUUAAU CUGAUGAG X CGAA ACAUUAGA	239	TCTAATGT A ATTAACCA	651
1629	CGUUGGUU CUGAUGAG X CGAA AUUACAUU	240	AATGTAAT T AACCAACG	652
1630	UCGUUGGU CUGAUGAG X CGAA AAUUACAU	241	ATGTAATT A ACCAACGA	653
1646	AGUCCGGA CUGAUGAG X CGAA AGCUUUUU	242	AAAAAGCT T TCCGGACT	654
1647	AAGUCCGG CUGAUGAG X CGAA AAGCUUUU	243	AAAAGCTT T CCGGACTT	655
.1648	AAAGUCCG CUGAUGAG X CGAA AAAGCUUU	244	AAAGCTTT C CGGACTTT	656
1655	GCAUUUAA CUGAUGAG X CGAA AGUCCGGA	245	TCCGGACT T TTAAATGC	657
1656	AGCAUUUA CUGAUGAG X CGAA AAGUCCGG	246	CCGGACTT T TAAATGCT	658
1657	UAGCAUUU CUGAUGAG X CGAA AAAGUCCG	247	CGGACTTT T AAATGCTA	659
1658	UUAGCAUU CUGAUGAG X CGAA AAAAGUCC	248	GGACTTTT A AATGCTAA	660
1665	AAAACAGU CUGAUGAG X CGAA AGCAUUUA	249	TAAATGCT A ACTGTTTT	661
1671	AGGGGAAA CUGAUGAG X CGAA ACAGUUAG	250	CTAACTGT T TTTCCCCT	662
1672	AAGGGGAA CUGAUGAG X CGAA AACAGUUA	251	TAACTGTT T TTCCCCTT	663
1673	GAAGGGGA CUGAUGAG X CGAA AAACAGUU	252	AACTGTTT T TCCCCTTC	664
1674	GGAAGGGG CUGAUGAG X CGAA AAAACAGU	253	ACTGTTTT T CCCCTTCC	665
1675	AGGAAGGG CUGAUGAG X CGAA AAAAACAG	254	CTGTTTTT C CCCTTCCT	666
1680	UAGACAGG CUGAUGAG X CGAA AGGGGAAA	255	TTTCCCCT T CCTGTCTA	667
1681	CUAGACAG CUGAUGAG X CGAA AAGGGGAA	256	TTCCCCTT C CTGTCTAG	668
1686	UUUUCCUA CUGAUGAG X CGAA ACAGGAAG	257	CTTCCTGT C TAGGAAAA	669
1688	CAUUUUCC CUGAUGAG X CGAA AGACAGGA	258	TCCTGTCT A GGAAAATG	670
1699	GAGCUUUA CUGAUGAG X CGAA AGCAUUUU	259	AAAATGCT A TAAAGCTC	672
1701	UUGAGCUU CUGAUGAG X CGAA AUAGCAUU	260	AATGCTAT A AAGCTCAA	673
1707	ACUAAUUU CUGAUGAG X CGAA AGCUUUAU	261	ATAAAGCT C AAATTAGT	674
1712	UCCUAACU CUGAUGAG X CGAA AUUUGAGC	262	GCTCAAAT T AGTTAGGA CTCAAATT A GTTAGGAA	675
1713	UUCCUAAC CUGAUGAG X CGAA AAUUUGAG	263	AAATTAGT T AGGAATGA	676
1716	UCAUUCCU CUGAUGAG X CGAA ACUAAUUU	264	AATTAGTT A GGAATGAC	677
1717.	GUCAUUCC CUGAUGAG X CGAA AACUAAUU	265	GAATGACT T ATACGTTT	678
1727	AAACGUAU CUGAUGAG X CGAA AGUCAUUC	266	AATGACTT A TACGTTT	679
1728	AAAACGUA CUGAUGAG X CGAA AAGUCAUU	268	TGACTTAT A CGTTTTGT	680
1730	ACAAAACG CUGAUGAG X CGAA AUAAGUCA	269	TTATACGT T TTGTTTTG	681
1734	CAAAACAA CUGAUGAG X CGAA ACGUAUAA	270	TATACGIT T TGTTTTGA	682
1735	UCAAAACA CUGAUGAG X CGAA AACGUAUA	271	ATACGTTT T GTTTTGAA	683
1736	UUCAAAAC CUGAUGAG X CGAA AAACGUAU GUAUUCAA CUGAUGAG X CGAA ACAAAACG	272	CGTTTTGT T TTGAATAC	684
1739	GUAUUCA CUGAUGAG X CGAA ACAAAACG	273	GTTTTGTT T TGAATACC	685
1740	AGGUAUUC CUGAUGAG X CGAA AACAAAAC	274	TTTTGTTT T GAATACCT	686
1741	CUCUUAGG CUGAUGAG X CGAA AUUCAAAA	275	TTTTGAAT A CCTAAGAG	687
1746		275	GAATACCT A AGAGATAC	688
1750	GUAUCUCU CUGAUGAG X CGAA AGGUAUUC	277	TAAGAGAT A CTTTTTGG	689
1757	CCAAAAAG CUGAUGAG X CGAA AUCUCUUA	2//	IMMOMOMI A CITITIO	009

Table 9

	Table .	,		
1760	UAUCCAAA CUGAUGAG X CGAA AGUAUCUC	278	GAGATACT T TTTGGATA	690
1761	AUAUCCAA CUGAUGAG X CGAA AAGUAUCU	279	AGATACTT T TTGGATAT	691
1762	AAUAUCCA CUGAUGAG X CGAA AAAGUAUC	280	GATACTTT T TGGATATT	692
1763	AAAUAUCC CUGAUGAG X CGAA AAAAGUAU	281	ATACTTTT T GGATATTT	693
1768	AAUAUAAA CUGAUGAG X CGAA AUCCAAAA	282	TTTTGGAT A TTTATATT	694
1770	GCAAUAUA CUGAUGAG X CGAA AUAUCCAA	283	TTGGATAT T TATATTGC	699
1771	GGCAAUAU CUGAUGAG X CGAA AAUAUCCA	284	TGGATATT T ATATTGCC	696
1772	UGGCAAUA CUGAUGAG X CGAA AAAUAUCC	285	GGATATTT A TATTGCCA	69
1774	UAUGGCAA CUGAUGAG X CGAA AUAAAUAU	286	ATATTTAT A TTGCCATA	69
1776	AAUAUGGC CUGAUGAG X CGAA AUAUAAAU	287	ATTTATAT T GCCATATT	69
1782	AGUAAGAA CUGAUGAG X CGAA AUGGCAAU	288	ATTGCCAT A TTCTTACT	70
1784	CAAGUAAG CUGAUGAG X CGAA AUAUGGCA	289	TGCCATAT T CTTACTTG	70
1785	UCAAGUAA CUGAUGAG X CGAA AAUAUGGC	290	GCCATATT C TTACTTGA	70
1787	AUUCAAGU CUGAUGAG X CGAA AGAAUAUG	291	CATATTCT T ACTTGAAT	70
1788	CAUUCAAG CUGAUGAG X CGAA AAGAAUAU	292	ATATTCTT A CTTGAATG	70
1791	AAGCAUUC CUGAUGAG X CGAA AGUAAGAA	293	TTCTTACT T GAATGCTT	70
1799	GUCAUUCA CUGAUGAG X CGAA AGCAUUCA	294	TGAATGCT T TGAATGAC	70
1800	AGUCAUUC CUGAUGAG X CGAA AAGCAUUC	295	GAATGCTT T GAATGACT	70
1809	ACUGGAUG CUGAUGAG X CGAA AGUCAUUC	296	GAATGACT A CATCCAGT	70
1813	CAGAACUG CUGAUGAG X CGAA AUGUAGUC	297	GACTACAT C CAGTTCTG	70
1818	AGGUGCAG CUGAUGAG X CGAA ACUGGAUG	298	CATCCAGT T CTGCACCT	71
1819	UAGGUGCA CUGAUGAG X CGAA AACUGGAU	299	ATCCAGTT C TGCACCTA	71
1827	AGAGGGUA CUGAUGAG X CGAA AGGUGCAG	300	CTGCACCT A TACCCTCT	71
1829	CCAGAGGG CUGAUGAG X CGAA AUAGGUGC	301	GCACCTAT A CCCTCTGG	71
1834	CAACACCA CUGAUGAG X CGAA AGGGUAUA	302	TATACCCT C TGGTGTTG	71
1841	UAAAAAGC CUGAUGAG X CGAA ACACCAGA	303	TCTGGTGT T GCTTTTTA	71
1845	AGGUUAAA CUGAUGAG X CGAA AGCAACAC	304	GTGTTGCT T TTTAACCT	71
1846	AAGGUUAA CUGAUGAG X CGAA AAGCAACA	305	TGTTGCTT T TTAACCTT	71
1847	GAAGGUUA CUGAUGAG X CGAA AAAGCAAC	306	GTTGCTTT T TAACCTTC	71
1848	GGAAGGUU CUGAUGAG X CGAA AAAAGCAA	307	TTGCTTTT T AACCTTCC	71
1849	AGGAAGGU CUGAUGAG X CGAA AAAAAGCA	308	TGCTTTTT A ACCTTCCT	72
1854	AUUCCAGG CUGAUGAG X CGAA AGGUUAAA	309	TTTAACCT T CCTGGAAT	72
1855	GAUUCCAG CUGAUGAG X CGAA AAGGUUAA	310	TTAACCTT C CTGGAATC	72
1863	AGAAAAUG CUGAUGAG X CGAA AUUCCAGG	311	CCTGGAAT C CATTTTCT	72
1867	UUUUAGAA CUGAUGAG X CGAA AUGGAUUC	312	GAATCCAT T TTCTAAAA	72
1868	UUUUUAGA CUGAUGAG X CGAA AAUGGAUU	313	AATCCATT T TCTAAAAA	72
1869	INTERNITIAG CUGAUGAG X CGAA AAAUGGAU	314	ATCCATTT T CTAAAAAA	72
1870	AUUUUUUA CUGAUGAG X CGAA AAAAUGGA	315	TCCATTTT C TAAAAAAT	7:
1872	UUAUUUUU CUGAUGAG X CGAA AGAAAAUG	316	CATTITCT A AAAAATAA	72
1879	UGUGUCUU CUGAUGAG X CGAA AUUUUUUA	317	TAAAAAAT A AAGACACA	7:
1889	CUGAGAAG CUGAUGAG X CGAA AUGUGUCU	318	AGACACAT T CTTCTCAG	7
1890	GCUGAGAA CUGAUGAG X CGAA AAUGUGUC	319	GACACATT C TTCTCAGC	7:
1892	GUGCUGAG CUGAUGAG X CGAA AGAAUGUG	320	CACATTCT T CTCAGCAC	7:
1893	GGUGCUGA CUGAUGAG X CGAA AAGAAUGU	321	ACATTCTT C TCAGCACC	73
1895	GUGGUGCU CUGAUGAG X CGAA AGAAGAAU	322	ATTETTET C AGCACCAC	7:
1913	UUUUGGAA CUGAUGAG X CGAA AGGUGUUG	323	CAACACCT A TTCCAAAA	7:
1915	GAUUUUGG CUGAUGAG X CGAA AUAGGUGU	324	ACACCTAT T CCAAAATC	73
A 7 L 3	CHESSES COGNOGNO A COM. MONOGOGO	1		1

Table 9

1916	CGAUUUUG CUGAUGAG X CGAA AAUAGGUG	325	CACCTATT C CAAAATCG	737
1923	AUGUGGUC CUGAUGAG X CGAA AUUUUGGA	326	TCCAAAAT C GACCACAT	738
1932	CUUCCAAA CUGAUGAG X CGAA AUGUGGUC	327	GACCACAT A TTTGGAAG	739
1934	UACUUCCA CUGAUGAG X CGAA AUAUGUGG	328	CCACATAT T TGGAAGTA	740
1935	UUACUUCC CUGAUGAG X CGAA AAUAUGUG	329	CACATATT T GGAAGTAA	741
1942	GAGAGCUU CUGAUGAG X CGAA ACUUCCAA	330	TTGGAAGT A AAGCTCTC	742
1948	GCUGAGGA CUGAUGAG X CGAA AGCUUUAC	331	GTAAAGCT C TCCTCAGC	743
1950	UUGCUGAG CUGAUGAG X CGAA AGAGCUUU	332	AAAGCTCT C CTCAGCAA	744
1953	CAUUUGCU CUGAUGAG X CGAA AGGAGAGC	333	GCTCTCCT C AGCAAATG	745
1963	UGUUCUUU CUGAUGAG X CGAA ACAUUUGC	334	GCAAATGT A AAAGAACA	746
1977	UUUGUUAU CUGAUGAG X CGAA AUUUCUGU	335	ACAGAAAT T ATAACAAA	747
1978	GUUUGUUA CUGAUGAG X CGAA AAUUUCUG	336	CAGAAATT A TAACAAAC	748
1980	CAGUUUGU CUGAUGAG X CGAA AUAAUUUC	337	GAAATTAT A ACAAACTG	749
1990	GUCUGAGA CUGAUGAG X CGAA ACAGUUUG	338	CAAACTGT C TCTCAGAC	750
1992	UGGUCUGA CUGAUGAG X CGAA AGACAGUU	339 ′	AACTGTCT C TCAGACCA	751
1994	UGUGGUCU CUGAUGAG X CGAA AGAGACAG	340	CTGTCTCT C AGACCACA	752
2005	UJUGGUUA CUGAUGAG X CGAA ACUGUGGU	341	ACCACAGI A TAACCAAA	753
2007	AGUUUGGU CUGAUGAG X CGAA AUACUGUG	342	CACAGTAT A ACCAAACT	754
2016	CUGAGUUC CUGAUGAG X CGAA AGUUUGGU	343	ACCAAACT A GAACTCAG	755
2022	UUAAUCCU CUGAUGAG X CGAA AGUUCUAG	344	CTAGAACT C AGGATTAA	756
2028	AGUUUCUU CUGAUGAG X CGAA AUCCUGAG	345	CTCAGGAT T AAGAAACT	757
2029	GAGUUUCU CUGAUGAG X CGAA AAUCCUGA	346	TCAGGATT A AGAAACTC	758
2037	UUUUGAGU CUGAUGAG X CGAA AGUUUCUU	347	AAGAAACT C ACTCAAAA	759
2041	GUGGUUUU CUGAUGAG X CGAA AGUGAGUU	348	AACTCACT C AAAACCAC	760
2056	UUUCCAUG CUGAUGAG X CGAA AGUUGUGU	349	ACACAACT A CATGGAAA	761
2079	UCAUUCAG CUGAUGAG X CGAA AGCAGGUU	350	AACCTGCT C CTGAATGA	762
2090	GUAUCCAG CUGAUGAG X CGAA AGUCAUUC	351	GAATGACT A CTGGATAC	763
2097	UUGUUAUG CUGAUGAG X CGAA AUCCAGUA	352	TACTGGAT A CATAACAA	764
2101	CAUUUUGU CUGAUGAG X CGAA AUGUAUCC	353	GGATACAT A ACAAAATG	765
2121	AACAUCUU CUGAUGAG X CGAA AUUUCUGC	354	GCAGAAAT A AAGATGTT	766 767
2129	UUUUAAAG CUGAUGAG X CGAA ACAUCUUU	355	AAAGATGT T CTTTAAAA	768
2130	GUUUUAAA CUGAUGAG X CGAA AACAUCUU	356	AAGATGTT C TTTAAAAC	769
2132	UGGUUUUA CUGAUGAG X CGAA AGAACAUC	357 358	GATGTTCT T TAAAACCA	770
2133	UUGGUUUU CUGAUGAG X CGAA AAGAACAU		TGTTCTT A AAACCAAT	771
2134	AUUGGUUU CUGAUGAG X CGAA AAAGAACA GAITICIGG CUGAUGAG X CGAA AUGUUGUG	359	CACAACAT A CCAGAATC	772
2162			ACCAGAAT C TCTGGGAC	773
2170	GUCCCAGA CUGAUGAG X CGAA AUUCUGGU	361	CAGAATCT C TGGGACAC	774
2172	GUGUCCCA CUGAUGAG X CGAA AGAUUCUG	363	GGACACAT T CAAAGCAG	775
2183	CUGCUUUG CUGAUGAG X CGAA AUGUGUCC ACUGCUUU CUGAUGAG X CGAA AAUGUGUC	363	GACACATT C AAAGCAGT	776
2184	UUUCCCUC CUGAUGAG X CGAA ACACACUG	365	CAGTGTGT A GAGGGAAA	777
2197	GUGCUAUA CUGAUGAG X CGAA ACACACOG	366	AGGGAAAT T TATAGCAC	778
	AGUGCUAU CUGAUGAG X CGAA AAUUUCCC	367	GGGAAATT T ATAGCACT	779
2208	UAGUGCUA CUGAUGAG X CGAA AAAUUUCC	368	GGAAATTT A TAGCACTA	780
2209	UUUAGUGC CUGAUGAG X CGAA AAADUUCC	369	AAATTTAT A GCACTAAA	781
2211	HOGGCAUU CUGAUGAG X CGAA AGUGCUAU	370	ATAGCACT A AATGCCCA	782
2217	AUTITUAGA CUGAUGAG X CGAA AUUUCCUG	370	CAGGAAAT A TCTAAAAT	783
2244	AUUUUAGA CUGAUGAG X CGAA AUUUCCUG	3/1	CACCIMANT A TOTANOMI	, 63

Table 9

2246	CAAUUUUA CUGAUGAG X CGAA AUAUUUCC	372	GGAAATAT C TAAAATTG	784
2248	GUCAAUUU CUGAUGAG X CGAA AGAUAUUU	373	AAATATCT A AAATTGAC	785
2253	AGGGUGUC CUGAUGAG X CGAA AUUUUAGA	374	TCTAAAAT T GACACCCT	786
2262	UGUGAUGU CUGAUGAG X CGAA AGGGUGUC	375	GACACCCT A ACATCACA	787
2267	UUAAUUGU CUGAUGAG X CGAA AUGUUAGG	376	CCTAACAT C ACAATTAA	788
2273	GUUCUUUU CUGAUGAG X CGAA AUUGUGAU	377	ATCACAAT T AAAAGAAC	789
2274	AGUUCUUU CUGAUGAG X CGAA AAUUGUGA	378	TCACAATT A AAAGAACT	790
2283	UGCUUCUC CUGAUGAG X CGAA AGUUCUUU	379	AAAGAACT A GAGAAGCA	791
2305	AGCUUUUC CUGAUGAG X CGAA AUGUGUUU	380	AAACACAT T GAAAAGCT	792
2314	CCUUCUCU CUGAUGAG X CGAA AGCUUUUC	381	GAAAAGCT A AGAGAAGG	793
2331	AUCUUAGU CUGAUGAG X CGAA AUUUCUUG	382	CAAGAAAT A ACTAAGAT	794
2335	UCUGAUCU CUGAUGAG X CGAA AGUUAUUU	383	AAATAACT A AGATCAGA	795
2340	UCUGCUCU CUGAUGAG X CGAA AUCUUAGU	384	ACTAAGAT C AGAGCAGA	796
2361	UGUGUCUC CUGAUGAG X CGAA AUUUCCUU	385	AAGGAAAT A GAGACACA	797
2377	UUUUUGAA CUGAUGAG X CGAA AGUUUUUU	386	AAAAAACT C TTCAAAAA	798
2379	AUUUUUUG CUGAUGAG X CGAA AGAGUUUU	387	AAAACTCT T CAAAAAAT	799
2380	GAUUUUUU CUGAUGAG X CGAA AAGAGUUU	388	AAACTCTT C AAAAAATC	800
2388	GAUUCAUU CUGAUGAG X CGAA AUUUUUUUG	389	CAAAAAAT C AATGAATC	801
2396	AGCUCCUG CUGAUGAG X CGAA AUUCAUUG	390	CAATGAAT C CAGGAGCT	802
2408	UUUCAAAA CUGAUGAG X CGAA ACCAGCUC	391	GAGCTGGT T TTTTGAAA	803
2409	GUUUCAAA CUGAUGAG X CGAA AACCAGCU	392	AGCTGGTT T TTTGAAAC	804
2410	CGUUUCAA CUGAUGAG X CGAA AAACCAGC	393	GCTGGTTT T TTGAAACG	805
2411	UCGUUUCA CUGAUGAG X CGAA AAAACCAG	394	CTGGTTTT T TGAAACGA	806
2412	AUCGUUUC CUGAUGAG X CGAA AAAAACCA	395	TGGTTTTT T GAAACGAT	807
2421	AUUUUGUU CUGAUGAG X CGAA AUCGUUUC	396	GAAACGAT C AACAAAAT	808
2430	UGUCUAUC CUGAUGAG X CGAA AUUUUGUU	397	AACAAAAT T GATAGACA	809
2434	CUAGUGUC CUGAUGAG X CGAA AUCAAUUU	398	AAATTGAT A GACACTAG	810
2441	AGUCUUGC CUGAUGAG X CGAA AGUGUCUA	399	TAGACACT A GCAAGACT	811
2450	. UUCUUUAU CUGAUGAG X CGAA AGUCUUGC	400	GCAAGACT A ATAAAGAA	812
2453	UUCUUCUU CUGAUGAG X CGAA AUUAGUCU	401	AGACTAAT A AAGAAGAA	813
2475	UUCUAUUU CUGAUGAG X CGAA AUUCUUCU	402	AGAAGAAT C AAATAGAA	814
2480	AUUGCUUC CUGAUGAG X CGAA AUUUGAUU	403	AATCAAAT A GAAGCAAT	815
2489	UCAUUUUU CUGAUGAG X CGAA AUUGCUUC	404	GAAGCAAT A AAAAATGA	816
2499	AUCCCCUU CUGAUGAG X CGAA AUCAUUUU	405	AAAATGAT A AAGGGGAT	817
2508	GGUGGUGA CUGAUGAG X CGAA AUCCCCUU	406	AAGGGGAT A TCACCACC	818
2510	UUGGUGGU CUGAUGAG X CGAA AUAUCCCC	407	GGGGATAT C ACCACCAA	819
2520	UUCUGUGG CUGAUGAG X CGAA AUUGGUGG	408	CCACCAAT C CCACAGAA	820
2531	UGGUGGUU CUGAUGAG X CGAA AUUUCUGU	409	ACAGAAAT A AACCACCA	821
2541	UAUUCUCU CUGAUGAG X CGAA AUGGUGGU	410	ACCACCAT C AGAGAATA	822
2549	GUUUGUAG CUGAUGAG X CGAA AUUCUCUG	411	CAGAGAAT A CTACAAAC	823
2552	GGUGUUUG CUGAUGAG X CGAA AGUAUUCU	412	AGAATACT A CAAACACC	824

Input Sequence = HSU29607. Cut Site = UH/.

Stem Length = 8. Core Sequence = CUGAUGAG X CGAA (X = GCCGUUAGGC or other stem II)

Seq1 = HSU29607 (Human methionine aminopeptidase mRNA, complete cds., 2569 bp)

Table 10

Table 10: Human methionine aminopeptidase type 2 (MetAP-2) NCH Ribozyme and Target Sequence

Nt. position	Ribozyme Sequence	Seq. ID Nos.	Substrate Sequence	Seq. ID Nos.
10	CCCGAGAG CUGAUGAG X CGAA IACGAGGG	825	CCCTCGTC T CTCTCGGG	1255
12	UGCCCGAG CUGAUGAG X CGAA IAGACGAG	826	CTCGTCTC T CTCGGGCA	1256
14	GUUGCCCG CUGAUGAG X CGAA IAGAGACG	827	CGTCTCTC T CGGGCAAC	1257
20	CGCCAUGU CUGAUGAG X CGAA ICCCGAGA	828	TCTCGGGC A ACATGGCG	1258
23	GCCCGCCA CUGAUGAG X CGAA IUUGCCCG	829	CGGGCAAC A TGGCGGGC	1259
49	CUCCCGGA CUGAUGAG X CGAA ICCGCUAC	830	GTAGCGGC C TCCGGGAG	1260
50	GCUCCCGG CUGAUGAG X CGAA IGCCGCUA	831	TAGCGGCC T CCGGGAGC	1261
52	UGGCUCCC CUGAUGAG X CGAA IAGGCCGC	832	GCGGCCTC C GGGAGCCA	1262
59	AUUCAGGU CUGAUGAG X CGAA ICUCCOGG	833	CCGGGAGC C ACCTGAAT	1263
60	CAUUCAGG CUGAUGAG X CGAA IGCUCCCG	834	CGGGAGCC A CCTGAATG	1264
62	GCCAUUCA CUGAUGAG X CGAA IUGGCUCC	835	GGAGCCAC C TGAATGGC	1265
63	CGCCAUUC CUGAUGAG X CGAA IGUGGCUC	836	GAGCCACC T GAATGGCG	1266
74	UGGAUCCA CUGAUGAG X CGAA IUCGCCAU	837	ATGGCGAC C TGGATCCA	1267
75	CUGGAUCC CUGAUGAG X CGAA IGUCGCCA	838	TGGCGACC T GGATCCAG	1268
81	UGUCGUCU CUGAUGAG X CGAA IAUCCAGG	839	CCTGGATC C AGACGACA	1269
82	CUGUCGUC CUGAUGAG X CGAA IGAUCCAG	840	CTGGATCC A GACGACAG	1270
89	UUCUUCCC CUGAUGAG X CGAA IUCGUCUG	841	CAGACGAC A GGGAAGAA	1271
103	GUAGAGGC CUGAUGAG X CGAA ICUCCUUC	842	GAAGGAGC T GCCTCTAC	1272
106	GCCGUAGA CUGAUGAG X CGAA ICAGCUCC	843	GGAGCTGC C TCTACGGC	1273
107	AGCCGUAG CUGAUGAG X CGAA IGCAGCUC	844	GAGCTGCC T CTACGGCT	1274
109	UCAGCCGU CUGAUGAG X CGAA IAGGCAGC	845	GCTGCCTC T ACGGCTGA	1275
115	GCUUCCUC CUGAUGAG X CGAA ICCGUAGA	846	TCTACGGC T GAGGAAGC	1276
124	UUCUUGGC CUGAUGAG X CGAA ICUUCCUC	847	GAGGAAGC A GCCAAGAA	1277
127	UUUUUCUU CUGAUGAG X CGAA ICUGCUUC	848	GAAGCAGC C AAGAAAAA	1278
128	UUUUUUCU CUGAUGAG X CGAA IGCUGCUU	849	AAGCAGCC A AGAAAAA	1279
158	AGGCCCUU CUGAUGAG X CGAA ICUCUUCU	850	AGAAGAGC A AAGGGCCT	1280
165	CUGCAGAA CUGAUGAG X CGAA ICCCUUUG	851	CAAAGGC C TTCTGCAG	1281
166	GCUGCAGA CUGAUGAG X CGAA IGCCCUUU	852	AAAGGGCC T TCTGCAGC	1282
169	CCUGCUGC CUGAUGAG X CGAA IAAGGCCC	853	GGGCCTTC T GCAGCAGG	1283
172	UCCCCUGC CUGAUGAG X CGAA ICAGAAGG	854	CCTTCTGC A GCAGGGGA	1284
175	UGUUCCCC CUGAUGAG X CGAA ICUGCAGA	855	TCTGCAGC A GGGGAACA	1285
183	CAGGUUCC CUGAUGAG X CGAA IUUCCCCU	856	AGGGGAAC A GGAACCTG	1286
189	CUUUAUCA CUGAUGAG X CGAA IUUCCUGU	857	ACAGGAAC C TGATAAAG	1287
190	UCUUUAUC CUGAUGAG X CGAA IGUUCCUG	858	CAGGAACC T GATAAAGA	1288
202	GAGGCUCC CUGAUGAG X CGAA IAUUCUUU	859	AAAGAATC A GGAGCCTC	1289
208	UCCACUGA CUGAUGAG X CGAA ICUCCUGA	860	TCAGGAGC C TCAGTGGA	1290
209	AUCCACUG CUGAUGAG X CGAA IGCUCCUG	861	CAGGAGCC T CAGTGGAT	1291
211	UCAUCCAC CUGAUGAG X CGAA IAGGCUCC	862	GGAGCCTC A GTGGATGA	1292
226	AACUGUCU CUGAUGAG X CGAA ICUACUUC	863	GAAGTAGC A AGACAGTT	1293
231	UUUCCAAC CUGAUGAG X CGAA IUCUUGCU	864	AGCAAGAC A GTTGGAAA	1294
244	UCCAAUGC CUGAUGAG X CGAA IAUCUUUC	865	GAAAGATC A GCATTGGA	1295
247	UCUUCCAA CUGAUGAG X CGAA ICUGAUCU	866	AGATCAGC A TTGGAAGA	1296

Table 10

307	UUUCCAGU CUGAUGAG X CGAA ICUCCAUC			
310	UUCUUUCC CUGAUGAG X CGAA ICUCCAUC	867	GATGGAGC A ACTGGAAA	1297
348	GAACUUUU CUGAUGAG X CGAA IUCCUCUC	868	GGAGCAAC T GGAAAGAA	1298
349	UGAACUUU CUGAUGAG X CGAA TUCCUCUC	869	GAGAGGAC C AAAAGTTC	1299
357	GGUCUGUU CUGAUGAG X CGAA IAACUUUU	870	AGAGGACC A AAAGTTCA	1300
361	GGAGGGUC CUGAUGAG X CGAA IAACUUUU GGAGGGUC CUGAUGAG X CGAA IUUUGAAC	871	AAAAGTTC A AACAGACC	1301
365	UGAGGGAG CUGAUGAG X CGAA IUCUGUUU	872	GTTCAAAC A GACCCTCC	1302
366	CUGAGGGA CUGAUGAG X CGAA IUCUGUUU	873	AAACAGAC C CTCCCTCA	1303
367		874	AACAGACC C TCCCTCAG	1304
369	ACUGAGGG CUGAUGAG X CGAA IGGUCUGU GAACUGAG CUGAUGAG X CGAA IAGGGUCU	875	ACAGACCC T CCCTCAGT	1305
370	GGAACUGA CUGAUGAG X CGAA IAGGGUCU	876	AGACCCTC C CTCAGTTC	1306
371	UGGAACUG CUGAUGAG X CGAA IGAGGGUC	877	GACCCTCC C TCAGTTCC	1307
373	AUUGGAAC CUGAUGAG X CGAA IAGGGAGG	878	ACCCTCCC T CAGTTCCA	1308
378	CACAUAUU CUGAUGAG X CGAA IAACUGAG	879	CCTCCCTC A GTTCCAAT	1309
379	UCACAUAU CUGAUGAG X CGAA IAACUGAG	880	CTCAGTTC C AATATGTG	1310
389	AGGAUACA CUGAUGAG X CGAA IUCACAUA	881	TCAGTTCC A ATATGTGA	1311
390	UAGGAUAC CUGAUGAG X CGAA IGUCACAU	882	TATGTGAC C TGTATCCT	1312
396	CACCAUUA CUGAUGAG X CGAA IAUACAGG	883	ATGTGACC T GTATCCTA	1313
397	ACACCAUU CUGAUGAG X CGAA IAUACAG	884	CCTGTATC C TAATGGTG	1314
411	GUCCUUUG CUGAUGAG X CGAA IAAAUACA	885	CTGTATCC T AATGGTGT	1315
412	UGUCCUUU CUGAUGAG X CGAA IGAAAUAC	886	TGTATTTC C CAAAGGAC	1316
413	UUGUCCUU CUGAUGAG X CGAA IGGAAAUA	887	GTATTTCC C AAAGGACA	1317
420	CGCAUUCU CUGAUGAG X CGAA IUCCUJUG	888	TATTTCCC A AAGGACAA	1318
434	UGUGGGUG CUGAUGAG X CGAA IUAUUCGC	889	CAAAGGAC A AGAATGCG	1319
435	GUGUGGGU CUGAUGAG X CGAA IGUAUUCG	890	GCGAATAC C CACCCACA	1320
436	UGUGUGGG CUGAUGAG X CGAA IGUAUUC	891	CGAATACC C ACCCACAC	1321
438	CUUGUGUG CUGAUGAG X CGAA IUGGGUAU	892	GAATACCC A CCCACACA	1322
439	UCUUGUGU CUGAUGAG X CGAA IGUGGGUA	893	ATACCCAC C CACACAAG	1323
440	AUCUUGUG CUGAUGAG X CGAA IGGUGGGU	894	TACCCACC C ACACAAGA	1324
442	CCAUCUUG CUGAUGAG X CGAA IUGGGUGG	895	ACCCACCC A CACAAGAT	1325
444	GCCCAUCU CUGAUGAG X CGAA IUGUGGGU	896	CCACCCAC A CAAGATGG	1326
457	CAAGCAGC CUGAUGAG X CGAA IUUCGCCC	898	ACCCACAC A AGATGGGC	1327
460	CUCCAAGC CUGAUGAG X CGAA ICUGUUCG	899	GGGCGAAC A GCTGCTTG	1328
463	GUUCUCCA CUGAUGAG X CGAA ICAGCUGU	900	CGAACAGC T GCTTGGAG	1329
472	UCACUUGU CUGAUGAG X CGAA IUUCUCCA	900	ACAGCTGC T TGGAGAAC	1330
475	UCUUCACU CUGAUGAG X CGAA IUAGUUCU	902	TGGAGAAC T ACAAGTGA AGAACTAC A AGTGAAGA	1331
493	UGAUCUAA CUGAUGAG X CGAA ICUUUCUU	903		1332
501	CACUUGCC CUGAUGAG X CGAA IAUCUAAU	904	AAGAAAGC A TTAGATCA	1333
505	UCUUCACU CUGAUGAG X CGAA ICCUGAUC	905	ATTAGATC A GGCAAGTG	1334
538	GCUUCUGC CUGAUGAG X CGAA ICUUCUCG	906	GATCAGGC A AGTGAAGA	1335
541	UGUGCUUC CUGAUGAG X CGAA ICAGCUUC	907	CGAGAAGC T GCAGAAGC	1336
547	UGUCGAUG CUGAUGAG X CGAA ICUUCUGC	908	GAAGCTGC A GAAGCACA	1337
549	CUUGUCGA CUGAUGAG X CGAA IUGCUUCU	909	GCAGAAGC A CATCGACA	1338
555	UUCUAACU CUGAUGAG X CGAA IUCGAUGU	910	AGAAGCAC A TCGACAAG	1339
578	CUUGAUCC CUGAUGAG X CGAA ICUCAUUA	911	ACATCGAC A AGTTAGAA	1340
584	CCCAGGCU CUGAUGAG X CGAA IAUCCAGC	911	TAATGAGC T GGATCAAG	1341
588	UCAUCCCA CUGAUGAG X CGAA ICUUGAUC	912	GCTGGATC A AGCCTGGG	1342
	X COAN ICHOGAUC	913	GATCAAGC C TGGGATGA	1343

Table 10

589	GUCAUCCC CUGAUGAG X CGAA IGCUUGAU	914	ATCAAGCC T GGGATGAC	1344
598	UCUAUCAU CUGAUGAG X CGAA IUCAUCCC	915	GGGATGAC A ATGATAGA	1345
611	CUUUUCAC CUGAUGAG X CGAA IAUUUCUA	916	TAGAAATC T GTGAAAAG	1346
629	GCGUGAAC CUGAUGAG X CGAA IUCUUCCA	917	TGGAAGAC T GTTCACGC	1347
634	AACUUGCG CUGAUGAG X CGAA IAACAGUC	918	GACTGTTC A CGCAAGTT	1348
638	UAUUAACU CUGAUGAG X CGAA ICGUGAAC	919	GTTCACGC A AGTTAATA	1349
667	GCCAGGCC CUGAUGAG X CGAA ICAUUUAA	920	TTAAATGC A GGCCTGGC	1350
671	AAAUGCCA CUGAUGAG X CGAA ICCUGCAU	921	ATGCAGGC C TGGCATTT	1351
672	GAAAUGCC CUGAUGAG X CGAA IGCCUGCA	922	TGCAGGCC T GGCATTTC	1352
676	GUAGGAAA CUGAUGAG X CGAA ICCAGGCC	923	GGCCTGGC A TTTCCTAC	1353
681	AUCCAGUA CUGAUGAG X CGAA IAAAUGCC	924	GGCATTTC C TACTGGAT	1354
682	CAUCCAGU CUGAUGAG X CGAA IGAAAUGC	925	GCATTTCC T ACTGGATG	1355
685	GAACAUCC CUGAUGAG X CGAA IUAGGAAA	926	TTTCCTAC T GGATGTTC	1356
694	UUAUUGAG CUGAUGAG X CGAA IAACAUCC	927	GGATGTTC T CTCAATAA	1357
696	AAUUAUUG CUGAUGAG X CGAA IAGAACAU	928	ATGTTCTC T CAATAATT	1358
698	ACAAUUAU CUGAUGAG X CGAA IAGAGAAC	929	GTTCTCTC A ATAATTGT	1359
709	UAAUGGGC CUGAUGAG X CGAA ICACAAUU	930	AATTGTGC T GCCCATTA	1360
712	GUAUAAUG CUGAUGAG X CGAA ICAGCACA	931	TGTGCTGC C CATTATAC	1361
713	AGUAUAAU CUGAUGAG X CGAA IGCAGCAC	932	GTGCTGCC C ATTATACT	1362
714	GAGUAUAA CUGAUGAG X CGAA IGGCAGCA	933	TGCTGCCC A TTATACTC	1363
721	GCAUUGGG CUGAUGAG X CGAA IUAUAAUG	934	CATTATAC T CCCAATGC	1364
723	CGGCAUUG CUGAUGAG X CGAA IAGUAUAA	935	TTATACTC C CAATGCCG	1365
724	CCGGCAUU CUGAUGAG X CGAA IGAGUAUA	936	TATACTCC C AATGCCGG	1366
725	ACCGGCAU CUGAUGAG X CGAA IGGAGUAU	937	ATACTCCC A ATGCCGGT	1367
730	GUGUCACC CUGAUGAG X CGAA ICAUUGGG	938	CCCAATGC C GGTGACAC	1368
737	UACUGUUG CUGAUGAG X CGAA IUCACCGG	939	CCGGTGAC A CAACAGTA	1369
739	AAUACUGU CUGAUGAG X CGAA IUGUCACC	940	GGTGACAC A ACAGTATT	1370
742	UGUAAUAC CUGAUGAG X CGAA IUUGUGUC	941	GACACAAC A GTATTACA	1371
750	CAUCAUAC CUGAUGAG X CGAA IUAAUACU	942	AGTATTAC A GTATGATG	1372
761	UUUACAGA CUGAUGAG X CGAA IUCAUCAU	943	ATGATGAC A TCTGTAAA	1373
764	UAUUUUAC CUGAUGAG X CGAA IAUGUCAU	944	ATGACATC T GTAAAATA	1374
776	UGUUCCAA CUGAUGAG X CGAA IUCUAUUU	945	AAATAGAC T TTGGAACA	1375
784	CUUAUAUG CUGAUGAG X CGAA IUUCCAAA	946	TTTGGAAC A CATATAAG	1376
786	CACUUAUA CUGAUGAG X CGAA IUGUUCCA	947	TGGAACAC A TATAAGTG	1377
809	AAAAGCAC CUGAUGAG X CGAA IUCAAUAA	948	TTATTGAC T GTGCTTTT	1378
814	ACAGUAAA CUGAUGAG X CGAA ICACAGUC	949	GACTGTGC T TTTACTGT	1379
820	AAAGUGAC CUGAUGAG X CGAA IUAAAAGC	950	GCTTTTAC T GTCACTTT	1380
824	AUUAAAAG CUGAUGAG X CGAA IACAGUAA	951	TTACTGTC A CTTTTAAT	1381
826	GGAUUAAA CUGAUGAG X CGAA IUGACAGU	952	ACTGTCAC T TTTAATCC	1382
834	CAUAUUUG CUGAUGAG X CGAA IAUUAAAA	953	TTTTAATC C CAAATATG	1383
835	UCAUAUUU CUGAUGAG X CGAA IGAUUAAA	954	TTTAATCC C AAATATGA	1384
836	AUCAUAUU CUGAUGAG X CGAA IGGAUUAA	955	TTAATCCC A AATATGAT	1385
859	UCUUUUAC CUGAUGAG X CGAA ICUUUUAA	956	TTAAAAGC T GTAAAAGA	1386
871	GUGUUAGU CUGAUGAG X CGAA ICAUCUUU	957	AAAGATGC T ACTAACAC	1387
874	CCAGUGUU CUGAUGAG X CGAA IUAGCAUC	958	GATGCTAC T AACACTGG	1388
878	UAUUCCAG CUGAUGAG X CGAA IUUAGUAG	959	CTACTAAC A CTGGAATA	1389
088	UUUAUUCC CUGAUGAG X CGAA IUGUUAGU	960	ACTAACAC T GGAATAAA	1390

Table 10

895	UCAAUUCC CUGAUGAG X CGAA ICACACUU	961	AAGTGTGC T GGAATTGA	1391
912	CAUCACAC CUGAUGAG X CGAA IACGAACA	962	TGTTCGTC T GTGTGATG	1392
931	UCUUGGAU CUGAUGAG X CGAA ICCUCACC	963	GGTGAGGC C ATCCAAGA	1393
932	UUCUUGGA CUGAUGAG X CGAA IGCCUCAC	964	GTGAGGCC A TCCAAGAA	1394
935	AACUUCUU CUGAUGAG X CGAA IAUGGCCU	965	AGGCCATC C AAGAAGTT	1395
936	UAACUUCU CUGAUGAG X CGAA IGAUGGCC	966	GGCCATCC A AGAAGTTA	1396
952	ACUUCAUA CUGAUGAG X CGAA IACUCCAU	967	ATGGAGTC C TATGAAGT	1397
953	AACUUCAU CUGAUGAG X CGAA IGACUCCA	968	TGGAGTCC T ATGAAGTT	1398
979	ACUUGAUA CUGAUGAG X CGAA IUCUUCCC	969	GGGAAGAC A TATCAAGT	1399
984	GUUUCACU CUGAUGAG X CGAA IAUAUGUC	970	GACATATC A AGTGAAAC	1400
993	UACGGAUU CUGAUGAG X CGAA IUUUCACU	971	AGTGAAAC C AATCCGTA	1401
994	UUACGGAU CUGAUGAG X CGAA IGUUUCAC	972	GTGAAACC A ATCCGTAA	1402
998	UAGAUUAC CUGAUGAG X CGAA IAUUGGUU	973	AACCAATC C GTAATCTA	1403
1005	GUCCAUUU CUGAUGAG X CGAA IAUUACGG	974	CCGTAATC T AAATGGAC	1404
1014	CAAUUGAA CUGAUGAG X CGAA IUCCAUUU	975	AAATGGAC A TTCAATTG	1405
1018	UGCCCAAU CUGAUGAG X CGAA IAAUGUCC	976	GGACATTC A ATTGGGCA	1406
1026	UUCUAUAU CUGAUGAG X CGAA ICCCAAUU	977	AATTGGGC A ATATAGAA	1407
1038	UUCCAGCA CUGAUGAG X CGAA IUAUUCUA	978	TAGAATAC A TGCTGGAA	1408
1042	GUUUUUCC CUGAUGAG X CGAA ICAUGUAU	979	ATACATGC T GGAAAAAC	1409
1051	AUCGGCAC CUGAUGAG X CGAA IUUUUUCC	980	GGAAAAAC A GTGCCGAT	1410
1056	UCACAAUC CUGAUGAG X CGAA ICACUGUU	981	AACAGTGC C GATTGTGA	1411
1078	AUUCUUGU CUGAUGAG X CGAA ICCUCCCC	982	GGGGAGGC A ACAAGAAT	1412
1081	UCCAUUCU CUGAUGAG X CGAA IUUGCCUC	983	GAGGCAAC A AGAATGGA	1413
1108	GUUUCAAU CUGAUGAG X CGAA ICAUAUAC	984	GTATATGC A ATTGAAAC	1414
1117	CUACCAAA CUGAUGAG X CGAA IUUUCAAU	985	ATTGAAAC C TTTGGTAG	1415
1118	ACUACCAA CUGAUGAG X CGAA IGUUUCAA	986	TTGAAACC T TTGGTAGT	1416
1129	CCUUUUCC CUGAUGAG X CGAA IUACUACC	987	GGTAGTAC A GGAAAAGG	1417
1146	UAUCAUCA CUGAUGAG X CGAA IAACAACA	988	TGTTGTTC A TGATGATA	1418
1165	AUGUAAUG CUGAUGAG X CGAA IAACAUUC	989	GAATGTTC A CATTACAT	1419
1167	UCAUGUAA CUGAUGAG X CGAA IUGAACAU	990	ATGTTCAC A TTACATGA	1420
1172	AUUUUUCA CUGAUGAG X CGAA IUAAUGUG	991	CACATTAC A TGAAAAAT	1421
1194	UUGGCACA CUGAUGAG X CGAA IUCCAACA	992	TGTTGGAC A TGTGCCAA	1422
1200	GCCUUAUU CUGAUGAG X CGAA ICACAUGU	993	ACATGTGC C AATAAGGC	1423
1201	AGCCUUAU CUGAUGAG X CGAA IGCACAUG	994	CATGTGCC A ATAAGGCT	1424
1209	UUCUUGGA CUGAUGAG X CGAA ICCUUAUU	995	AATAAGGC T TCCAAGAA	1425
1212	UUGUUCUU CUGAUGAG X CGAA IAAGCCUU	996	AAGGCTTC C AAGAACAA	1426
1213	UUUGUUCU CUGAUGAG X CGAA IGAAGCCU	997	AGGCTTCC A AGAACAAA	1427
1219	AAGUGUUU CUGAUGAG X CGAA TUUCUUGG	998	CCAAGAAC A AAACACTT	1428
1224	UUAACAAG CUGAUGAG X CGAA IUUUUGUU	999	AACAAAAC A CTTGTTAA	1429
1226	AUUUAACA CUGAUGAG X CGAA IUGUUUUG	1000	CAAAACAC T TGTTAAAT	1430
1238	UUCAUUGA CUGAUGAG X CGAA IACAUUUA	1001	TAAATGTC A TCAATGAA	1431
1241	GUUUUCAU CUGAUGAG X CGAA IAUGACAU	1002	ATGTCATC A ATGAAAAC	1432
1250	GGUUCCAA CUGAUGAG X CGAA IUUUUCAU	1003	ATGAAAAC T TTGGAACC	1433
1258	AAGGCAAG CUGAUGAG X CGAA IUUCCAAA	1004	TTTGGAAC C CTTGCCTT	1434
1259	GAAGGCAA CUGAUGAG X CGAA IGUUCCAA	1005	TTGGAACC C TTGCCTTC	1435
1260	AGAAGGCA CUGAUGAG X CGAA IGGUUCCA	1006	TGGAACCC T TGCCTTCT	1436
1264	CGGCAGAA CUGAUGAG X CGAA ICAAGGGU	1007	ACCUTTGC C TTCTGCCG	1437

Table 10

1265	GCGGCAGA CUGAUGAG X CGAA IGCAAGGG	1008	CCCTTGCC T TCTGCCGC	1438
1268	UCUGCGGC CUGAUGAG X CGAA IAAGGCAA	1009	TTGCCTTC T GCCGCAGA	1439
1271	CCAUCUGC CUGAUGAG X CGAA ICAGAAGG	1010	CCTTCTGC C GCAGATGG	1440
1274	CAGCCAUC CUGAUGAG X CGAA ICGGCAGA	1011	TCTGCCGC A GATGGCTG	1441
1281	AGCGAUCC CUGAUGAG X CGAA ICCAUCUG	1012	CAGATGGC T GGATCGCT	1442
1289	UUCUCCCA CUGAUGAG X CGAA ICGAUCCA	1013	TGGATCGC T TGGGAGAA	1443
1307	AGCCAUCA CUGAUGAG X CGAA IUAUUUAC	1014	GTAAATAC T TGATGGCT	1444
1315	UUCUUCAG CUGAUGAG X CGAA ICCAUCAA	1015	TTGATGGC T CTGAAGAA	1445
1317	GAUUCUUC CUGAUGAG X CGAA IAGCCAUC	1016	GATGGCTC T GAAGAATC	1446
1326	AGUCACAC CUGAUGAG X CGAA IAUUCUUC	1017	GAAGAATC T GTGTGACT	1447
1334	AAUGCCCA CUGAUGAG X CGAA IUCACACA	1018	TGTGTGAC T TGGGCATT	1448
1340	AUCUACAA CUGAUGAG X CGAA ICCCAAGU	1019	ACTTGGGC A TTGTAGAT	1449
1350	GUGGAUAU CUGAUGAG X CGAA IAUCUACA	1020	TGTAGATC C ATATCCAC	1450
1351	GGUGGAUA CUGAUGAG X CGAA IGAUCUAC	1021	GTAGATCC A TATCCACC	1451
1356	AUAAUGGU CUGAUGAG X CGAA IAUAUGGA	1022	TCCATATC C ACCATTAT	1452
1357	CAUAAUGG CUGAUGAG X CGAA IGAUAUGG	1023	CCATATCC A CCATTATG	1453
1359	CACAUAAU CUGAUGAG X CGAA IUGGAUAU	1024	ATATCCAC C ATTATGTG	1454
1360	UCACAUAA CUGAUGAG X CGAA IGUGGAUA	1025	TATCCACC A TTATGTGA	1455
1370	UCCUJUAA CUGAUGAG X CGAA IUCACAUA	1026	TATGTGAC A TTAAAGGA	1456
1381	GCUGUAUA CUGAUGAG X CGAA IAUCCUUU	1027	AAAGGATC A TATACAGC	1457
1387	AAUUGCGC CUGAUGAG X CGAA IUAUAUGA	1028	TCATATAC A GCGCAATT	1458
1392	GUUCAAAU CUGAUGAG X CGAA ICGCUGUA	1029	TACAGCGC A ATTTGAAC	1459
1401	GGAUGGUA CUGAUGAG X CGAA IUUCAAAU	1030	ATTTGAAC A TACCATCC	1460
1405	AACAGGAU CUGAUGAG X CGAA IUAUGUUC	1031	GAACATAC C ATCCTGTT	1461
1406	CAACAGGA CUGAUGAG X CGAA IGUAUGUU	1032	AACATACC A TCCTGTTG	1462
1409	ACGCAACA CUGAUGAG X CGAA IAUGGUAU	1033	ATACCATC C TGTTGCGT	1463
1410	GACGCAAC CUGAUGAG X CGAA IGAUGGUA	1034	TACCATCC T GTTGCGTC	1464
1419	UACAUGUU CUGAUGAG X CGAA IACGCAAC	1035	GTTGCGTC C AACATGTA	1465
1420	UUACAUGU CUGAUGAG X CGAA IGACGCAA	1036	TTGCGTCC A ACATGTAA	1466
1423	UCUUUACA CUGAUGAG X CGAA IUUGGACG	1037	CGTCCAAC A TGTAAAGA	1467
1439	UCCUCUGC CUGAUGAG X CGAA IACAACUU	1038	AAGTTGTC A GCAGAGGA	1468
1442	AUCUCCUC CUGAUGAG X CGAA ICUGACAA	1039	TTGTCAGC A GAGGAGAT	1469
1454	AGUUUAAU CUGAUGAG X CGAA IUCAUCUC	1040	GAGATGAC T ATTAAACT	1470
1462	UUGGACUA CUGAUGAG X CGAA IUUUAAUA	1041	TATTAAAC T TAGTCCAA	1471
1468	GUGGCUUU CUGAUGAG X CGAA IACUAAGU	1042	ACTTAGTC C AAAGCCAC	1472
1469	GGUGGCUU CUGAUGAG X CGAA IGACUAAG	1043	CTTAGTCC A AAGCCACC	1473
1474	GUUGAGGU CUGAUGAG X CGAA ICUUUGGA	1044	TCCAAAGC C ACCTCAAC	1474
1475	UGUUGAGG CUGAUGAG X CGAA IGCUUUGG	1045	CCAAAGCC A CCTCAACA	1475
1477	GGUGUUGA CUGAUGAG X CGAA IUGGCUUU	1046	AAAGCCAC C TCAACACC	1476
1478	AGGUGUUG CUGAUGAG X CGAA IGUGGCUU	1047	AAGCCACC T CAACACCT	1477
1480	AAAGGUGU CUGAUGAG X CGAA IAGGUGGC	1048	GCCACCTC A ACACCTTT	1478
1483	AAUAAAGG CUGAUGAG X CGAA IUUGAGGU	1049	ACCTCAAC A CCTTTATT	1479
1485	AAAAUAAA CUGAUGAG X CGAA IUGUUGAG	1050	CTCAACAC C TTTATTTT	1480
1486	GAAAAUAA CUGAUGAG X CGAA IGUGUUGA	1051	TCAACACC T TTATTTTC	1481
1495	CAAAGCUC CUGAUGAG X CGAA IAAAAUAA	1052	TTATTTTC T GAGCTTTG	1482
1500	UCCAACAA CUGAUGAG X CGAA ICUCAGAA	1053	TTCTGAGC T TTGTTGGA	1483
1513	UGGUAUCA CUGAUGAG X CGAA IUUUUCCA	1054	TGGAAAAC A TGATACCA	1484
1			1	

Table 10

1520	UUAAUUCU CUGAUGAG X CGAA IUAUCAUG	1055	CATGATAC C AGAATTAA	1485
1521	AUUAAUUC CUGAUGAG X CGAA IGUAUCAU	1056	ATGATACC A GAATTAAT	1486
1534	CAACAUGU CUGAUGAG X CGAA ICAAAUUA	1057	TAATTTGC C ACATGTTG	1487
1535	ACAACAUG CUGAUGAG X CGAA IGCAAAUU	1058	AATTTGCC A CATGTTGT	1488
1537	AGACAACA CUGAUGAG X CGAA IUGGCAAA	1059	TTTGCCAC A TGTTGTCT	1489
1545	GUUAAAAC CUGAUGAG X CGAA IACAACAU	1060	ATGTTGTC T GTTTTAAC	1490
1554	GGGUCCAC CUGAUGAG X CGAA IUUAAAAC	1061	GTTTTAAC A GTGGACCC	1491
1561	AUUACAUG CUGAUGAG X CGAA IUCCACUG	1062	CAGTGGAC C CATGTAAT	1492
1562	UAUUACAU CUGAUGAG X CGAA IGUCCACU	1063	AGTGGACC C ATGTAATA	1493
1563	GUAUUACA CUGAUGAG X CGAA IGGUCCAC	1064	GTGGACCC A TGTAATAC	1494
1572	UGGAUAAA CUGAUGAG X CGAA IUAUUACA	1065	TGTAATAC T TTTATCCA	1495
1579	UUAAACAU CUGAUGAG X CGAA IAUAAAAG	1066	CTTTTATC C ATGTTTAA	1496
1580	UUUAAACA CUGAUGAG X CGAA IGAUAAAA	1067	TTTTATCC A TGTTTAAA	1497
1606	UUUGCCUU CUGAUGAG X CGAA IUCCAAAU	1068	ATTTGGAC A AAGGCAAA	1498
1612	AGACGGUU CUGAUGAG X CGAA ICCUUUGU	1069	ACAAAGGC A AACCGTCT	1499
1616	CAUUAGAC CUGAUGAG X CGAA IUUUGCCU	1070	AGGCAAAC C GTCTAATG	1500
1620	AUUACAUU CUGAUGAG X CGAA IACGGUUU	1071	AAACCGTC T AATGTAAT	1501
1633	UUUUCGUU CUGAUGAG X CGAA IUUAAUUA	1072	TAATTAAC C AACGAAAA	1502
1634	UUUUUCGU CUGAUGAG X CGAA IGUUAAUU	1073	AATTAACC A ACGAAAAA	1503
1645	GUCCGGAA CUGAUGAG X CGAA ICUUUUUC	1074	GAAAAAGC T TTCCGGAC	1504
1649	AAAAGUCC CUGAUGAG X CGAA IAAAGCUU	1075	AAGCTTTC C GGACTTTT	1505
1654	CAUUUAAA CUGAUGAG X CGAA IUCCGGAA	1076	TTCCGGAC T TTTAAATG	1506
1664	AAACAGUU CUGAUGAG X CGAA ICAUUUAA	1077	TTAAATGC T AACTGTTT	1507
1668	GGAAAAAC CUGAUGAG X CGAA IUUAGCAU	1078	ATGCTAAC T GTTTTTCC	1508
1676	CAGGAAGG CUGAUGAG X CGAA IAAAAACA	1079	TGTTTTC C CCTTCCTG	1509
1677	ACAGGAAG CUGAUGAG X CGAA IGAAAAAC	1080	GTTTTCC C CTTCCTGT	1510
1678	GACAGGAA CUGAUGAG X CGAA IGGAAAAA	1081	TTTTTCCC C TTCCTGTC	1511
1679	AGACAGGA CUGAUGAG X CGAA IGGGAAAA	1082	TTTTCCCC T TCCTGTCT	1512
1682	CCUAGACA CUGAUGAG X CGAA IAAGGGGA	1083	TCCCCTTC C TGTCTAGG	1513
1683	UCCUAGAC CUGAUGAG X CGAA IGAAGGGG	1084	CCCCTTCC T GTCTAGGA	1514
1687	AUUUUCCU CUGAUGAG X CGAA IACAGGAA	1085	TTCCTGTC T AGGAAAAT	1515
1698	AGCUUUAU CUGAUGAG X CGAA ICAUUUUC	1086	GAAAATGC T ATAAAGCT	1516
1706	CUAAUUUG CUGAUGAG X CGAA ICUUUAUA	1087	TATAAAGC T CAAATTAG	1517
1708	AACUAAUU CUGAUGAG X CGAA IAGCUUUA	1088	TAAAGCTC A AATTAGTT	1518
1726	AACGUAUA CUGAUGAG X CGAA IUCAUUCC	1089	GGAATGAC T TATACGTT	1519
1748	AUCUCUUA CUGAUGAG X CGAA IUAUUCAA	1090	TTGAATAC C TAAGAGAT	1520
1749	UAUCUCUU CUGAUGAG X CGAA IGUAUUCA	1091	TGAATACC T AAGAGATA	1521
1759	AUCCAAAA CUGAUGAG X CGAA IUAUCUCU	1092	AGAGATAC T TTTTGGAT	1522
1779	AAGAAUAU CUGAUGAG X CGAA ICAAUAUA	1093	TATATTGC C ATATTCTT	1523
1780	UAAGAAUA CUGAUGAG X CGAA IGCAAUAU	1094	ATATTGCC A TATTCTTA	1524
1786	UUCAAGUA CUGAUGAG X CGAA IAAUAUGG	1095	CCATATTC T TACTTGAA	1525
1790	AGCAUUCA CUGAUGAG X CGAA IUAAGAAU	1096	ATTCTTAC T TGAATGCT	1526
1798	UCAUUCAA CUGAUGAG X CGAA ICAUUCAA	1097	TTGAATGC T TTGAATGA	1527
1808	CUGGAUGU CUGAUGAG X CGAA IUCAUUCA	1098	TGAATGAC T ACATCCAG	1528
1811	GAACUGGA CUGAUGAG X CGAA IUAGUCAU	1099	ATGACTAC A TCCAGTTC	1529
1814	GCAGAACU CUGAUGAG X CGAA IAUGUAGU	1100	ACTACATC C AGTTCTGC	1530
1815	UGCAGAAC CUGAUGAG X CGAA IGAUGUAG	1101	CTACATCC A GTTCTGCA	1531

Table 10

1820	AUAGGUGC CUGAUGAG X CGAA IAACUGGA	1102	TCCAGTTC T GCACCTAT	1532
1823	GGUAUAGG CUGAUGAG X CGAA ICAGAACU	1103	AGTTCTGC A CCTATACC	1533
1825	AGGGUAUA CUGAUGAG X CGAA IUGCAGAA	1104	TTCTGCAC C TATACCCT	1534
1826	GAGGGUAU CUGAUGAG X CGAA IGUGCAGA	1105	TCTGCACC T ATACCCTC	1535
1831	CACCAGAG CUGAUGAG X CGAA IUAUAGGU	1106	ACCTATAC C CTCTGGTG	1536
1832	ACACCAGA CUGAUGAG X CGAA IGUAUAGG	1107	CCTATACC C TCTGGTGT	1537
1833	AACACCAG CUGAUGAG X CGAA IGGUAUAG	1108	CTATACCC T CTGGTGTT	1538
1835	GCAACACC CUGAUGAG X CGAA IAGGGUAU	1109	ATACCCTC T GGTGTTGC	1539
1844	GGUUAAAA CUGAUGAG X CGAA ICAACACC	1110	GGTGTTGC T TTTTAACC	1540
1852	UCCAGGAA CUGAUGAG X CGAA IUUAAAAA	1111	TTTTTAAC C TTCCTGGA	1541
1853	UUCCAGGA CUGAUGAG X CGAA IGUUAAAA	1112	TTTTAACC T TCCTGGAA	1542
1856	GGAUUCCA CUGAUGAG X CGAA IAAGGUUA	1113	TAACCTTC C TGGAATCC	1543
1857	UGGAUUCC CUGAUGAG X CGAA IGAAGGUU	1114	AACCTTCC T GGAATCCA	1544
1864	UAGAAAAU CUGAUGAG X CGAA IAUUCCAG	1115	CTGGAATC C ATTTTCTA	1545
1865	UUAGAAAA CUGAUGAG X CGAA IGAUUCCA	1116	TGGAATCC A TTTTCTAA	1546
1871	UAUUUUUU CUGAUGAG X CGAA IAAAAUGG	1117	CCATTTTC T AAAAAATA	1547
1885	GAAGAAUG CUGAUGAG X CGAA IUCUUUAU	1118	ATAAAGAC A CATTCTTC	1548
1887	GAGAAGAA CUGAUGAG X CGAA IUGUCUUU	1119	AAAGACAC A TTCTTCTC	1549
1891	UGCUGAGA CUGAUGAG X CGAA IAAUGUGU	1120	ACACATTC T TCTCAGCA	1550
1894	UGGUGCUG CUGAUGAG X CGAA IAAGAAUG	1121	CATTCTTC T CAGCACCA	1551
1896	UGUGGUGC CUGAUGAG X CGAA IAGAAGAA	1122	TTCTTCTC A GCACCACA	1552
1899	UUGUGUGG CUGAUGAG X CGAA ICUGAGAA	1123	TTCTCAGC A CCACACAA	1553
1901	UGUUGUGU CUGAUGAG X CGAA IUGCUGAG	1124	CTCAGCAC C ACACAACA	1554
1902	GUGUUGUG CUGAUGAG X CGAA IGUGCUGA	1125	TCAGCACC A CACAACAC	1555
1904	AGGUGUUG CUGAUGAG X CGAA IUGUGUGU AUAGGUGU CUGAUGAG X CGAA IUGUGGUG	1126	AGCACCAC A CAACACCT CACCACAC A ACACCTAT	1556
1909	GGAAUAGG CUGAUGAG X CGAA IUUGUGUG	1127	CACACAC A ACACCTAT	1558
1911	UUGGAAUA CUGAUGAG X CGAA IUGUUGUG	1129	CACACAC C TATTCCAA	1559
1912	UUUGGAAU CUGAUGAG X CGAA IGUGUUGU	1130	ACAACACC T ATTCCAAA	1560
1917	UCGAUUUU CUGAUGAG X CGAA IAAUAGGU	1131	ACCTATTC C AAAATCGA	1561
1918	GUCGAUUU CUGAUGAG X CGAA IGAAUAGG	1132	CCTATTCC A AAATCGAC	1562
1927	AAAUAUGU CUGAUGAG X CGAA IUCGAUUU	1133	AAATCGAC C ACATATTT	1563
1928	CAAAUAUG CUGAUGAG X CGAA IGUCGAUU	1134	AATCGACC A CATATITG	1564
1930	UCCAAAUA CUGAUGAG X CGAA IUGGUCGA	1135	TCGACCAC A TATTTGGA	1565
1947	CUGAGGAG CUGAUGAG X CGAA ICUUUACU	1136	AGTAAAGC T CTCCTCAG	1566
1949	UGCUGAGG CUGAUGAG X CGAA IAGCUUUA	1137	TAAAGCTC T CCTCAGCA	1567
1951	UUUGCUGA CUGAUGAG X CGAA IAGAGCUU	1138	AAGCTCTC C TCAGCAAA	1568
1952	AUUUGCUG CUGAUGAG X CGAA IGAGAGCU	1139	AGCTCTCC T CAGCAAAT	1569
1954	ACAUUUGC CUGAUGAG X CGAA IAGGAGAG	1140	CTCTCCTC A GCAAATGT	1570
1957	UUUACAUU CUGAUGAG X CGAA ICUGAGGA	1141	TCCTCAGC A AATGTAAA	1571
1971	AUAAUUUC CUGAUGAG X CGAA IUUCUUUU	1142	AAAAGAAC A GAAATTAT	1572
1983	AGACAGUU CUGAUGAG X CGAA IUUAUAAU	1143	ATTATAAC A AACTGTCT	1573
1987	UGAGAGAC CUGAUGAG X CGAA IUUUGUUA	1144	TAACAAAC T GTCTCTCA	1574
1991	GGUCUGAG CUGAUGAG X CGAA IACAGUUU	1145	AAACTGTC T CTCAGACC	1575
1993	GUGGUCUG CUGAUGAG X CGAA IAGACAGU	1146	ACTGTCTC T CAGACCAC	1576
1995	CUGUGGUC CUGAUGAG X CGAA IAGAGACA	1147	TGTCTCTC A GACCACAG	1577
1999	UAUACUGU CUGAUGAG X CGAA IUCUGAGA	1148	TCTCAGAC C ACAGTATA	1578

Table 10

2000	UUAUACUG CUGAUGAG X CGAA IGUCUGAG	1149	CTCAGACC A CAGTATAA	1579
2002	GGUUAUAC CUGAUGAG X CGAA IUGGUCUG	1150	CAGACCAC A GTATAACC	1580
2010	UCUAGUUU CUGAUGAG X CGAA IUUAUACU	1151	AGTATAAC C AAACTAGA	1581
2011	UUCUAGUU CUGAUGAG X CGAA IGUUAUAC	1152	GTATAACC A AACTAGAA	1582
2015	UGAGUUCU CUGAUGAG X CGAA IUUUGGUU	1153	AACCAAAC T AGAACTCA	1583
2021	UAAUCCUG CUGAUGAG X CGAA IUUCUAGU	1154	ACTAGAAC T CAGGATTA	1584
2023	CUUAAUCC CUGAUGAG X CGAA IAGUUCUA	1155	TAGAACTC A GGATTAAG	1585
2036	UUUGAGUG CUGAUGAG X CGAA IUUUCUUA	1156	TAAGAAAC T CACTCAAA	1586
2038	GUUUUGAG CUGAUGAG X CGAA IAGUUUCU	1157	AGAAACTC A CTCAAAAC	1587
2040	UGGUUUUG CUGAUGAG X CGAA IUGAGUUU	1158	AAACTCAC T CAAAACCA	1588
2042	UGUGGUUU CUGAUGAG X CGAA IAGUGAGU	1159	ACTCACTC A AAACCACA	1589
2047	AGUUGUGU CUGAUGAG X CGAA IUUUUGAG	1160	CTCAAAAC C ACACAACT	1590
2048	UAGUUGUG CUGAUGAG X CGAA IGUUUUGA	1161	TCAAAACC A CACAACTA	1591
2050	UGUAGUUG CUGAUGAG X CGAA IUGGUUUU	1162	AAAACCAC A CAACTACA	1592
2052	CAUGUAGU CUGAUGAG X CGAA IUGUGGUU	1163	AACCACAC A ACTACATG	1593
2055	UUCCAUGU CUGAUGAG X CGAA IUUGUGUG	1164	CACACAAC T ACATGGAA	1594
2058	AGUUUCCA CUGAUGAG X CGAA IUAGUUGU	1165	ACAACTAC A TGGAAACT	1595
2066	GGUUGUUC CUGAUGAG X CGAA IUUUCCAU	1166	ATGGAAAC T GAACAACC	1596
2071	GAGCAGGU CUGAUGAG X CGAA IUUCAGUU	1167	AACTGAAC A ACCTGCTC	1597
2074	CAGGAGCA CUGAUGAG X CGAA IUUGUUCA	1168	TGAACAAC C TGCTCCTG	1598
2075	UCAGGAGC CUGAUGAG X CGAA IGUUGUUC	1169	GAACAACC T GCTCCTGA	1599
2078	CAUUCAGG CUGAUGAG X CGAA ICAGGUUG	1170	CAACCTGC T CCTGAATG	1600
2080	GUCAUUCA CUGAUGAG X CGAA IAGCAGGU	1171	ACCTGCTC C TGAATGAC	1601
2081	AGUCAUUC CUGAUGAG X CGAA IGAGCAGG	1172	CCTGCTCC T GAATGACT	1602
2089	UAUCCAGU CUGAUGAG X CGAA IUCAUUCA	1173	TGAATGAC T ACTGGATA	1603
2092	AUGUAUCC CUGAUGAG X CGAA IUAGUCAU	1174	ATGACTAC T GGATACAT	1604
2099	UUUUGUUA CUGAUGAG X CGAA IUAUCCAG	1175	CTGGATAC A TAACAAAA	1605
2104	CUUCAUUU CUGAUGAG X CGAA IUUAUGUA	1176	TACATAAC A AAATGAAG	1606
2115	UUUAUUUC CUGAUGAG X CGAA ICCUUCAU	1177	ATGAAGGC A GAAATAAA	1607
2131	GGUUUUAA CUGAUGAG X CGAA IAACAUCU	1178	AGATGTTC T TTAAAACC	1608
2139	UUCUCAUU CUGAUGAG X CGAA IUUUUAAA	1179	TTTAAAAC C AATGAGAA	1610
2140	GUUCUCAU CUGAUGAG X CGAA IGUUUUAA	1180	TTAAAACC A ATGAGAAC	
2149	UGUGUCUU CUGAUGAG X CGAA IUUCUCAU	1181	ATGAGAAC A AAGACACA ACAAAGAC A CAACATAC	1611
2155	GUAUGUUG CUGAUGAG X CGAA IUCUUUGU	1182	AAAGACAC A ACATACCA	1613
2157	UGGUAUGU CUGAUGAG X CGAA IUGUCUUU	1183	GACACAAC A TACCAGAA	1614
2160	UUCUGGUA CUGAUGAG X CGAA IUUGUGUC	1184	CAACATAC C AGAATCTC	1615
2164	GAGAUUCU CUGAUGAG X CGAA IUAUGUUG AGAGAUUC CUGAUGAG X CGAA IGUAUGUU	1186	AACATACC A GAATCTCT	1616
2165	UGUCCCAG CUGAUGAG X CGAA IAUUCUGG	1187	CCAGAATC T CTGGGACA	1617
2171	UGUGUCCC CUGAUGAG X CGAA IAGAUUCU	1188	AGAATOTO T GGGACACA	1618
2173	UUUGAAUG CUGAUGAG X CGAA IUCCCAGA	1189	TCTGGGAC A CATTCAAA	1619
2179	GCUUUGAA CUGAUGAG X CGAA IUGUCCCA	1190	TGGGACAC A TTCAAAGC	1620
2181	CACUGCUU CUGAUGAG X CGAA IAGUGUGU	1191	ACACATTC A AAGCAGTG	1621
2190	CUACACAC CUGAUGAG X CGAA ICUUUGAA	1192	TTCAAAGC A GTGTGTAG	1622
2190	GCAUUJAG CUGAUGAG X CGAA ICUAUAAA	1193	TITATAGC A CTAAATGC	1623
2214	GGGCAUUU CUGAUGAG X CGAA IUGCUAUA	1194	TATAGCAC T AAATGCCC	1624
2216	CUCUUGUG CUGAUGAG X CGAA ICAUUUAG	1194	CTAAATGC C CACAAGAG	1625
2223	COCCORDO COGNOGNO V CONV ICHODONG	**33	CILIBRIOC C CHONINGHO	1

Table 10

2224	UCUCUUGU CUGAUGAG X CGAA IGCAUUUA	1196	TAAATGCC C ACAAGAGA	1626
2225	UUCUCUUG CUGAUGAG X CGAA IGGCAUUU	1197	AAATGCCC A CAAGAGAA	1627
2227	CUUUCUCU CUGAUGAG X CGAA IUGGGCAU	1198	ATGCCCAC A AGAGAAAG	1628
2237	AUAUUUCC CUGAUGAG X CGAA ICUUUCUC	1199	GAGAAAGC A GGAAATAT	1629
2247	UCAAUUUU CUGAUGAG X CGAA IAUAUUUC	1200	GAAATATC T AAAATTGA	1630
2257	UGUUAGGG CUGAUGAG X CGAA IUCAAUUU	1201	AAATTGAC A CCCTAACA	1631
2259	GAUGUUAG CUGAUGAG X CGAA IUGUCAAU	1202	ATTGACAC C CTAACATC	1632
2260	UGAUGUUA CUGAUGAG X CGAA IGUGUCAA	1203	TTGACACC C TAACATCA	1633
2261	GUGAUGUU CUGAUGAG X CGAA IGGUGUCA	1204	TGACACCC T AACATCAC	1634
2265	AAUUGUGA CUGAUGAG X CGAA IUUAGGGU	1205	ACCCTAAC A TCACAATT	1635
2268	UUUAAUUG CUGAUGAG X CGAA IAUGUUAG	1206	CTAACATC A CAATTAAA	1636
2270	CUUUUAAU CUGAUGAG X CGAA IUGAUGUU	1207	AACATCAC A ATTAAAAG	1637
2282	GCUUCUCU CUGAUGAG X CGAA IUUCUUUU	1208	AAAAGAAC T AGAGAAGC	1638
2291	UUUGCUCU CUGAUGAG X CGAA ICUUCUCU	1209	AGAGAAGC A AGAGCAAA	1639
2297	AAUGUGUU CUGAUGAG X CGAA ICUCUUGC	1210	GCAAGAGC A AACACATT	1640
2301	UUUCAAUG CUGAUGAG X CGAA IUUUGCUC	1211	GAGCAAAC A CATTGAAA	1641
2303	CUUUUCAA CUGAUGAG X CGAA IUGUUUGC	1212	GCAAACAC A TTGAAAAG	1642
2313	CUUCUCUU CUGAUGAG X CGAA ICUUUUCA	1213	TGAAAAGC T AAGAGAAG	1643
2324	UUAUUUCU CUGAUGAG X CGAA ICCUUCUC	1214	GAGAAGGC A AGAAATAA	1644
2334	CUGAUCUU CUGAUGAG X CGAA IUUAUUUC	1215	GAAATAAC T AAGATCAG	1645
2341	UUCUGCUC CUGAUGAG X CGAA IAUCUUAG	1216	CTAAGATC A GAGCAGAA	1646
2346	UUCAGUUC CUGAUGAG X CGAA 1CUCUGAU	1217	ATCAGAGC A GAACTGAA	1647
2351	UUUCCUUC CUGAUGAG X CGAA IUUCUGCU	1218	AGCAGAAC T GAAGGAAA	1648
2367	GUUUUUUG CUGAUGAG X CGAA IUCUCUAU	1219	ATAGAGAC A CAAAAAAC	1649
2369	GAGUUUUU CUGAUGAG X CGAA IUGUCUCU	1220	AGAGACAC A AAAAACTC	1650
2376	UUUUGAAG CUGAUGAG X CGAA IUUUUUUG	1221	CAAAAAAC T CTTCAAAA	1651
2378	UUUUUUGA CUGAUGAG X CGAA IAGUUUUU	1222	AAAAACTC T TCAAAAAA	1652
2381	UGAUUUUU CUGAUGAG X CGAA IAAGAGUU	1223	AACTCTTC A AAAAATCA	1653
2389	GGAUUCAU CUGAUGAG X CGAA IAUUUUUU	1224	AAAAAATC A ATGAATCC	1654
2397	CAGCUCCU CUGAUGAG X CGAA TAUUCAUU	1225	AATGAATC C AGGAGCTG	1655
2398	CCAGCUCC CUGAUGAG X CGAA IGAUUCAU	1226	ATGAATCC A GGAGCTGG	1656
2404	AAAAAACC CUGAUGAG X CGAA ICUCCUGG	1227	CCAGGAGC T GGTTTTTT	1657
2422	AAUUUUGU CUGAUGAG X CGAA IAUCGUUU	1228	AAACGATC A ACAAAATT	1658
2425	AUCAAUUU CUGAUGAG X CGAA IUUGAUCG	1229	CGATCAAC A AAATTGAT	1659
2438	CUUGCUAG CUGAUGAG X CGAA IUCUAUCA	1230	TGATAGAC A CTAGCAAG	1660
2440	GUCUUGCU CUGAUGAG X CGAA IUGUCUAU	1231	ATAGACAC T AGCAAGAC	1662
2444	AUUAGUCU CUGAUGAG X CGAA ICUAGUGU	1232	ACACTAGC A AGACTAAT AGCAAGAC T AATAAAGA	1663
2449	UCUUUAUU CUGAUGAG X CGAA IUCUUGCU	1233	GAAGAATC A AATAGAAG	1664
2476	CUUCUAUU CUGAUGAG X CGAA IAUUCUUC	1234	ATAGAAGC A ATAAAAA	1665
2486	UUUUUUAU CUGAUGAG X CGAA ICUUCUAU	1235	GGGATATC A CCACCAAT	1666
2511	AUUGGUGG CUGAUGAG X CGAA IAUAUCCC	1236	GATATCAC C ACCAATCC	1667
2513	GGAUUGGU CUGAUGAG X CGAA IUGAUAUC		ATATCACC A CCAATCC	1668
2514	GGGAUUGG CUGAUGAG X CGAA IGUGAUAU	1238	ATCACCAC C AATCCCAC	1669
2516	GUGGGAUU CUGAUGAG X CGAA IUGGUGAU	1239	TCACCACC A ATCCCACA	1670
2517	UGUGGGAU CUGAUGAG X CGAA IGUGGUGA	1240	CACCACT C CACAGAAA	1671
2521	UUUCUGUG CUGAUGAG X CGAA IAUUGGUG AUUUCUGU CUGAUGAG X CGAA IGAUUGGU	1241	ACCAATCC C ACAGAAAT	1672
2522	AUUUCUGU CUGAUGAG X CGAA IGAUUGGU	1242	ACCAMICC C ACAGAAAT	1 20.2

2523

UAUUUCUG CUGAUGAG X CGAA IGGAUUGG 2523 UAUUUCUG CUGAUGAG X CGAA IGGAUUGG 1243 2525 UUUAUUUC CUGAUGAG X CGAA IUGGGAUU 1244 CCAATCCC A CAGAAATA 1673 AATCCCAC A GAAATAAA

2535	CUGAUGGU CUGAUGAG X CGAA IUUUAUUU	1245	AAATAAAC C ACCATCAG	1675
2536	UCUGAUGG CUGAUGAG X CGAA IGUUUAUU	1246	AATAAACC A CCATCAGA	1676
2538	UCUCUGAU CUGAUGAG X CGAA IUGGUUUA	1247	TAAACCAC C ATCAGAGA	1677
2539	UUCUCUGA CUGAUGAG X CGAA IGUGGUUU	2248	AAACCACC A TCAGAGAA	1678
2542	GUAUUCUC CUGAUGAG X CGAA TAUGGUGG	1249	CCACCATC A GAGAATAC	1679
2551	GUGUUUGU CUGAUGAG X CGAA IUAUUCUC	1250	GAGAATAC T ACAAACAC	1680
2554	GAGGUGUU CUGAUGAG X CGAA IUAGUAUU	1251	AATACTAC A AACACCTC	1681
2558	CGUAGAGG CUGAUGAG X CGAA IUUUGUAG	1252	CTACAAAC A CCTCTACG	1682
2560	UGCGUAGA CUGAUGAG X CGAA IUGUUUGU	1253	ACAAACAC C TCTACGCA	1683
2561	UUGCGUAG CUGAUGAG X CGAA IGUGUUUG	1254	CAAACACC T CTACGCAA	1684

Input Sequence = HSU29607. Cut Site = CH/.	
Stem Length = 8. Core Sequence = CUGAUGAG X CGAA (X = GCCGUUAGGC or other stem II)	
Scq1 = HSU29607 (Human methionine aminopeptidase mRNA, complete eds., 2569 bp)	
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Table 11: Human Methionine Aminopeptidase type 2 (MetAP-2) G-cleaver Ribozyme and Target Sequence

Ž.	Substrate Sequence	Seq. ID	Ribozyme Sequence	Sed. ID Nos.
64	GGAGCCACCU G AAUGG	1685	CCAUU UGAUGGCAUGCACUAUGCGCG AGGUGGCUCC	1834
7.1	CCUGAAUGGC G ACCUG	1686	CAGGU UGAUGGCAUGCACUAUGCGCG GCCAUUCAGG	1835
98	GGAUCCAGAC G ACAGG	1687	CCUGU UGAUGGAUGCACUAUGCGCG GUCUGGAUCC	1836
104	AGAAGGAGCU G CCUCU	1688	AGAGG UGAUGGCAUGCACUAUGCGCG AGCUCCUUCU	1837
116	CUCUACGGCU G AGGAA	1689	UUCCU UGAUGGCAUGCACUAUGCGCG AGCCGUAGAG	1838
141	ABANAAGAC G AAAGA	1690	UCUUU UGAUGGCAUGCACUAUGCGCG GUCUUUUUUU	1839
170	AGGGCCUUCU G CAGCA	1691	UGCUG UGAUGGCAUGCACUAUGCGCG AGAAGGCCCU	1840
191	ACAGGAACCU G AUAAA	1692	UUUNAU UGAUGGCAUSCACUAUGCGCG AGGUUCCUGU	1841
218	CUCAGUGGAU G AAGUA	1693	UACUU UGAUGGCAUGCACUAUGCGCG AUCCACUGAG	1842
269	AGAAAGAGAU G AAGAU	1694	AUCUU UGAUGGCAUGCACUAUGCGCG AUCUCUUUCU	1843
275	AGAUGAAGAU G AUGAA	1695	UUCAU UGAUGGCAUGCACUAUGCGCG AUCUUCAUCU	1844
278	UGANGAUGAU G ANGAU	1696	AUCUU UGAUGGCAUGCACUAUGCGCG AUCAUCUUCA	1845
293	UGGAGAUGGC G AUGGA	1691	UCCAU UGAUGGCAUGCACUAUGCGCG GCCAUCUCCA	1846
384	GUUCCAAUAU G UGACC	1698	GGUCA UGAUGGCAUGCACUAUGCGCG AUAUUGGAAC	1847
386	UCCAAUAUGU G ACCUG	1699	CAGGU UGAUGGCAUGCACUAUGCGCG ACAUAUUGGA	1848
391	UNUGUGACCU G UNUCC	1700	GGAUA UGAUGGCAUGCACUAUGCGCG AGGUCACAUA.	1849
404	UCCURAUGGU G UNUUU	1701	AAAUA UGAUGGCAUGCACUAUGCGCG ACCAUUAGGA	1850
426	GGACAAGAAU G CGAAU	1702	AUUCG UGAUGGCAUGCACUAUGCGCG AUUCUUGUCC	1821
428	ACAAGAAUGC G AAUAC	1703	GUALU UGAUGICAUUGCACUAUGICGICG GCAUUCUUGU	1852
453	CAAGAUGGGC G AACAG	1704	CUGUU UGAUGGCAUGCACUAUGCGCG GCCCAUCUUG	1853
461	GCGAACAGCU G CUUGG	1705	CCAAG UGAUGGCAUGCACUAUGCGCG AGCUGUUCGC	1854
479	AACUACAAGU G AAGAA	1706	UUCUU UGAUGCAUGCACUAUGCGCG ACUUGUAGUU	1855
509	UCAGGCAAGU G AAGAG	1707	CUCUT UGAUGGCAUGCACUAUGCGCG ACUUGCCUGA	1856
524	GAUUUGGAAU G AUUUU	1708	AAAAU UGAUGGCAUGCACUAUGCGCG AUUCCAAAUC	1857
531	AAUGAUJUJUC G AGAAG	1709	CUIJCU UGAUGGCAUGCACUAUGCGCG GAAAAUCAUU	1858
539	UCGAGAAGCU G CAGAA	1710	UNCUG UGAUGGCAUGCACUAUGCGCG AGCUUCUCGA	1859
552	GAAGCACAUC G ACAAG	1711	CUUGU UGAUGGCAUGCACUAUGCGCG GAUGUGCUUC	1860
	Olione of the strong street	1712	CARCIT HEATIGGCAUGCACUAUGCGCG AUUACGUAUU	1861

595	AGCCUGGGAU G ACAAU	1713	AUDGU UGAUGGCAUGCACUAUGCGCG AUCCCAGGCU	1862
109	GGAUGACAAU G AUAGA	1714	UCUAU UGAUGGCAUGCACUAUGCGCG AUUGUCAUCC	1863
612	AUAGAAAUCU G UGAAA	5121.	UUUCA UGAUGGCAUGCACUAUGCGCG AGAUUUCUAU	1864
614	AGAAAUCUGU G AAAAG	1716	CUUTU UGAUGGCAUGCACUAUGCGCG ACAGAUTUCU	1865
630	UNGGAAGACU G UUCAC	1717	GUGAA UGAUGGCAUGCACUAUGCGCG AGUCUUCCAA	1866
636	GACUGUUCAC G CAAGU	1718	ACUUG UGAUGGCAUGCACUAUGCGCG GUGAACAGUC	1867
665	UGGAUUAAAU G CAGGC	1719	GCCUG UGAUGGCAUGCACUAUGCGCG AUUUAAUCCA	1868
069	CCUACUGGAU G UUCUC	1720	GAGAA UGAUGGCAUGCACUAUGCGCG AUCCAGUAGG	1869
705	CUCAAUAAUU G UGCUG	1721	CAGCA UGAUGGCAUGCACUAUGCGCG AAUUAUUGAG	1870
707	CAAUAAUUGU G CUGCC	1722	GGCAG UGAUGGCAUGCACUAUGCGCG ACAAUUAUUG	1811
710	UAAUUGUGCU G CCCAU	1723	AUGGG UGAUGGCAUGCACUAUGCGCG AGCACAAUUA	1872
728	UACUCCCAAU G CCGGU	1724	ACCGG UGAUGGCAUGCACUAUGCGCG AUUGGGAGUA	1873
734	CAAUGCCGGU G ACACA	1725	UGUGU UGAUGGCAUGCACUAUGCGCG ACCGGCAUUG	1874
755	AUUACAGUAU G AUGAC	1726	GUCAU UGAUGGCAUGCACUAUGCGCG AUACUGUAAU	1875
758	ACAGUAUGAU G ACAUC	1727	GAUGU UGAUGGCAUGCACUAUGCGCG AUCAUACUGU	1876
765	GAUGACAUCU G UAAAA	1728	UUUUA UGAUGGCAUGCACUAUGCGCG AGAUGUCAUC	1877
806	UAGGAUUAUU G ACUGU	1729	ACAGU UGAUGGCAUGCACUAUGCGCG AAUAAUCCUA	1878
810	AUUAUUGACU G UGCUU	1730	AAGCA UGAUGGCAUGCACUAUGCGCG AGUCAAUAAU	1879
812	UAUUGACUGU G CUUUU	1731	AAAAG UGAUGGCAUGCACUAUGCGCG ACAGUCAAUA	1880
821	UGCULUDACU G UCACU	1732	AGUGA UGAUGCAUGCACUAUGCGCG AGUAAAAGCA	1881
842	UCCCAAAUAU G AUACG	1733	CGUAU UGAUGGCAUGCACUAUGCGCG AUAUUUGGGA	1882
860	AUUAAAAGCU G UAAAA	1734	UUUUN UGAUGGCAUGCACUAUGCGCG AGCUUUUAAU	1883
869	UGUAAAAGAU G CUACU	1735	AGUAG UGAUGGCAUGCACUAUGCGCG AUCUUUUACA	1884
891	GGAAUAAAGU G UGCUG	1736	CAGCA UGAUGCCAUGCACUAUGCGCG ACUUUAUUCC	1885
893	AAUAAAGUGU G CUGGA	1737	UCCAG UGAUGGCAUGCACUAUGCGCG ACACUTUAUTU	1886
905	UGCUGGAAUU G AUGUU	1738	AACAU UGAUGGCAUGCACUAUGCGCG AAUUCCAGCA	1887
908	UGGAAUUGAU G UUCGU	1739	ACGAA UGAUGCAUGCACUAUGCGCG AUCAAUUCCA	1888
913	AUGUUCGUCU G UGUGA	1740	UCACA UGAUGICAUGCACUAUGCGCG AGACGAACAU	1889
915	GUUCGUCUGU G UGAUG	1741	CAUCA UGAUGGCAUGCACUAUGCGCG ACAGACGAAC	1890
917	uceucuanan a Auann	1742	AACAU UGAUGGCAUGCACUAUGCGCG ACACAGACGA	1831
920	UCUGUGUGAU G UUGGU	1743	ACCAA UGAUGGCAUGCACUAUGCGCG AUCACACAGA	1892

926	0.0000 0 000000	1744	GGCCU UGAUGGCAUGCACOAGGCGCG ACCAACAGCA	
926	GGAGUCCUAU G AAGUU	1745	AACUU UGAUGGCAUGCACUAUGCGCG AUAGGACUCC	1894
962	CUAUGAAGUU G AAAUA	1746	UAUUU UGAUGGCAUGCACUAUGGGCG AACUUCAUAG	1895
988	CAUAUCAAGU G AAACC	1747	GGUUU UGAUGGCAUGCACUAUGCGCG ACUUGAUAUG	1896
1040	UAGAAUACAU G CUGGA	1748	UCCAG UGAUGGCAUGCACUAUGCGCG AUGUAUUCUA	1897
1054	GARARCAGU G CCGAU	1749	AUCGG UGAUGGCAUGCACUAUGCGCG ACUGUUUUC	1898
1057	AAACAGUGCC G AUUGU	1750	ACAAU UGAUGGCAUGCACUAUGCGCG GGCACUGUUU	1899
1061	AGUGCCGAUU G UGAAA	1751	UUUCA UGAUGGCAUGCACUAUGCGCG AAUCGGCACU	1900
1063	UGCCGAUUGU G AAAGG	1752	CCUUU UGAUGGCAUGCACUAUGCGCG ACAAUCGGCA	1901
1106	AGAAGUAUAU G CAAUU	1753	AAUUG UGAUGGCAUGCACUAUGCGCG AUAUACUUCU	1902
1112	AUAUGCAAUU G AAACC	1754	GGUUU UGAUGGCAUGCACUAUGCGCG AAUUGCAUAU	1903
1139	AGGAAAGGU G UUGUU	1755	AACAA UGAUGGCAUGCACUAUGCGCG ACCUUUUCCU	1904
1142	AAAAGGUGUU G UUCAU	1756	AUGAA UGAUGCAUGCACUAUGCGCG AACACCUUUU	1905
1148	UGUUGUUCAU G AUGAU	1757	AUCAU UGAUGGCAUGCACUAUGCGCG AUGAACAACA	1906
1151	UGUUCAUGAU G AUAUG	1758	CAUAU UGAUGGCAUGCACUAUGCGCG AUCAUGAACA	1907
1161	GAUAUGGAAU G UUCAC	1759	GUGAA UGAUGGCAUGCACUAUGCGCG AUUCCAUAUC	1908
1174	CACAUUACAU G AAAAA	1760	UNUUU UGAUGGCAUGCACUAUGCGCG AUGUAAUGUG	1909
1184	GAAAAUUUU G AUGUU	1761	AACAU UGAUGGCAUGCACUAUGCGCG AAAAUUUUUC	1910
1187	AAAUUUGAU G UUGGA	1762	UCCAA UGAUGCCAUGCACUAUGCGCG AUCAAAAUUU	1911
1196	UGUUGGACAU G UGCCA	1763	UGGCA UGAUGGCAUGCACUAUGCGCG AUGUCCAACA	1912
1198	UNGGACAUGU G CCAAU	1764	AUUGG UGAUGGCAUGCACUAUGCGCG ACAUGUCCAA	1913
1228	CAAAACACUU G UUAAA	1765	UUUDA UGAUGGCAUGCACUAUGCGCG AAGUGUUUUG	1914
1235	CUUGUUAAAU G UCAUC	1766	GAUGA UGAUGGCAUGCACUAUGCGCG AUUUAACAAG	1915
1244	UGUCAUCAAU G AAAAC	1767	GUUUU UGAUGCCAUGCACUAUGCGCG AUUGAUGACA	1916
1262	UGGNACCCUU G CCUUC	1768	GAAGG UGAUGCAUGCACUAUGCGCG AAGGGUUCCA	1917
1269	CUUGCCUUCU G CCGCA	1769	UGCGG UGAUGGCAUGCACUAUGCGCG AGAAGGCAAG	1918
1272	GCCUUCUGCC G CAGAU	1770	AUCUG UGAUGGCAUGCACUAUGCGCG GGCAGAAGGC	1919
1287	UGGCUGGAUC G CUUGG	1771	CCAAG UGAUGGCAUGCACUAUGCGCG GAUCCAGCCA	1920
1309	GUANAUACUU G AUGGC	1772	GCCAU UGAUGGCAUGCACUAUGCGCG AAGUAUUUAC	1921
1318	UGAUGGCUCU G AAGAA	1773	UUCUU UGAUGGCAUGCACUAUGCGCG AGAGCCAUCA	1922
1337	ADDITION OF HOLICE	1774	TICACA UGAUGGCAUGCACUAUGCGCG AGAUUCUUCA	1923

GAAUCUGUGU G ACUUG CUUGGGCAUU G UAGAU CCACCAUUAU G UGACA	3776	Ollian School Sc	
NU G UGACA	0//7	CAAGO UGAOGCAOGCACOAOGCACA ACACACAGO	1925
AU G UGACA	1777	AUCUA UGAUGGCAUGCACUAUGCGCG AAUGCCCAAG	1926
	1778	UGUCA UGAUGGCAUGCACUAUGCGCG AUAAUGGUGG	1927
ACCAUDADED G ACAUD	1779	AAUGU UGAUGGCAUGCACUAUGCGCG ACAUAAUGGU	1928
CAUAUACAGC G CAAUU	1780	AAUUG UGAUGGCAUGCACUAUGGGCG GCUGUAUAUG	1929
AGCGCAAUUU G AACAU	1781	AUGUU UGAUGGCAUGCACUAUGCGCG AAAUUGCGCU	1930
AUACCAUCCU G UUGCG	1782	CGCAA UGAUGGCAUGCACUAUGCGCG AGGAUGGUAU	1931
CCAUCCUGUU G CGUCC	1783	GGACG UGAUGGCAUGCACUAUGCGCG AACAGGAUGG	1932
CGUCCAACAU G UNAAG	1784	CUUUA UGAUGGCAUGCACUAUGCGCG AUGUUGGACG	1933
UAAAGAAGUU G UCAGC	1785	GCUGA UGAUGGCAUGCACUAUGCGCG AACUUCUUUA	1934
CAGAGGAGAU G ACUAU	1786	AUAGU UGAUGGCAUGCACUAUGCGCG AUCUCCUCUG	1935
UUUAUUUUCU G AGCUU	1787	AAGCU UGAUGGCAUGCACUAUGCGCG AGAAAAUAAA	1936
UCUGAGCUUU G UUGGA	1788	UCCAA USAUGGCAUGCACUAUGCGCG AAAGCUCAGA	1937
UGGAAAACAU G AUACC	1789	GGUAU UGAUGGCAUGCACUAUGCGCG AUGUUTUCCA	1938
GAAUUAAUUU G CCACA	1790	UGUGG UGAUGGCAUGCACUAUGCGCG AAAUUAAUUC	1939
UNIGCCACAU G UUGUC	1791	GACAA UGAUGGCAUGCACUAUGCGCG AUGUGGCAAA	1940
GCCACAUGUU G UCUGU	1792	ACAGA UGAUGGCAUGCACUAUGCGCG AACAUGUGGC	1941
CAUGUIGUCU G UUUUA	1793	UNANA UGAUGGCAUGCACUAUGCGCG AGACMACAUG	1942
GUGGACCCAU G UAAUA	1794	UAUUA UGAUGGCAUGCACUAUGCGCG AUGGGUCCAC	1943
UUUUAUCCAU G UUUAA	1795	UDANA UGAUGGCAUGCACUAUGCGCG AUGGAUAAAA	.1944
ACCGUCUAAU G UAAUU	1796	AAUUA UGAUGGCAUGCACUAUGCGCG AUUAGACGGU	1945
AUUAACCAAC G AAAAA	1797	UUUUU UGAUGGCAUAUGCGCG GUUGGUUAAU	1946
ACTUTUDADAU G CUAAC	1798	GUUAG UGAUGGCAUGCACUAUGCGCG AUUUAAAAGU	1947
AAUGCUAACU G UUUUU	1799	AAAAA UGAUGGCAUGCACUAUGCGCG AGUUAGCAUU	1948
ucceduaca a ucuna	1800	CUAGA UGAUGGCAUGCACUAUGCGCG AGGAAGGGGA	1949
CUAGGAAAN G CUAUA	1801	DAUAG UGAUGGCAUGCACUAUGCGCG AUUUUCCUAG	1950
AGUUAGGAAU G ACUUA	1802	UNAGU UGAUGCAUGCACUAUGCGCG AUUCCUAACU	1951
UAUACGUUUU G UUUUG	1803	CAAAA UGAUGGCAUGCACUAUGCGCG AAAACGUAUA	1952
GUUUUGUUU G AAUAC	1804	GUAUU UGAUGGCAUGCACUAUGCGCG AAAACAAAAC	1953
UAUTUDAUAUU G CCAUA	1805	UAUGG UGAUGCAUGCACUAUGCGCG AAUAUAAAUA	1954

Input Sequence = HSU29607. Cut Site = YG/M or UG/U.
Stem Length = 5/10. Core Sequence = UGAUG GCAUGCACUAUGC GCG

	_	_	$\overline{}$	_	_	_	_	_					$\overline{}$	r-	Γ.				$\overline{}$	_		$\overline{}$	$\overline{}$				
1955	1956	1957	1958	1959	1960	1961	1962	1963	1961	5961	1966	1961	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982
GCAUU UGAUGGCAUGCACUAUGCGCG AAGUAAGAAU	CAAAG UGAUGGCAUGCACUAUGCGCG AUUCAAGUAA	UCAUU UGAUGGCAUGCACUAUGCGCG AAAGCAUUCA	GUAGU UGAUGCAUGCACUAUGCGCG AUUCAAAGCA	AGGUG UGAUGGCAUGCACUAUGCGCG AGAACUGGAU	AGCAA UGAUGGCAUGCACUAUGCGCG ACCAGAGGGU	AAAAG UGAUGGCAUGCACUAUGCGCG AACACCAGAG	GUGGU UGAUGGCAUGCACUAUGCGCG GAUUUUGGAA	UJUJUA UGAUGGCAUGCACUAUGCGCG AUUUGCUGAG	AGAGA UGAUGGCAUGAGGCGCG AGUUUGUUAU	UUGUU UGAUGGCAUGCACUAUGCGCG AGUUUCCAUG	AGGAG UGAUGGCAUGCACUAUGCGCG AGGUUGUUCA	UCAUU UGAUGGCAUGCACUAUGCGCG AGGAGCAGGU	GUAGU UGAUGGCAUGCACUAUGCGCG AUUCAGGAGC	GCCUU UGAUGGCAUGCACUAUGCGCG AUUUUGUUAU	AAGAA UGAUGGCAUGCACUAUGCGCG AUCUUUAUUU	GUUCU UGAUGGCAUGCACUAUGCCCG AUUGGUUUUA	CUACA UGAUGGCAUGCACUAUGCGCG ACUGCUUUGA	CUCUA UGAUGGCAUGCACUAUGCGCG ACACUGCUUU	GUGGG UGAUGGCAUGCACUAUGCGCG AUTUAGUGCU	GGUGU UGAUGGCAUDAUGCGCG AAUUUUAGAU	CUUUU UGAUGGCAUGCACUAUGCGCG AAUGUGUUUG	uccuu ugauggcaugcacuaugcgcg aguucugcuc	GGAUU UGAUGGCAUGCACUAUGCGCG AUUGAUJUUU	CGUUU UGAUGGCAUGCACUAUGCGCG AAAAAACCAG	UUGAU UGAUGGCAUGCACUAUGCGCG GUUUCAAAAA	UCUAU UGAUGGCAUGCACUAUGCGCG AAUUUUGUUG	UTUAL UGAUGGCAUGCACUAUGCGCG AUUUUUAUU
1806	1807	1808	1809	1810	1811	1812	1813	1814	1815	1816	1817	1818	1819	1820	1821	1822	1823	1824	1825	1826	1827	1828	1829	1830	1831	1832	1833
AUDCUUACUU G AAUGC	UNACUUGAAU G CUUUG	UGAAUGCUUU G AAUGA	UGCUUUGAAU G ACUAC	AUCCAGUUCU G CACCU	ACCCUCUGGU G UUGCU	cocoedadan e canaa	UUCCAAAUC G ACCAC	CUCAGCAAAU G UAAAA	AUAACAAACU G UCUCU	CAUGGAAACU G AACAA	UGAACAACCU G CUCCU	ACCUGCUCCU G AAUGA	GCUCCUGAAU G ACUAC	AUAACAAAAU G AAGGC	AAAUAAAGAU G UUCUU	UAAAACCAAU G AGAAC	UCAAAGCAGU G UGUAG	AAAGCAGUGU G UAGAG	AGCACUAANU G CCCAC	AUCUAAAAUU G ACACC	CAAACACAUU G AAAAG	GAGCAGAACU G AAGGA	ANAMAUCAAU G AAUCC	CUGGUUUUUU G AAACG	UUUUUGAAAC G AUCAA	CAACAAAUU G AUAGA	AAUAAAAAU G AUAAA
1792	1796	1801	1805	1821	1839	1842	1924	1961	1988	2067	2076	2082	2086	2109	2127	2143	2193	2195	2221	2254	2306	2352	2392	2413	2418	2431	2496

Table 11

Seq1 - NSUZ8607 (Numan mathlonina aminopeptidawa mAVA, complete cds., 2569 [bp]

PCT/US00/23998

Table 12
Table 12: Anti Human MetAP-2 HH, NCH, and G-Cleaver Ribozymes

Alias	Ribozyme Sequence	Seq. ID	Substrate Seq.	Seq. ID
		Nos.	141	Nos.
HH				
MAP2-11	CCCGAGA CUGAUGAGGCCGUDAGGCCGAA AGACGAG	1983	cuceucu c ucuceee	2001
MAP2-15	GUUGCCC CUGAUGAGGCCGUUAGGCCGAA AGAGAGA	1984	UCUCUCU C GGGCAAC	2002
MAP2-464	GUUCUCC CUSAUSAGGCCGUUAGGCCGAA AGCAGCU	1985	AGCUGCU U GGAGAAC	2003
MAP2-911	UCACACA CUGAUGAGGCCGUUAGGCCGAA ACGAACA	1986	UGUUCGU C UGUGUGA	2004
MAP2-1290	UUCUCCC CUGAUGAGGCCGUUAGGCCGAA AGCGAUC	1987	GAUCGCU U GGGAGAA	2005
MAP2-1342	GAUCUAC CUGAUGAGGCCGUUAGGCCGAA AUGCCCA	1988	UGGGCAU U GUAGAUC	2006
MAP2-1479	AGGUGUU CUGAUGAGGCCGUUAGGCCGAA AGGUGGC	1989	GCCACCU C AACACCU	2007
MAP2-1646	GUCCGGA CUGAUGAGGCCGUUAGGCCGAA AGCUUUU	1990	AAAAGCU U UCCGGAC	2008
MAP2-1819	AGGUGCA CUGAUGAGGCCGUUAGGCCGAA AACUGGA	1991	uccaguu c ugcaccu	5005
MAP2-2262	GUGAUGU CUGAUGAGGCCGUUAGGCCGAA AGGGUGU	1992	ACACCCU A ACAUCAC	2010
MAP2-10	CCGAGAG CUGAUGAGGCCGUUAGGCCGAA GACGAGG	1993	cencene n enencee	2011
NCH				
MAP2-369	AACUGAG CUGAUGAGGCCGUDAGGCCGAA IAGGGUC	1994	GACCCUC C CUCAGUU	2012
MAP2-370	GAACUGA CUGAUGAGGCCGUVAGGCCGAA IGAGGGU	1995	ACCCUCC C UCAGUUC	2013
MAP2-1901	GUUSUGU CUGAUGAGGCCGUUAGGCCGAA IUGCUGA	1996	UCAGCAC C ACACAAC	2014
MAP2-1906	UNGGUGU CUGAUGAGGCCGUDAGGCCGAA IUGUGGU	1997	ACCACAC A ACACCUA	2015
G-Cleaver				
MAP2-1821	AGGUG UGAUGGCAUGCACUAUGCGCG AGAACUGGAU	1998	AUCCAGUUCU G CACCU	2016
MAP2-2076	AGGAG UGAUGGCAUGCACUAUGCGCG AGGUUGUUCA	1999	UGAACAACCU G CUCCU	2017
MAP2-2086	GUAGU UGAUGGCAUGCACUAUGCGCG AUUCAGGAGC	2000	GCUCCUGAAU G ACUAC	2018

Table 13: Human telomerase reverse transcriptase (TERT) Hammerhead Ribozyme and Target Sequence

nt. Position	Ribozyme Sequence	Seq ID Nos.	Substrate Sequence	Seq ID Nos.
13	CGCAGCAG CUGAUGAG X CGAA ACGCAGCG		CGCTGCGT C CTGCTGCG	
68	GCAGCGGG CUGAUGAG X CGAA AGCGCGCG		CGCGCGCT C CCCGCTGC	
90	GCAGCAGG CUGAUGAG X CGAA AGCGCACG		CGTGCGCT C CCTGCTGC	
108	CCUCGCGG CUGAUGAG X CGAA AGUGGCUG		CAGCCACT A CCGCGAGG	
135	GCCGCACG CUGAUGAG X CGAA ACGUGGCC		GGCCACGT T CGTGCGGC	
136	CGCCGCAC CUGAUGAG X CGAA AACGUGGC		GCCACGTT C GTGCGGCG	
194	CGCGCGGA CUGAUGAG X CGAA AGCCGCCG		CGGCGGCT T TCCGCGCG	
195	GCGCGCGG CUGAUGAG X CGAA AAGCCGCC		GGCGGCTT T CCGCGCGC	
196	AGCGCGCG CUGAUGAG X CGAA AAAGCCGC		GCGGCTTT C CGCGCGCT	
264	GGCGGAAG CUGAUGAG X CGAA AGGGGGCG		CGCCCCCT C CTTCCGCC	
267	CCUGGCGG CUGAUGAG X CGAA AGGAGGGG		CCCCTCCT T CCGCCAGG	
268	ACCUGGCG CUGAUGAG X CGAA AAGGAGGG		CCCTCCTT C CGCCAGGT	
279	UCAGGCAG CUGAUGAG X CGAA ACACCUGG		CCAGGTGT C CTGCCTGA	
351	CGAAGCCG CUGAUGAG X CGAA AGGCCAGC	-	GCTGGCCT T CGGCTTCG	
352	GCGAAGCC CUGAUGAG X CGAA AAGGCCAG	1	CIGGCCTT C GGCTTCGC	
357	GCAGCGCG CUGAUGAG X CGAA AGCCGAAG		CTTCGGCT T CGCGCTGC	
358	AGCAGCGC CUGAUGAG X CGAA AAGCCGAA		TTCGGCTT C GCGCTGCT	
399	UGGUGGUG CUGAUGAG X CGAA AGGCCUCG		CGAGGCCT T CACCACCA	
400	CUGGUGGU CUGAUGAG X CGAA AAGGCCUC		GAGGCCTT C ACCACCAG	
420	UGGGCAGG CUGAUGAG X CGAA AGCUGCGC		GCGCAGCT A CCTGCCCA	
505	AGCAGGUG CUGAUGAG X CGAA ACCAGCAC		GTGCTGGT T CACCTGCT	
506	CAGCAGGU CUGAUGAG X CGAA AACCAGCA	-	TGCTGGTT C ACCTGCTG	
529	AGCACAAA CUGAUGAG X CGAA AGCGCGCA		TGCGCGCT C TTTGTGCT	
531	CCAGCACA CUGAUGAG X CGAA AGAGCGCG	 	CGCGCTCT T TGTGCTGG	
532	ACCAGCAC CUGAUGAG X CGAA AAGAGCGC	-	GCGCTCTT T GTGCTGGT	
545	GCAGCUGG CUGAUGAG X CGAA AGCCACCA		TGGTGGCT C CCAGCTGC	
558	ACACCUGG CUGAUGAG X CGAA AGGCGCAG	_	CTGCGCCT A CCAGGTGT	1
582	CGAGCUGG CUGAUGAG X CGAA ACAGCGGC		GCCGCTGT A CCAGCTCG	
589	GCAGCGCC CUGAUGAG X CGAA AGCUGGUA	+	TACCAGCT C GGCGCTGC	
602	CCGGGCCU CUGAUGAG X CGAA AGUGGCAG	+	CTGCCACT C AGGCCCGG	
626	GGGUCCAC CUGAUGAG X CGAA AGCGUGUG		CACACGCT A GTGGACCC	
644	GCAUCCCA CUGAUGAG X CGAA ACGCCUUC	+	GAAGGCGT C TGGGATGC	
671	CCUGACGC CUGAUGAG X CGAA AUGGUUCC		GGAACCAT A GCGTCAGG	
676	GCCUCCCU CUGAUGAG X CGAA ACGCUAUG	-	CATAGCGT C AGGGAGGC	
691	CCCAGGG CUGAUGAG X CGAA ACCCCGGC	+	GCCGGGGT C CCCCTGGG	
749	CAACGCA CUGAUGAG X CGAA ACUUCGGC	+	GCCGAAGT C TGCCGTTG	
749	UCUUGGGC CUGAUGAG X CGAA ACGGCAGA	+	TCTGCCGT T GCCCAAGA	
	CCCUGCCC CUGAUGAG X CGAA ACGGCCGU	+	ACGCCCGT T GGGCAGGG	1
808	GGGCCAG CUGAUGAG X CGAA ACGGGCGG	-	GCAGGGGT C CTGGGCCC	+
819	CACACAGA CUGAUGAG X CGAA ACCACGGU	+	ACCGTGGT T TCTGTGTG	
863	CACACAGA CUGAUGAG X CGAA ACCACGGU CCACACAG CUGAUGAG X CGAA AACCACGG		CCGTGGTT T CTGTGTGG	
864			CGTGGTTT C TGTGTGGT	
865	ACCACACA CUGAUGAG X CGAA AAACCACG		TGTGGTGT C ACCTGCCA	+
876	UGGCAGGU CUGAUGAG X CGAA ACACCACA		10100101 C ACCIDECA	

		AGCCACCT C TTTGGAGG
906	CCUCCAAA CUGAUGAG X CGAA AGGUGGCU	CCACCTCT T TGGAGGT
908	ACCCUCCA CUGAUGAG X CGAA AGAGGUGG	
909	CACCCUCC CUGAUGAG X CGAA AAGAGGUG	CACCTCTT T GGAGGGTG GGTGCGCT C TCTGGCAC
922	GUGCCAGA CUGAUGAG X CGAA AGCGCACC	
924	GCGUGCCA CUGAUGAG X CGAA AGAGCGCA	TGCGCTCT C TGGCACGC
939	AUGGGUGG CUGAUGAG X CGAA AGUGGCGC	GCGCCACT C CCACCCAT
948	GGCCCACG CUGAUGAG X CGAA AUGGGUGG	CCACCCAT C CGTGGGCC
981	GCGAUGUG CUGAUGAG X CGAA AUGGGGGG	CCCCCCAT C CACATCGC .
987	GUGGCCGC CUGAUGAG X CGAA AUGUGGAU	ATCCACAT C GCGGCCAC
1001	GUCCCAGG CUGAUGAG X CGAA ACGUGGUG	CACCACGT C CCTGGGAC
1016	CGGGGGAC CUGAUGAG X CGAA AGGCGUGU	ACACGCCT T GTCCCCCG
1019	CACCGGGG CUGAUGAG X CGAA ACAAGGCG	CGCCTTGT C CCCCGGTG
1029	UCUCGGCG CUGAUGAG X CGAA ACACCGGG	CCCGGTGT A CGCCGAGA
1047	AGUAGAGG CUGAUGAG X CGAA AGUGCUUG	CAAGCACT T CCTCTACT
1048	GAGUAGAG CUGAUGAG X CGAA AAGUGCUU	AAGCACTT C CTCTACTC
1051	GAGGAGUA CUGAUGAG X CGAA AGGAAGUG	CACTTCCT C TACTCCTC
1053	CUGAGGAG CUGAUGAG X CGAA AGAGGAAG	CTTCCTCT A CTCCTCAG
1056	CGCCUGAG CUGAUGAG X CGAA AGUAGAGG	CCTCTACT C CTCAGGCG
1059	UGUCGCCU CUGAUGAG X CGAA AGGAGUAG	CTACTCCT C AGGCGACA
1086	GUAGGAAG CUGAUGAG X CGAA AGGGCCGC	GCGGCCCT C CTTCCTAC
1089	UGAGUAGG CUGAUGAG X CGAA AGGAGGGC	GCCCTCCT T CCTACTCA CCCTCCTT C CTACTCAG
1090	CUGAGUAG CUGAUGAG X CGAA AAGGAGGG	TCCTTCCT A CTCAGCTC
1093	GAGCUGAG CUGAUGAG X CGAA AGGAAGGA	TTCCTACT C AGCTCTCT
1096	AGAGAGCU CUGAUGAG X CGAA AGUAGGAA	ACTCAGCT C TCTGAGGC
1101	GCCUCAGA CUGAUGAG X CGAA AGCUGAGU	TCAGCTCT C TGAGGCCC
1103	GGGCCUCA CUGAUGAG X CGAA AGAGCUGA	CTGGCGCT C GGAGGCTC
1127	GAGCCUCC CUGAUGAG X CGAA AGCGCCAG	CGGAGGCT C GTGGAGAC
1135	GUCUCCAC CUGAUGAG X CGAA AGCCUCCG	GAGACCAT C TTTCTGGG
1147	CCCAGAAA CUGAUGAG X CGAA AUGGUCUC	GACCATCT T TCTGGGTT
1149	AACCCAGA CUGAUGAG X CGAA AGAUGGUC	ACCATCTT T CTGGGTTC
1150	GAACCCAG CUGAUGAG X CGAA AAGAUGGU	CCATCTTT C TGGGTTCC
1151	GGAACCCA CUGAUGAG X CGAA AAAGAUGG	TTCTGGGT T CCAGGCCC
1157	GGGCCUGG CUGAUGAG X CGAA ACCCAGAA AGGGCCUG CUGAUGAG X CGAA AACCCAGA	TCTGGGTT C CAGGCCCT
1158	CCUGCOGG CUGAUGAG X CGAA AGCCCAGA	CAGGGACT C CCCGCAGG
1181	GGCGGGC CUGAUGAG X CGAA ACCUGCGG	CCGCAGGT T GCCCCGCC
1191	UUUGCCAG CUGAUGAG X CGAA ACCUGCUGG	CCAGCGCT A CTGGCAAA
1212	GCUCCAGA CUGAUGAG X CGAA ACAGGGGC	GCCCCTGT T TCTGGAGC
1233	AGCUCCAGA CUGAUGAG X CGAA ACAGGGG	CCCCTGTT T CTGGAGCT
1234	CAGCUCCA CUGAUGAG X CGAA AAACAGGG	CCCTGTTT C TGGAGCTG
1235	UGGUUCCC CUGAUGAG X CGAA AGCAGCUC	GAGCTGCT T GGGAACCA
1246	GCACCCCG CUGAUGAG X CGAA AGGGGCAC	GTGCCCCT A CGGGGTGC
1269	GUCUUGAG CUGAUGAG X CGAA AGGACCCC	GGGGTGCT C CTCAAGAC
	UGCGUCUU CUGAUGAG X CGAA AGGAGCAC	GTGCTCCT C AAGACGCA
1282	GCUGGGGU CUGAUGAG X CGAA ACCGCAGC	GCTGCGGT C ACCCCAGC
1312	CGGGCACA CUGAUGAG X CGAA ACACCGGC	GCCGGTGT C TGTGCCCG
1330	CCGCCACA CUGAUGAG X CGAA ACCCCUGG	CCAGGGCT C TGTGGCGG
1356	CEGECACA CUGAUGAG A CGAA AGCEEGGG	

Table 13

1394	CACCAGGC CUGAUGAG X CGAA ACGGGGGU	ACCCCCGT C GCCTGGTG
1411	UGCUGGCG CUGAUGAG X CGAA AGCAGCUG	CAGCTGCT C CGCCAGCA
1440	CGAAGCCG CUGAUGAG X CGAA ACACCUGC	GCAGGTGT A CGGCTTCG
1446	CCCGCACG CUGAUGAG X CGAA AGCCGUAC	GTACGGCT T CGTGCGGG
1447	GCCCGCAC CUGAUGAG X CGAA AAGCCGUA	TACGGCTT C GTGCGGGC
1486	GAGCCCCA CUGAUGAG X CGAA AGGCCUGG	CCAGGCCT C TGGGGCTC
1494	UGUGCCUG CUGAUGAG X CGAA AGCCCCAG	CTGGGGCT C CAGGCACA
1515	UCCUGAGG CUGAUGAG X CGAA AGCGGCGU	ACGCCGCT T CCTCAGGA
1516	UUCCUGAG CUGAUGAG X CGAA AAGCGGCG	CGCCGCTT C CTCAGGAA
1519	GUGUUCCU CUGAUGAG X CGAA AGGAAGCG	CGCTTCCT C AGGAACAC
1536	GGGAGAUG CUGAUGAG X CGAA ACUUCUUG	CAAGAAGT T CATCTCCC
1537	AGGGAGAU CUGAUGAG X CGAA AACUUCUU	AAGAAGTT C ATCTCCCT
1540	CCCAGGGA CUGAUGAG X CGAA AUGAACUU	AAGTTCAT C TCCCTGGG
1542	UCCCCAGG CUGAUGAG X CGAA AGAUGAAC	GTTCATCT C CCTGGGGA
1564	UGCAGCGA CUGAUGAG X CGAA AGCUUGGC	GCCAAGCT C TCGCTGCA
1566	CCUGCAGC CUGAUGAG X CGAA AGAGCUUG	CAAGCTCT C GCTGCAGG
1610	GCGCAGCC CUGAUGAG X CGAA AGCGCAGU	ACTGCGCT T GGCTGCGC
1633	ACACAGCC CUGAUGAG X CGAA ACCCCUGG	CCAGGGGT T GGCTGTGT
1642	GCGGCCGG CUGAUGAG X CGAA ACACAGCC	GGCTGTGT T CCGGCCGC
1643	UGCGGCCG CUGAUGAG X CGAA AACACAGC	GCTGTGTT C CGGCCGCA
1661	CUCACGCA CUGAUGAG X CGAA ACGGUGCU	AGCACCGT C TGCGTGAG
1675	UUGGCCAG CUGAUGAG X CGAA AUCUCCUC	GAGGAGAT C CTGGCCAA
1686	AGUGCAGG CUGAUGAG X CGAA ACUUGGCC	GGCCAAGT T CCTGCACT
1687	CAGUGCAG CUGAUGAG X CGAA AACUUGGC	GCCAAGTT C CTGCACTG
1710	CGACGACG CUGAUGAG X CGAA ACACACUC	GAGTGTGT A CGTCGTCG
1714	AGCUCGAC CUGAUGAG X CGAA ACGUACAC	GTGTACGT C GTCGAGCT
1717	AGCAGCUC CUGAUGAG X CGAA ACGACGUA	TACGTCGT C GAGCTGCT
1726	AAAGACCU CUGAUGAG X CGAA AGCAGCUC	GAGCTGCT C AGGTCTTT
1731	AAAAGAAA CUGAUGAG X CGAA ACCUGAGC	GCTCAGGT C TTTCTTTT
1733	AUAAAAGA CUGAUGAG X CGAA AGACCUGA	TCAGGTCT T TCTTTTAT
1734	CAUAAAAG CUGAUGAG X CGAA AAGACCUG	CAGGTOTT T CTTTTATG
1735	ACAUAAAA CUGAUGAG X CGAA AAAGACCU	AGGTCTTT C TTTTATGT
1737	UGACAUAA CUGAUGAG X CGAA AGAAAGAC	GTCTTTCT T TTATGTCA
1738	GUGACAUA CUGAUGAG X CGAA AAGAAAGA	TCTTTCTT T TATGTCAC
1739	CGUGACAU CUGAUGAG X CGAA AAAGAAAG	CTTTCTTT T ATGTCACG
1740	CCGUGACA CUGAUGAG X CGAA AAAAGAAA	TTTCTTTT A TGTCACGG
1744	GUCUCCGU CUGAUGAG X CGAA ACAUAAAA	TTTTATGT C ACGGAGAC
1758	UCUUUUGA CUGAUGAG X CGAA ACGUGGUC	GACCACGT T TCAAAAGA
1759	UUCUUUUG CUGAUGAG X CGAA AACGUGGU	ACCACGTT T CAAAAGAA
1760	GUUCUUUU CUGAUGAG X CGAA AAACGUGG	CCACGTTT C AAAAGAAC
1774	UAGAAAA CUGAUGAG X CGAA AGCCUGUU	AACAGGCT C TTTTTCTA
1776	GGUAGAAA CUGAUGAG X CGAA AGAGCCUG	CAGGCTCT T TITCTACC
1777	CGGUAGAA CUGAUGAG X CGAA AAGAGCCU	AGGCTCTT T TTCTACCG
1778	CCGGUAGA CUGAUGAG X CGAA AAAGAGCC	GGCTCTTT T TCTACCGG
1779	UCCGGUAG CUGAUGAG X CGAA AAAAGAGC	GCTCTTTT T CTACCGGA
1780	UUCCGGUA CUGAUGAG X CGAA AAAAAGAG	CTCTTTT C TACCGGAA
1782	UCUUCCGG CUGAUGAG X CGAA AGAAAAAG	CTTTTCT A CCGGAAGA

1795	UUGCUCCA CUGAUGAG X CGAA ACACUCUU	AAGAGTGT C TGGAGCAA
1806	UGCUUUGC CUGAUGAG X CGAA ACUUGCUC	GAGCAAGT T GCAAAGCA
1816	CUGAUUCC CUGAUGAG X CGAA AUGCUUUG	CANAGCAT T GGAATCAG
1822	UGCUGUCU CUGAUGAG X CGAA AUUCCAAU	ATTGGAAT C AGACAGCA
1833	CCCUCUUC CUGAUGAG X CGAA AGUGCUGU	ACAGCACT T GAAGAGGG
1860	CUGCUUCC CUGAUGAG X CGAA ACAGCUCC	GGAGCTGT C GGAAGCAG
1873	UGCUGCCU CUGAUGAG X CGAA ACCUCUGC	GCAGAGGT C AGGCAGCA
1883	GGCUUCCC CUGAUGAG X CGAA AUGCUGCC	GGCAGCAT C GGGAAGCC
1911	GGAGUCUG CUGAUGAG X CGAA ACGUCAGC	GCTGACGT C CAGACTCC
1918	AUGAAGCG CUGAUGAG X CGAA AGUCUGGA	TCCAGACT C CGCTTCAT
	UGGGGAUG CUGAUGAG X CGAA AGCGGAGU	ACTCCCCT T CATCCCCA
1923	UUGGGGAU CUGAUGAG X CGAA AAGCGGAG	CTCCGCTT C ATCCCCAA
1924		CGCTTCAT C CCCAAGCC
1927	GGCUUGGG CUGAUGAG X CGAA AUGAAGCG	CGGCCGAT T GTGAACAT
1954	AUGUUCAC CUGAUGAG X CGAA AUCGGCCG	CATGGACT A CGTCGTGG
1968	CCACGACG CUGAUGAG X CGAA AGUCCAUG	
1972	GCUCCCAC CUGAUGAG X CGAA ACGUAGUC	GACTAGGT C GTGGGAGC
1989	CUCUGCGG CUGAUGAG X CGAA ACGUUCUG	CAGAACGT T CCGCAGAG
1990	UCUCUGCG CUGAUGAG X CGAA AACGUUCU	AGAACGTT C CGCAGAGA
2015	CGAGGUGA CUGAUGAG X CGAA ACGCUCGG	CCGAGCGT C TCACCTCG
2017	CUCGAGGU CUGAUGAG X CGAA AGACGCUC	GAGCGTCT C ACCTCGAG
2022	UCACCCUC CUGAUGAG X CGAA AGGUGAGA	TCTCACCT C GAGGGTGA
2040	GCACGCUG CUGAUGAG X CGAA ACAGUGCC	GGCACTGT T CAGCGTGC
2041	AGCACGCU CUGAUGAG X CGAA AACAGUGC	GCACTGTT C AGCGTGCT
2050	UCGUAGUU CUGAUGAG X CGAA AGCACGCU	AGCGTGCT C AACTACGA
2055	CCCGCUCG CUGAUGAG X CGAA AGUUGAGC	GCTCAACT A CGAGCGGG
2080	GCGCCCAG CUGAUGAG X CGAA AGGCCGGG	CCCGGCCT C CTGGGCGC
2091	CCAGCACA CUGAUGAG X CGAA AGGCGCCC	GGGCGCCT C TGTGCTGG
2111	CCUGUGGA CUGAUGAG X CGAA AUCGUCCA	TGGACGAT A TCCACAGG
2113	GCCCUGUG CUGAUGAG X CGAA AUAUCGUC	GACGATAT C CACAGGGC
2133	GCAGCACG CUGAUGAG X CGAA AGGUGCGC	GCGCACCT T CGTGCTGC
2134	CGCAGCAC CUGAUGAG X CGAA AAGGUGCG	CGCACCTT C GTGCTGCG
2175	UGACAAAG CUGAUGAG X CGAA ACAGCUCA	TGAGCTGT A CTTTGTCA
2178	CCUUGACA CUGAUGAG X CGAA AGUACAGC	GCTGTACT T TGTCAAGG
2179	ACCUUGAC CUGAUGAG X CGAA AAGUACAG	CTGTACTT T GTCAAGGT
2182	UCCACCUU CUGAUGAG X CGAA ACAAAGUA	TACTITGT C AAGGIGGA
2205	UGGUGUCG CUGAUGAG X CGAA ACGCGCCC	GGGCGCGT A CGACACCA
2215	UCCUGGGG CUGAUGAG X CGAA AUGGUGUC	GACACCAT C CCCCAGGA
2230	ACCUCCGU CUGAUGAG X CGAA AGCCUGUC	GACAGGCT C ACGGAGGT
2239	CUGGCGAU CUGAUGAG X CGAA ACCUCCGU	ACGGAGGT C ATCGCCAG
2242	AUGCUGGC CUGAUGAG X CGAA AUGACCUC	GAGGTCAT C GCCAGCAT
2251	GGUUUGAU CUGAUGAG X CGAA AUGCUGGC	GCCAGCAT C ATCAAACC
2254	UGGGGUUU CUGAUGAG X CGAA AUGAUGCU	AGCATCAT C AAACCCCA
2271	GCACGCAG CUGAUGAG X CGAA ACGUGUUC	GAACACGT A CTGCGTGC
2282	GGCAUACC CUGAUGAG X CGAA ACGCACGC	GCGTGCGT C GGTATGCC
2286	CCACGGCA CUGAUGAG X CGAA ACCGACGC	GCGTCGGT A TGCCGTGG
2296	GCCUUCUG CUGAUGAG X CGAA ACCACGGC	GCCGTGGT C CAGAAGGC
2320	GCCUUGCG CUGAUGAG X CGAA ACGUGCCC	GGGCACGT C CGCAAGGC
2320	GCCOOGCG COGMOGMG A CGMA ACGOGCCC	SSSENGOT C COGNICOO

23131 GGCUCUUG CUGAUGAG X CGAA AGGCCUUG CAAGGCCT C AGAGAGCC			
2344 AAGGUAGA CUGAUGAG X CGAA ACGUGGCU	2331	GGCUCUUG CUGAUGAG X CGAA AGGCCUUG	CAAGGCCT T CAAGAGCC
19346 UCARGGUA CUGAUGAG X CGAA AGAGCUGG CCACGTCT C TACCTTGA	2332	UGGCUCUU CUGAUGAG X CGAA AAGGCCUU	AAGGCCTT C AAGAGCCA
2352	2344	AAGGUAGA CUGAUGAG X CGAA ACGUGGCU	AGCCACGT C TCTACCTT
2352	2346		
2362	2348	UGUCAAGG CUGAUGAG X CGAA AGAGACGU	
2370 GUCGCAUG CUGAUGAG X CGAA ACCUGUGG CCAGCCGT A CATGCGAC	2352	GGUCUGUC CUGAUGAG X CGAA AGGUAGAG	
2382	2362	UACGGCUG CUGAUGAG X CGAA AGGUCUGU	
2383	2370	GUCGCAUG CUGAUGAG X CGAA ACGGCUGG	1
2390	2382		
2425 UCQAUGAC CUGAUGAG X CGAA ACOGCAUC GATCCCOT C GTCATCGA 2428 UGCUCCAU CUGAUGAG X CGAA ACGACGAGC GCCGTCGT C ATCGAGCA 2428 UGCUCCAU CUGAUGAG X CGAA AGGACGAGC GCCGTCGT C ATCGAGCA 2421 UCUCGGC CUGAUGAG X CGAA AGCUCUGC GCAGAGCT C CTCGCTGA 2442 UCAGGGGA CUGAUGAG X CGAA AGCUCUGC GCAGAGCT C CTCGATAG 2445 CAUUCAGC CUGAUGAG X CGAA AGGCCCU AGTRGCCT C CTGAATG 2476 ACGUCGAA CUGAUGAG X CGAA AGAGCCCU AGTRGCCT C T GCACGTT 2477 AGACGUC CUGAUGAG X CGAA AGAGGCCCA TGGCCTT C GACGTCT 2479 AGAGCUC CUGAUGAG X CGAA AGAGGCCCA TGGCCTT C GCACGTCT 2479 CGUAGGA CUGAUGAG X CGAA AGAGGCCCA TGCGCTT C GCACGTCT 2479 CGUAGGAC CUGAUGAG X CGAA AGAGGCCA TGCGCTT C CTACGCT 2481 AGAGGUAG CUGAUGAG X CGAA AGAGGCCA GACGTCTT C CTACGCT 2482 AAGCGUAG CUGAUGAG X CGAA AGAGGUAG GACGTCTT C CTACGCT 2483 AUGAGCAU CUGAUGAG X CGAA AGCUAGA CTTACGCT C CTACGCT 2494 GGCACAUG CUGAUGAG X CGAA AGCUAGA CTTACGCT C CACGCCT 2515 UUGACCCU CUGAUGAG X CGAA AGCUAGA CTTACGCT C CACGCCT			
2428 UGCUCGAU CUGAUGAG X CGAA ACGACGGC GCCCTCGT C ATCOAGCA 2431 CUCUGCUC CUGAUGAG X CGAA AUGACGAC GTCGTCAT C GAGCAGAG 2441 CUCAGGAC CUGAUGAG X CGAA AGCUCUGC GCAGAGAG 2445 CAAUGAGG CUGAUGAG X CGAA AGCUCUGC GCAGAGAG 2445 CAAUGAGG CUGAUGAG X CGAA AGGCCACU AGTGCCTC C CCTGAATG 2470 ACGUCGAA CUGAUGAG X CGAA AGGCCACU AGTGCCTC T CGACGTCT 2471 AGAGCUGC CUGAUGAG X CGAA AGAGGCCA TGGCCTCT T CGACGTCT 2473 AGAGCUGC CUGAUGAG X CGAA AGAGGCC GGCCTCTT C GACGTCTT 2473 AGAGCUGAG CUGAUGAG X CGAA AGAGCUCG GACCTCTT C CTCACCT 2481 AAGCUGAG CUGAUGAG X CGAA AGACGUCG GACCTCTT C CTCACCT 2482 AAGCUJAG CUGAUGAG X CGAA AGACGUCG GACCTCT C TCCACCT 2485 AUGAACCC CUGAUGAG X CGAA AGCGUAG GTCCTCT C TCACGCT T 2490 GGCCACAU CUGAUGAG X CGAA AGCGUAG CTCACGCT C AGCGCT C ACGGCA 2491 UGCCCCU CUGAUGAG X CGAA AUCCCCC GGCCACAU CUGAUGAG X CGAA ACGUAGC 2526 GGACGAU CUGAUGAG X CGAA ACGUAGG CTACGCT C ACGGCAC 25279 ACUGAGC CUGAUGAG X CGAA ACCUAGCC GGCACAU C CACGGGG </th <th>2390</th> <th>CUGCAGGU CUGAUGAG X CGAA AGCCACGA</th> <th></th>	2390	CUGCAGGU CUGAUGAG X CGAA AGCCACGA	
2411 CUCUGUIC CURAUDAG X CORA AUGACGAC GTOTTCAT C GAGCAGAG 2442 UCAGGGAG CUGAUGAG X CORA AGCUCUGC GCAGAGCT C CTCCCTGA 2445 CAULCAGG CUGAUGAG X CORA AGGAGCUC GACCTCCT C CCTCAATG 2470 ACGUCGAA CUGAUGAG X CORA AGGAGCUC AGTGGCCT C TTCGAGT 2470 AGGUCGA CUGAUGAG X CORA AGGCCAU AGTGGCCT C TCGAGTCT 2473 AGACGUC CUGAUGAG X CORA AGGCCCA TGGCCTCT T CGAGCTCT 2473 AGACGUC CUGAUGAG X CORA AGGCCCG GGCCTCTT C GACCTCT 2473 COUAGGAA CUGAUGAG X CORA AGGCCUCG GGCCTCTT C CTCACCCT 2481 AGGCUAG CUGAUGAG X CORA AGGCCUCG GGACTCTT C CTCACCCT 2482 AGGCUAG CUGAUGAG X CORA AGGCUCG GCCTCACCT T CATCACCT 2483 AUGAACC CUGAUGAG X CORA AGGCUAG GTCTTCCT A CGCTTCAT 2489 GGCACAUG CUGAUGAG X CORA AGCUAGG GTCTCCCT C ATGTGCCA 2491 LUGCCCCU CUGAUGAG X CORA AGCUAGGA GTCTCCCT C ATGTGCCA 2515 LUGCCCCU CUGAUGAG X CORA AGCUAGCA GTGCCAT C AGGCCA 2526 GGACGURG CUGAUGAG X CORA AGCUUGC GGCCACACT C CATCGTC 2529 ACUGGCACC CUGAUGAG X CORA AGCUAGGA TCCACCT C CATCGTC <th>2425</th> <th></th> <th></th>	2425		
2442 UCAGGGAC CUGAUGAG X CORA AGCUCUGC GCAGAGCT C CTCCCTGA 2445 CAUUCAGG CUGAUGAG X CORA AGGCACU GACCTCCT C CCTGAATG 2470 ACQUCAGA CUGAUGAG X CORA AGGCCACU AGTGCCT C CCTGAATG 2472 ACGACGAC CUGAUGAG X CORA AGGCCACU AGTGCCTC T COACGTCT 2473 AAGACGUC CUGAUGAG X CORA AGGCCCA TIGGCCTC T COACGTCT 2473 AAGACGUC CUGAUGAG X CORA AGGUCGAA TITCGACGT C TTCCTACG 24749 COUAGGAA CUGAUGAG X CORA AGAGUCG GGCCTCT T CCTACGCT 24811 AGGGUAG CUGAUGAG X CORA AGACGUCG GACGTCT C CTACGCT 2482 AAGCGUAG CUGAUGAG X CORA AGACGUCG GACGTCT C CTACGCT 2485 AUGAGCG CUGAUGAG X CORA AGGAGGC GTCTTCCT A GCCTTCAT 2486 AUGAGCGCAU CUGAUGAG X CORA AGGAUGG CTACCCT T C ATUTOCC 2491 UGCCCCU CUGAUGAG X CORA AGGACUG CTACCCT C ATUTOCC 2521 AUGCCCU CUGAUGAG X CORA AUGUSCC GTCCCCAT C AGGGCACA 2529 ACUGGCACU CUGAUGAG X CORA AGGACUG CTACCCT C AGGGCACA 2529 ACUGGCACU CUGAUGAG X CORA AGGACUG CAAGGGAGT C CTACCGC 2529 ACUGGCACU CUGAUGAG X CORA AGCUGAC CAAGGGGAT C CTACCGC <	2428		
2445 CAJUCAGG CUGALGAG X CGAA AGGAGCUC GAGCTCCT C CTGAATG 2470 AGGUCGAA CUGAUGAG X CGAA AGGCCACU AGTRGCCT C TTGGACGT 2471 AGAGCUGC CUGAUGAG X CGAA AGGGCCACU AGTRGCCT C TTGGACGTC 2472 AGAGCUGC CUGAUGAG X GGAA AGGGCCA TGGCCTCT C GACGTCT 2473 AGAGCUCC CUGAUGAG X GGAA AGGGCC GGCCTCTT C GACGTCT 2479 CAUGAGAA CUGAGAA CACUGCAA TTGGACGT C TTCCTACG 2481 AGCGUAG CUGAUGAG X CGAA AGAGCUCG CCACUTCT C CTACGCT 2482 AAGCGUAG CUGAUGAG X CGAA AGAGCUCG GACUTCT C CTACGCT 2483 AUGAGACC CUGAUGAG X CGAA AGACGUAG GTCTTCCT A CCCTTCAT 2499 GGCACAUG CUGAUGAG X CGAA AGCGUAG CTACGCT C ACCTTCAT 2491 LUGCCCCU CUGAUGAG X CGAA AGCGUAG CTACGCT C CATGTCC 2515 LUUGCCCCU CUGAUGAG X CGAA AUGCCCCC GGGCACHAC CUGAUGAG X CGAA ACCUAGG 2526 GACGGUAC CUGAUGAG X CGAA ACCUAGG CAGGGCAC CUCAUGAGA X CGAA ACCUAGG 2529 ACUGGAC CUGAUGAG X CGAA ACCUAGG CAGGGGAT C CCGCGGC 2539 ACUGGAC CUGAUGAG X CGAA ACCCUG CAGGGGAT C CCGCGGCG 2549 CCCUGGGC CUGAUGAG X CGAA ACCCUG CAGGGGAT C CCGCC			
2470 ACGUCGAA CUGAUGAG X COAA AGGCCACU AGTGGCCT C TTGGACGT 2472 AGAGGUGC CUGAUGAG X COAA AGAGGCCA TGGCCTCT T GGACGTCT 2473 AAGAGUGC CUGAUGAG X COAA AGAGGCCG GGCCTCTT C GACGTCT 2479 CQUAGGAA CUGAUGAG X COAA AGAGGCCG GGCCTCTT C GACGTCT 2479 CQUAGGAA CUGAUGAG X COAA AGACGUCG CGACGTCT T CCTACGCT 2481 AGCGUAGC CUGAUGAG X COAA AGACGUCG GCACGTCT C CTACGCT 2482 AAGCGUA CUGAUGAG X COAA AGACGUCG GCACGTCT C CTACGCT 2483 AUBAACCC CUGAUGAG X COAA AGACGUAG GTCTTCCT A CGCTTCAT 2499 GGCACAUG CUGAUGAG X COAA AGACGUAG CCTACGCT T CATGTCC 2491 UGGCACAU CUGAUGAG X COAA AGACGUAG CTACGCT T CATGTCC 2526 GAGGUAG CUGAUGAG X COAA AGCUUGC GGCCAAAC C CUAGAGAG X COAA 2526 GAGGUAG CUGAUGAG X COAA AUCUSCCC GGCCAACT C CTACGCTC 2529 ACUGGACG CUGAUGAG X COAA AUCUSCCC GGCAACT C CTACGCTC 2533 UGGCACU CUGAUGAG X COAA AUCUSCCC CAAGGGAT C CTACGCTC 2548 CCCTUCCGC CUGAUGAG X COAA AUCCCCUG CAAGGGAT C CTACCCTC 2559 AGAGGAGA CUGAUGAGA X COAA AUCCCCUG CAAGGGCT C CATCCCTC			
2472 AGAGGUGG CUGAUGAG X CGAA AGAGGCCA TGGCCTCT T CGACGTCT 2473 AAGACGUC CUGAUGAG X CGAA AGAGGGCC GGCCTCTT C CGACGTCTT 2479 CAUGAGGA X CGGAA AGAGGGGC GGCCTCTT C CTACGCT 2481 AGAGGUAG CUGAUGAG X CGAA AGACGUGGA TTCGACGCT C TTCCTACGCT 2482 AAGGGUAG CUGAUGAG X CGAA AGAGGUCG GACGTCT T CCTACGCTT 2485 AUGAGGUAG CUGAUGAG X CGAA AGAGGUGG GACGTCT C TACGCTT 2489 GGCACAUC CUGAUGAG X CGAA AGAGGUAG CTACGCT C ACTCCT 2491 UGGCACU CUGAUGAG X CGAA AGCGUAG CTACGCT C AGTGCCA 2491 UGGCACU CUGAUGAG X CGAA AGCGUAG CTACGCAT C CAGGCAC 2515 UUGCCCCU CUGAUGAG X CGAA ACUGCCC GGCAAGAT C CTACGTCC 2526 GGACGAC CUCAUGAGA X CGAA ACUGCCCC GGCAGACT C CTACGTCC 25279 ACUGGACC CUCAUGAGA X CGAA ACUGCCCC CGGGGACT C CTACGCCC 2549 ACUGGACC CUCAUGAGA X CGAA ACUCCCCC CAGGGGAT C CCACGGG 2559 ACUGGACC CUCAUGAGA X CGAA ACUCCCCC CAGGGGAT C CCACGGGC 2559 ACUGGACC CUCAUGAGA X CGAA ACCCCCC CAGGGGAT C CCACGGGC 2559 ACUGGAGC CUCAUGAGA X CGAA AGCCCCC GCGCAGCC CCACGGGG <			
2473 AAGACGUC CUGAUGAG X CGAA AAGAGGCC GGCCTCTT C GACGTCTT 2479 COUAGGAA CUGAUGAG X CGAA ACGUCGAA TTCGACGT C TTCCTACG 2481 AAGGUUAG CUGAUGAG X CGAA AGACGUCG GACGTCTT C CTACGCT 2482 AAGCGUGA CUGAUGAG X CGAA AGACGUCG GACGTCTT C CTACGCTT 2482 AAGCGUGA CUGAUGAG X CGAA AGAGGUCG GACGTCTT C CTACGCTT 2489 GGCACAUG CUGAUGAG X CGAA AGAGGUAG CTACGCTT C ATGTGCCA 2491 UGGCACAU CUGAUGAG X CGAA AGAGGUAG CTACGCTT C ATGTGCCA 2515 LUGCCCCU CUGAUGAG X CGAA AGAGGUAG CTACGCTT C ATGTGCCA 2516 GGACGUAG CUGAUGAG X CGAA AGAGGUUG CTACGCTT C ATGTGCCA 2526 GGACGUAG CUGAUGAG X CGAA AGAGCUUG CAAGTCCT A COTCCAGT 2539 ACCUGACAU CUGAUGAG X CGAA AGCCUUGG CAAGTCCT C CATCCTCT 2539 AGAGGAUG CUGAUGAG X CGAA AGCCUGAGA TCCTACCT C CATCCTCT 2548 CCCUGCGC CUGAUGAG X CGAA AGCCCUGC CAAGGGAT C COACGAGG 2559 AGAGGAUG CUGAUGAG X CGAA AGCGAGG GCATCCAT C CATCCTCT 2563 GGGAGAGAC CUGAUGAG X CGAA AGCGAGG GCATCCAT C CATCCTCT 2566 AGCCUGA CUGAUGAG X CGAA AGCAGGG CATCCTCT C CACCCT			
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2563 GUGGABAS CUGAUGAS X CGAA AUGGAGCC GGCTCCAT C CTCTCCAC			
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2568 GCAGCGUG CUGNUGAG X CGAA AGAGGAUG			
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2592			ACGCTGCT C TGCAGCCT
2616 UCCCCGCA CUGAUGAG X CGAA ACAGCUUG CAAGCTGT T TGCGGGGA 2617 AUCCCGGC CUGAUGAG X CGAA AACAGCUU AAGCTGTT T GGGGGGAT 2628 UCCCGGC CUGAUGAG X CGAA AACGCCGC GGGGGGAT T GGGGGGGA 2627 GUCCGGC CUGAUGAG X CGAA AAUCCCCG CGGGGAT C GGCGGGA 2644 AAAGGCAG CUGAUGAG X CGAA AACCAGC GGGCTGCT C CTGGTTT 2651 AAUCCACAC CUGAUGAG X CGAA ACCAGGA TCCTGCTT T GGTGGAT 2652 CAUCCAC CUGAUGAG X CGAA AACCAGG CCTGCGTT T GGTGGAT 2653 CAACAAGA CUGAUGAG X CGAA AUCAUCCA TGGATGAT T TCTTGTTG 2654 CCAACAAG CUGAUGAG X CGAA AUCAUCC GGATGATT T CTTGTTG 2655 ACCACAAG CUGAUGAG X CGAA AUCAUCCA GGATGATT T CTTGTTGG 2655 ACCACACAA CUGAUGAG X CGAA AUCAUCCA GGATGATT T CTTGTTGG			CCTGTGCT A CGGCGACA
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2644 AAAGGCAG CUGAUGAG X CGAA AGCAGCCC GGGCTGCT C CTGCGTTT 2651 AUCCACCA CUGAUGAG X CGAA AGCGCAGGA TCCTGCGT T TGGTGGAT 2652 CAUCCACC CUGAUGAG X CGAA AAGCGAGG CCTGGGTT T GGTGGATG 2653 CAACAAGA CUGAUGAG X CGAA AUCAUCCA TGGATGAT T TCTTGTTG 2654 CCAACAAG CUGAUGAG X CGAA AUCAUCC GQATGATT T CTTGTTGG 2655 ACCAACAA CUGAUGAG X CGAA AAAUCAUC GATGATT T CTTGTTGGT		UCCCGCCG CUGAUGAG X CGAA AUCCCCGC	GCGGGGAT T CGGCGGGA
2651 AUCCACCA CUGAUGAG X CGAA ACGCAGGA TCCTGCGT T TGGTGGAT 2652 CAUCCACC CUGAUGAG X CGAA AAGGCAGG CCTGCGTT T GGTGGATG 2663 CAACAAGA CUGAUGAG X CGAA AAGCACCA TGGATGAT T TCTTGTTG 2654 CCAACAAG CUGAUGAG X CGAA AAUCAUCC GGATGATT T CTTGTTGG 2655 ACCAACAA CUGAUGAG X CGAA AAAAUCAUC GATGATT C TTGTTGGT	2627	GUCCCGCC CUGAUGAG X CGAA AAUCCCCG	CGGGGATT C GGCGGGAC
2652 CAUCCACC CUGAUGAG X CGAA AACGCAGG CCTGCGTT T GGTGGATG 2653 CAACAAGA CUGAUGAG X CGAA AUCAUCCA TGGATGAT T TCTTGTTG 2654 CCAACAAG CUGAUGAG X CGAA AUCAUCC GGATGATT T CTTGTTGG 2655 ACCAACAA CUGAUGAG X CGAA AAUCAUC GATGATT T C TTGTTGGT	2644	AAACGCAG CUGAUGAG X CGAA AGCAGCCC	GGGCTGCT C CTGCGTTT
2653 CAACAAGA CUGAUGAG X CGAA AUCAUCCA TGGATGAT T TCTTGTTG 2654 CCAACAAG CUGAUGAG X CGAA AAUCAUCC GGATGATT T CTTGTTGG 2655 ACCAACAA CUGAUGAG X CGAA AAAUCAUC GATGATT C TTGTTGGT	2651	AUCCACCA CUGAUGAG X CGAA ACGCAGGA	TCCTGCGT T TGGTGGAT
2664 CCAACAG CUGAUGAG X CGAA AAUCAUCC GGATGATT T CTTGTTGG 2665 ACCAACAA CUGAUGAG X CGAA AAAUCAUC GATGATTT C TTGTTGGT	2652	CAUCCACC CUGAUGAG X CGAA AACGCAGG	CCTGCGTT T GGTGGATG
2665 ACCAACAA CUGAUGAG X CGAA AAAUCAUC GATGATTT C TTGTTGGT	2663	CAACAAGA CUGAUGAG X CGAA AUCAUCCA	TGGATGAT T TCTTGTTG
	2664	CCAACAAG CUGAUGAG X CGAA AAUCAUCC	GGATGATT T CTTGTTGG
2667 UCACCAAC CUGAUGAG X CGAA AGAAAUCA TGATTTCT T GTTGGTGA	2665	ACCAACAA CUGAUGAG X CGAA AAAUCAUC	GATGATTT C TTGTTGGT
	2667	UCACCAAC CUGAUGAG X CGAA AGAAAUCA	TGATTTCT T GTTGGTGA

Table 13

2670	GUGUCACC CUGAUGAG X CGAA ACAAGAAA	TTTCTTGT T GGTGACAC
2681	GGUGAGGU CUGAUGAG X CGAA AGGUGUCA	TGACACCT C ACCTCACC
2686	GCGUGGGU CUGAUGAG X CGAA AGGUGAGG	CCTCACCT C ACCCACGC
2703	UCCUGAGG CUGAUGAG X CGAA AGGUUUUC	GAAAACCT T CCTCAGGA
2704	GUCCUGAG CUGAUGAG X CGAA AAGGUUUU	AAAACCTT C CTCAGGAC
2707	AGGGUCCU CUGAUGAG X CGAA AGGAAGGU	ACCTTCCT C AGGACCCT
2719	ACACCUCG CUGAUGAG X CGAA ACCAGGGU	ACCCTGGT C CGAGGTGT
2728	UACUCAGG CUGAUGAG X CGAA ACACCUCG	CGAGGTGT C CCTGAGTA
2736	CGCAGCCA CUGAUGAG X CGAA ACUCAGGG	CCCTGAGT A TGGCTGCG
2754	UCUUCCGC CUGAUGAG X CGAA AGUUCACC	GGTGAACT T GCGGAAGA
2775	CUACAGGG CUGAUGAG X CGAA AGUUCACC	GGTGAACT T CCCTGTAG
2776	UCUACAGG CUGAUGAG X CGAA AAGUUCAC	GTGAACTT C CCTGTAGA
2782	UCGUCUUC CUGAUGAG X CGAA ACAGGGAA	TTCCCTGT A GAAGACGA
2810	CUGAACAA CUGAUGAG X CGAA AGCCGUGC	GCACGGCT T TTGTTCAG
2811	UCUGAACA CUGAUGAG X CGAA AAGCCGUG	CACGGCTT T TGTTCAGA
2812	AUCUGAAC CUGAUGAG X CGAA AAAGCCGU	ACGGCTTT T GTTCAGAT
2815	GGCAUCUG CUGAUGAG X CGAA ACAAAAGC	GCTTTTGT T CAGATGCC
2816	CGGCAUCU CUGAUGAG X CGAA AACAAAAG	CTTTTGTT C AGATGCCG
2836	CAGGGGAA CUGAUGAG X CGAA AGGCCGUG	CACGGCCT A TTCCCCTG
2838	ACCAGGGG CUGAUGAG X CGAA AUAGGCCG	CGGCCTAT T CCCCTGGT
2839	CACCAGGG CUGAUGAG X CGAA AAUAGGCC	GGCCTATT C CCCTGGTG
2864	GGUCCGGG CUGAUGAG X CGAA AUCCAGCA	TGCTGGAT A CCCGGACC
2892	AGCUGGAG CUGAUGAG X CGAA AGUCGCUC	GAGCGACT A CTCCAGCT
2895	CAUAGCUG CUGAUGAG X CGAA AGUAGUCG	CGACTACT C CAGCTATG
2901	UCCGGGCA CUGAUGAG X CGAA AGCUGGAG	CTCCAGCT A TGCCCGGA
2913	CUCUGAUG CUGAUGAG X CGAA AGGUCCGG	CCGGACCT C CATCAGAG
2917	CUGGCUCU CUGAUGAG X CGAA AUGGAGGU	ACCTCCAT C AGAGCCAG
2927	GAAGGUGA CUGAUGAG X CGAA ACUGGCUC	GAGCCAGT C TCACCTTC
2929	UUGAAGGU CUGAUGAG X CGAA AGACUGGC	GCCAGTCT C ACCTTCAA
2934	CGCGGUUG CUGAUGAG X CGAA AGGUGAGA	TCTCACCT T CAACCGCG
2935	CCGCGGUU CUGAUGAG X CGAA AAGGUGAG	CTCACCTT C AACCGCGG
2946	CAGCCUUG CUGAUGAG X CGAA AGCCGCGG	CCGCGGCT T CAAGGCTG
2947	CCAGCCUU CUGAUGAG X CGAA AAGCCGCG	CGCGGCTT C AAGGCTGG
2969	GAGUUUGC CUGAUGAG X CGAA ACGCAUGU	ACATGCGT C GCAAACTC
2977	ACCCCAAA CUGAUGAG X CGAA AGUUUGCG	CGCAAACT C TTTGGGGT
2979	AGACCCCA CUGAUGAG X CGAA AGAGUUUG	CAAACTCT T TGGGGTCT
2980	AAGACCCC CUGAUGAG X CGAA AAGAGUUU	AAACTCTT T GGGGTCTT
2986	AGCCGCAA CUGAUGAG X CGAA ACCCCAAA	TTTGGGGT C TTGCGGCT
2988	UCAGCCGC CUGAUGAG X CGAA AGACCCCA	TGGGGTCT T GCGGCTGA
3002	CAGGCUGU CUGAUGAG X CGAA ACACUUCA	TGAAGTGT C ACAGCCTG
3012	AAUCCAGA CUGAUGAG X CGAA ACAGGCUG	CAGCCTGT T TCTGGATT
3013	AAAUCCAG CUGAUGAG X CGAA AACAGGCU	AGCCTGTT T CTGGATTT
3014	CAAAUCCA CUGAUGAG X CGAA AAACAGGC	GCCTGTTT C TGGATTTG
3020	CACCUGCA CUGAUGAG X CGAA AUCCAGAA	TTCTGGAT T TGCAGGTG
3021	UCACCUGC CUGAUGAG X CGAA AAUCCAGA	TCTGGATT T GCAGGTGA
3037	ACCGUCUG CUGAUGAG X CGAA AGGCUGUU	AACAGCCT C CAGACGGT
3058	AUCUUGUA CUGAUGAG X CGAA AUGUUGGU	ACCAACAT C TACAAGAT

1966			
1970	3060	GGAUCUUG CUGAUGAG X CGAA AGAUGUUG	CAACATCT A CAAGATCC
GARACCUG CUGAUGAG X CORA ACCUGUAC GCAGGCCT A CAGCTTIC	3067		
AUGOGUGA CUGAUGAG X CGAA ACCUGUAC	3070		
CAUGCOUG CUGAUGAG X CGAA AACCUGUA	3084		
ACAUGGU CUGAUGAG X CGAA AAACCUGU ACAGGTTT C ACCCATGT	3090		
1112			
1117 GCUQAUGA CUGAUGAG X CGAA AUGGGAGC			
13.11			
1122			
3122			
1310			
13111 GUUCUUCC CUGAUGAG X CGAA AACUUCCU			
13147 GCAGGRAA CUGAURAG X CGRA AURUGOGG CCCCACAT T TITCCTGC			
3149			
3149 GCGCAGGA CUGAUGAG X CGAA AAAUGUUG CCACATTT T TCCTGCCC			
3150			
3151 ACGCGCAG CUGAUGAG X CGAA AAAAADUGU			
150			
3153			
3165			
3197			
13181			
3186 GGAUGGAG CUGAUGAG X CGAA AGCAGAGG CCTCTGCT A CTCCATCC			
1899			
3193 GCUUUCAG CUGAUGAG X CGAA AUGGAGUA			
3219 CCCCCAGC CUGAUGAG X CGAA ACAUCCCU			
3248			
3255 CGGCCUCG CUGAUGAG X CGAA AGGGCAGA TCTGCCCT C CGAGGCCCG			
3288			TCTGCCCT C CGAGGCCG
3289			
3305 ACGGUGUE CUGAUGAG X CGAA AGUCAGEU	3289		CAAGCATT C CTGCTCAA
3316 ACGUAGGU CUGAUGAG X CGAA ACACCGUG CACCGTGT C ACCTACGT	3295	GUCAGCUU CUGAUGAG X CGAA AGCAGGAA	TTCCTGCT C AAGCTGAC
3321 GUGGCAGG CUGAURAG X CGRA AGGUGACA TGTCACCT A COTGCCAC	3305	ACGGUGUC CUGAUGAG X CGAA AGUCAGCU	AGCTGACT C GACACCGT
3331	3316	ACGUAGGU CUGAUGAG X CGAA ACACGGUG	CACCGTGT C ACCTACGT
3339 UCCUGAGU CUGAUGAG X CGAA ACCCCAGG CCTGGGGT C ACTCAGGA	3321	GUGGCACG CUGAUGAG X CGAA AGGUGACA	TGTCACCT A CGTGCCAC
3343 GCUGUCCU CUGAUGAG X CGAA AGUGACCC GGGTCACT C AGGACAGC	3331 -	GACCCCAG CUGAUGAG X CGAA AGUGGCAC	GTGCCACT C CTGGGGTC
3368	3339	UCCUGAGU CUGAUGAG X CGAA ACCCCAGG	CCTGGGGT C ACTCAGGA
3376 GUCCCCGG CUGANGAG X CGAA AGCUNCCG CGGAAGCT C CCGGGAAC	3343	GCUGUCCU CUGAUGAG X CGAA AGUGACCC	GGGTCACT C AGGACAGC
3429 UGRAGUCU CUGAUGAG X CGRA AGGGCAGU ACTGCCCT C AGACTTCA 3435 UGGUCUU CUGAUGAG X CGRA AGUCUGAG CTCAGACT T CAAGACCA 3436 AUGGUCUU CUGAUGAG X CGRA AGUCUGA TCAGACTT C AGACCAT 3445 CAGUCCAG CUGAUGAG X CGRA AUGCUCU AAAACCAT C CTGGACTG 3503 CCCGGCGU CUGAUGAG X CGRA ACAGGGCU AGCCCTGT C ACGCCGGG	3368	GAGCUUCC CUGAUGAG X CGAA ACUCAGCU	
3435 UGGUCUUG CUGAUGAG X CGAA AGUCUGAG CTCAGACT T CAAGACCA 3436 AUGGUCUU CUGAUGAG X CGAA AAGUCUGA TCAGACTT C AAGACCAT 3445 CAGUCCAG CUGAUGAG X CGAA AUGUCUCU AAAACACAT C CTGGACTG 3503 CCCGGGGU CUGAUGAG X CGAA ACAGGGCU AGCCCTGT C ACGCCGGG	3376	GUCCCCGG CUGAUGAG X CGAA AGCUUCCG	
3436 AUGGUCUU CUGAUGAG X CGAA AAGUCUGA TCAGACTT C AAGACCAT 3445 CAGUCCAG CUGAUGAG X CGAA AUGGUCUU AAGACCAT C CTGGACTG 3503 CCCGGCGU CUGAUGAG X CGAA ACAGGGCU AGCCCTGT C ACGCCCGG	3429	UGAAGUCU CUGAUGAG X CGAA AGGGCAGU	ACTGCCCT C AGACTTCA
3445 CAGUCCAG CUGAUGAG X CGAA AUGGUCUU AAGACCAT C CTGGACTG 3503 CCCGGCGU CUGAUGAG X CGAA ACAGGGCU AGCCCTGT C ACGCCGGG	3435		
3503 CCCGGCGU CUGAUGAG X CGAA ACAGGGCU AGCCCTGT C ACGCCGGG	3436		
1313	3445	CAGUCCAG CUGAUGAG X CGAA AUGGUCUU	
3514 GGGACGUA CUGAUGAG X CGAA AGCCCGGC GCCGGGCT C TACGTCCC			
	3514	GGGACGUA CUGAUGAG X CGAA AGCCCGGC	GCCGGGCT C TACGTCCC

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Table 13

		L agggeren 1 Avenue
3516	CUGGGACG CUGAUGAG X CGAA AGAGCCCG	CGGGCTCT A CGTCCCAG
3520	CUCCCUGG CUGAUGAG X CGAA ACGUAGAG	CTCTACGT C CCAGGGAG
3568	AGGCCUCA CUGAUGAG X CGAA ACUCCCAG	CTGGGAGT C TGAGGCCT
3587	CUCGGCCA CUGAUGAG X CGAA ACACUCAC	GTGAGTGT T TGGCCGAG
3588	CCUCGGCC CUGAUGAG X CGAA AACACUCA	TGAGTGTT T GGCCGAGG
3606	UUCAGCCG CUGAUGAG X CGAA ACAUGCAG	CTGCATGT C CGGCTGAA
3625	CUCAGCCG CUGAUGAG X CGAA ACACUCAG	CTGAGTGT C CGGCTGAG
3648	CUUGGCUG CUGAUGAG X CGAA ACACUCGC	GCGAGTGT C CAGCCAAG
3667	GUGUGCUG CUGAUGAG X CGAA ACACUCAG	CTGAGTGT C CAGCACAC
3683	GAAGUGAA CUGAUGAG X CGAA ACGGCAGG	CCTGCCGT C TTCACTTC
3685	GGGAAGUG CUGAUGAG X CGAA AGACGGCA	TGCCGTCT T CACTTCCC
3686	GGGGAAGU CUGAUGAG X CGAA AAGACGGC	GCCGTCTT C ACTTCCCC
3690	CUGUGGGG CUGAUGAG X CGAA AGUGAAGA	TCTTCACT T CCCCACAG
3691	CCUGUGGG CUGAUGAG X CGAA AAGUGAAG	CTTCACTT C CCCACAGG
3708	GUGGAGCC CUGAUGAG X CGAA AGCGCCAG	CTGGCGCT C GGCTCCAC
3713	CUGUGGUG CUGAUGAG X CGAA AGCCGAGC	GCTCGGCT C CACCCCAG
3730	GUGAGGAA CUGAUGAG X CGAA AGCUGGCC	GGCCAGCT T TTCCTCAC
3731	GGUGAGGA CUGAUGAG X CGAA AAGCUGGC	GCCAGCTT T TCCTCACC
3732	UGGUGAGG CUGAUGAG X CGAA AAAGCUGG	CCAGCTTT T CCTCACCA
3733	CUGGUGAG CUGAUGAG X CGAA AAAAGCUG	CAGCTTTT C CTCACCAG
3736	CUCCUGGU CUGAUGAG X CGAA AGGAAAAG	CTTTTCCT C ACCAGGAG
3752	GGGAGUGG CUGAUGAG X CGAA AGCCGGGC	GCCCGGCT T CCACTCCC
3753	GGGGAGUG CUGAUGAG X CGAA AAGCCGGG	CCCGGCTT C CACTCCCC
3758	UAUGUGGG CUGAUGAG X CGAA AGUGGAAG	CTTCCACT C CCCACATA
3766	ACUAUUCC CUGAUGAG X CGAA AUGUGGGG	CCCCACAT A GGAATAGT
3772	GGAUGGAC CUGAUGAG X CGAA AUUCCUAU	ATAGGAAT A GTCCATCC
3775	UGGGGAUG CUGAUGAG X CGAA ACUAUUCC	GGAATAGT C CATCCCCA
3779	AAUCUGGG CUGAUGAG X CGAA AUGGACUA	TAGTCCAT C CCCAGATT
3787	CAAUGGCG CUGAUGAG X CGAA AUCUGGGG	CCCCAGAT T CGCCATTG
3788	ACAAUGGC CUGAUGAG X CGAA AAUCUGGG	CCCAGATT C GCCATTGT
3794	GGGUGAAC CUGAUGAG X CGAA AUGGCGAA	TTCGCCAT T GTTCACCC
3797	GAGGGGUG CUGAUGAG X CGAA ACAAUGGC	GCCATTGT T CACCCCTC
3798	CGAGGGGU CUGAUGAG X CGAA AACAAUGG	CCATTGTT C ACCCCTCG
3805	GGCAGGGC CUGAUGAG X CGAA AGGGGUGA	TCACCCCT C GCCCTGCC
3816	AGGCAAAG CUGAUGAG X CGAA AGGGCAGG	CCTGCCCT C CTTTGCCT
3819	GGAAGGCA CUGAUGAG X CGAA AGGAGGGC	GCCTCCT T TGCCTTCC
3820	UGGAAGGC CUGAUGAG X CGAA AAGGAGGG	
3825	GGGGGUGG CUGAUGAG X CGAA AGGCAAAG	CTTTGCCT T CCACCCCC
3826	UGGGGGUG CUGAUGAG X CGAA AAGGCAAA	TTTGCCTT C CACCCCCA CCCACCAT C CAGGTGGA
3839	UCCACCUG CUGAUGAG X CGAA AUGGUGGG	
3873	AAUUCCCA CUGAUGAG X CGAA AGCUCCCA	TGGGAGCT C TGGGAATT
3881	UCACUCCA CUGAUGAG X CGAA AUUCCCAG	CTGGGAAT T TGGAGTGA TGGGAATT T GGAGTGAC
3882	GUCACUCC CUGAUGAG X CGAA AAUUCCCA	TGCCCTGT A CACAGGCG
3907	CGCCUGUG CUGAUGAG X CGAA ACAGGGCA	ATGGGGGT C CCTGTGGG
3940	CCCACAGG CUGAUGAG X CGAA ACCCCCAU	CTGTGGGT C AAATTGGG
3950	CCCAAUUU ÇUGAUGAG X CGAA ACCCACAG	***************************************
3955	CUCCCCC CUGAUGAG X CGAA AUUUGACC	GGTCAAAT T GGGGGGAG

Table 13

3977	CAGUAUUU CUGAUGAG X CGAA ACUCCCAC	GTGGGAGT A AAATACTG
3982	AUAUUCAG CUGAUGAG X CGAA AUUUUACU	AGTAAAAT A CTGAATAT
3989	AACUCAUA CUGAUGAG X CGAA AUUCAGUA	TACTGAAT A TATGAGTT
3991	AAAACUCA CUGAUGAG X CGAA AUAUUCAG	CTGAATAT A TGAGTTTT
3997	AACUGAAA CUGAUGAG X CGAA ACUCAUAU	ATATGAGT T TTTCAGTT
3998	AAACUGAA CUGAUGAG X CGAA AACUCAUA	TATGAGTT T TTCAGTTT
3999	AAAACUGA CUGAUGAG X CGAA AAACUCAU	ATGAGTTT T TCAGTTTT
4000	CAAAACUG CUGAUGAG X CGAA AAAACUCA	TGAGTTTT T CAGTTTTG
4001	UCAAAACU CUGAUGAG X CGAA AAAAACUC	GAGTTTTT C AGTTTTGA
4005	UUUUUCAA CUGAUGAG X CGAA ACUGAAAA	TTTTCAGT T TTGAAAAA
4006	UUUUUUCA CUGAUGAG X CGAA AACUGAAA	TTTCAGTT T TGAAAAAA
4007	UUUUUUUC CUGAUGAG X CGAA AAACUGAA	TTCAGTTT T GAAAAAA

Stem Length = 8. Core Sequence = CUGAUGAG X CGAA (X = GCCGUUAGGC or other stem II sequence and length (greater than or equal to 2 base-pairs))
Seql = TERT (Homo supiens telomerase reverse transcriptase (TERT) mRNA, 4015 bp); Nakamura et al., Science 277 (5328), 955-959 (1997)

2.0

Table 14: Human telomerase reverse transcriptase (TERT) NCH Ribozyme and Target Sequence

nt. Position	Ribozyme Sequence	Seq ID Nos	Substrate Sequence	Seq ID Nos
14	GCGCAGCA CUGAUGAG X CGAA IACGCAGC		GCTGCGTC C TGCTGCGC	
15	UGCGCAGC CUGAUGAG X CGAA IGACGCAG	1	CTGCGTCC T GCTGCGCA	
18	ACGUGCGC CUGAUGAG X CGAA ICAGGACG		CGTCCTGC T GCGCACGT	
23	UUCCCACG CUGAUGAG X CGAA ICGCAGCA		TGCTGCGC A CGTGGGAA	
34	GGGGCCAG CUGAUGAG X CGAA ICUUCCCA		TGGGAAGC C CTGGCCCC	
35	CGGGGCCA CUGAUGAG X CGAA IGCUUCCC		GGGAAGCC C TGGCCCCG	
36	CCGGGGCC CUGAUGAG X CGAA IGGCUUCC		GGAAGCCC T GGCCCCGG	
40	GUGGCCGG CUGAUGAG X CGAA ICCAGGGC	1	GCCCTGGC C CCGGCCAC	
41	GGUGGCCG CUGAUGAG X CGAA IGCCAGGG		CCCTGGCC C CGGCCACC	
42	GGGUGGCC CUGAUGAG X CGAA IGGCCAGG		CCTGGCCC C GGCCACCC	
46	GCGGGGGU CUGAUGAG X CGAA ICCGGGGC		GCCCCGGC C ACCCCCGC	
47	CGCGGGGG CUGAUGAG X CGAA IGCCGGGG		CCCCGGCC A CCCCCGCG	
4.9	AUCGCGGG CUGAUGAG X CGAA IUGGCCGG		COGGCCAC C CCCGCGAT	1
50	CAUCGCGG CUGAUGAG X CGAA IGUGGCCG		CGGCCACC C CCGCGATG	
51	GCAUCGCG CUGAUGAG X CGAA IGGUGGCC		GGCCACCC C CGCGATGC	
52	GGCAUCGC CUGAUGAG X CGAA 1GGGUGGC		GCCACCCC C GCGATGCC	
60	GAGCGCGC CUGAUGAG X CGAA ICAUCGCG		CGCGATGC C GCGCGCTC	
67	CAGCGGGG CUGAUGAG X CGAA ICGCGCGG		CCGCGCGC T CCCCGCTG	
69	GGCAGCGG CUGAUGAG X CGAA IAGCGCGC		GCGCGCTC C CCGCTGCC	
70	CGGCAGCG CUGAUGAG X CGAA IGAGCGCG		CGCGCTCC C CGCTGCCG	
71	UCGGCAGC CUGAUGAG X CGAA IGGAGCGC		GCGCTCCC C GCTGCCGA	
74	GGCUCGGC CUGAUGAG X CGAA ICGGGGAG	1	CTCCCCGC T GCCGAGCC	
77	CACGGCUC CUGAUGAG X CGAA ICAGCGGG		CCCGCTGC C GAGCCGTG	
82	GAGCGCAC CUGAUGAG X CGAA ICUCGGCA	1	TGCCGAGC C GTGCGCTC	
89	CAGCAGGG CUGAUGAG X CGAA ICGCACGG		CCGTGCGC T CCCTGCTG	
91	CGCAGCAG CUGAUGAG X CGAA IAGCGCAC		GTGCGCTC C CTGCTGCG	
92	GCGCAGCA CUGAUGAG X CGAA IGAGCGCA		TGCGCTCC C TGCTGCGC	
93	UGCGCAGC CUGAUGAG X CGAA IGGAGCGC		GCGCTCCC T GCTGCGCA	
96	GGCUGCGC CUGAUGAG X CGAA ICAGGGAG		CTCCCTGC T GCGCAGCC	
101	GUAGUGGC CUGAUGAG X CGAA ICGCAGCA		TGCTGCGC A GCCACTAC	
104	GCGGUAGU CUGAUGAG X CGAA ICUGCGCA		TGCGCAGC C ACTACCGC	
105	CGCGGUAG CUGAUGAG X CGAA IGCUGCGC		GCGCAGCC A CTACCGCG	
107	CUCGCGGU CUGAUGAG X CGAA IUGGCUGC		GCAGCCAC T ACCGCGAG	
110	CACCUCGC CUGAUGAG X CGAA IUAGUGGC		GCCACTAC C GCGAGGTG	
120	CCAGCGGC CUGAUGAG X CGAA ICACCUCG		CGAGGTGC T GCCGCTGG	
123	UGGCCAGC CUGAUGAG X CGAA ICAGCACC	1	GGTGCTGC C GCTGGCCA	
126	ACGUGGCC CUGAUGAG X CGAA ICGGCAGC		GCTGCCGC T GGCCACGT	
130	ACGAACGU CUGAUGAG X CGAA ICCAGCGG	T	CCGCTGGC C ACGTTCGT	
131	CACGAACG CUGAUGAG X CGAA IGCCAGCG		CGCTGGCC A CGTTCGTG	
146	GGGCCCCA CUGAUGAG X CGAA ICGCCGCA	1	TGCGGCGC C TGGGGCCC	
147	GGGGCCCC CUGAUGAG X CGAA IGCGCCGC		GCGGCGCC T GGGGCCCC	
153	AGCCCUGG CUGAUGAG X CGAA ICCCCAGG	1	CCTGGGGC C CCAGGGCT	
154	CAGCCCUG CUGAUGAG X CGAA IGCCCCAG	1	CTGGGGCC C CAGGGCTG	1

Table 14

155	CCAGCCCU CUGAUGAG X CGAA IGGCCCCA	TGGGGCCC C AGGGCTGG
156	GCCAGCCC CUGAUGAG X CGAA IGGGCCCC	GGGGCCCC A GGGCTGGC
161	CAGCCGCC CUGAUGAG X CGAA ICCCUGGG	CCCAGGGC T GGCGGCTG
168	GCUGCACC CUGAUGAG X CGAA ICCGCCAG	CTGGCGGC T GGTGCAGC
174	CCCCGCGC CUGAUGAG X CGAA ICACCAGC	GCTGGTGC A GCGCGGGG
185	AGCCGCCG CUGAUGAG X CGAA IUCCCCGC	GCGGGGAC C CGGCGGCT
186	AAGCCGCC CUGAUGAG X CGAA IGUCCCCG	CGGGGACC C GGCGGCTT
193	GCGCGGAA CUGAUGAG X CGAA ICCGCCGG	CCGGCGGC T TTCCGCGC
197	CAGCGCGC CUGAUGAG X CGAA IAAAGCCG	CGGCTTTC C GCGCGCTG
204	GGGCCACC CUGAUGAG X CGAA ICGCGCGG	CCGCGCGC T GGTGGCCC
211	AGGCACUG CUGAUGAG X CGAA ICCACCAG	CTGGTGGC C CAGTGCCT
212	CAGGCACU CUGAUGAG X CGAA IGCCACCA	TGGTGGCC C AGTGCCTG
213	CCAGGCAC CUGAUGAG X CGAA IGGCCACC	GGTGGCCC A GTGCCTGG
218	GCACACCA CUGAUGAG X CGAA ICACUGGG	CCCAGTGC C TGGTGTGC
219	CGCACACC CUGAUGAG X CGAA IGCACUGG	CCAGTGCC T GGTGTGCG
231	CGUCCCAG CUGAUGAG X CGAA ICACGCAC	GTGCGTGC C CTGGGACG
232	GCGUCCCA CUGAUGAG X CGAA IGCACGCA	TGCGTGCC C TGGGACGC
233	UGCGUCCC CUGAUGAG X CGAA IGGCACGC	GCGTGCCC T GGGACGCA
241	GGCGGCCG CUGAUGAG X CGAA ICGUCCCA	TGGGACGC A CGGCCGCC
246	CGGGGGGC CUGAUGAG X CGAA ICCGUGCG	CGCACGGC C GCCCCCCG
249	CGGCGGGG CUGAUGAG X CGAA ICGGCCGU	ACGGCCGC C CCCCGCCG
250	GCGGCGGG CUGAUGAG X CGAA IGCGGCCG	CGGCCGCC C CCCGCCGC
251	GGCGGCGG CUGAUGAG X CGAA IGGCGGCC	GGCCGCCC C CCGCCGCC
252	GGGCGGCG CUGAUGAG X CGAA IGGGCGGC	GCCGCCCC C CGCCGCCC
253	GGGGCGGC CUGAUGAG X CGAA IGGGGCGG	CCGCCCCC C GCCGCCCC
256	GAGGGGGC CUGAUGAG X CGAA ICGGGGGG	CCCCCCCC C GCCCCCTC
259	AAGGAGGG CUGAUGAG X CGAA ICGGCGGG	CCCGCCGC C CCCTCCTT
260	GAAGGAGG CUGAUGAG X CGAA IGCGGCGG	CCGCCGCC C CCTCCTTC
261	GGAAGGAG CUGAUGAG X CGAA IGGCGGCG	CGCCGCCC C CTCCTTCC
262	CGGAAGGA CUGAUGAG X CGAA IGGGCGGC	GCCGCCCC C TCCTTCCG
263	GCGGAAGG CUGAUGAG X CGAA IGGGGCGG	GCCCCCCC C TTCCGCCA
265	UGGCGGAA CUGAUGAG X CGAA IAGGGGGC	COCCTCC T TCCGCCAG
266	CUGGCGGA CUGAUGAG X CGAA IGAGGGGG	CCTCCTTC C GCCAGGTG
269	CACCUGGC CUGAUGAG X CGAA IAAGGAGG	CCTCCGC C AGGTGTCC
272	GGACACCU CUGAUGAG X CGAA ICGGAAGG	CTTCCGCC A GGTGTCCT
273	AGGACACC CUGAUGAG X CGAA IGCGGAAG	CAGGTGTC C TGCCTGAA
280	UUCAGGCA CUGAUGAG X CGAA IACACCUG	AGGTGTCC T GCCTGAAG
281	CUUCAGGC CUGAUGAG X CGAA IGACACCU	TGTCCTGC C TGAAGGAG
284	CUCCUUCA CUGAUGAG X CGAA ICAGGACA	GTCCTGCC T GAAGGAGC
285	GCUCCUUC CUGAUGAG X CGAA IGCAGGAC	GAAGGAGC T GGTGGCCC
294	GGGCCACC CUGAUGAG X CGAA ICUCCUUC	CTGGTGGC C CGAGTGCT
301	AGCACUCG CUGAUGAG X CGAA ICCACCAG	TGGTGGCC C GAGTGCTG
302	CAGCACUC CUGAUGAG X CGAA IGCCACCA	CCGAGTGC T GCAGAGGC
309	GCCUCUGC CUGAUGAG X CGAA ICACUCGG	AGTGCTGC A GAGGCTGT
312	ACAGCCUC CUGAUGAG X CGAA ICAGCACU GCUCGCAC CUGAUGAG X CGAA ICCUCUGC	GCAGAGGC T GTGCGAGC
318	CGAAGGCC CUGAUGAG X CGAA ICACGUUC	GAACGTGC T GGCCTTCG
345	CGAAGGCC CUGAUGAG X CGAA TCACGUUC	

Table 14

349	AAGCCGAA CUGAUGAG X CGAA ICCAGCAC	GTGCTGGC C TTCGGCTT
350	GAAGCCGA CUGAUGAG X CGAA IGCCAGCA	TGCTGGCC T TCGGCTTC
356	CAGCGCGA CUGAUGAG X CGAA ICCGAAGG	CCTTCGGC T TCGCGCTG
363	CGUCCAGC CUGAUGAG X CGAA ICGCGAAG	CTTCGCGC T GCTGGACG
366	CCCCGUCC CUGAUGAG X CGAA ICAGCGCG	CGCGCTGC T GGACGGGG
376	CCCCCGCG CUGAUGAG X CGAA ICCCCGUC	GACGGGGC C CGCGGGGG
377	GCCCCCGC CUGAUGAG X CGAA IGCCCCGU	ACGGGGCC C GCGGGGGC
386	CUCGGGGG CUGAUGAG X CGAA ICCCCCGC	GCGGGGC C CCCCGAG
387	CCUCGGGG CUGAUGAG X CGAA IGCCCCCG	CGGGGGCC C CCCCGAGG
388	GCCUCGGG CUGAUGAG X CGAA IGGCCCCC	GGGGCCC C CCCGAGGC
389	GGCCUCGG CUGAUGAG X CGAA IGGGCCCC	GGGGCCCC C CCGAGGCC
390	AGGCCUCG CUGAUGAG X CGAA IGGGGCCC	GGGCCCCC C CGAGGCCT
391	AAGGCCUC CUGAUGAG X CGAA IGGGGGCC	GGCCCCC C GAGGCCTT
397	GUGGUGAA CUGAUGAG X CGAA ICCUCGGG	CCCGAGGC C TTCACCAC
398	GGUGGUGA CUGAUGAG X CGAA IGCCUCGG	CCGAGGCC T TCACCACC
401	GCUGGUGG CUGAUGAG X CGAA IAAGGCCU	AGGCCTTC A CCACCAGC
403	ACGCUGGU CUGAUGAG X CGAA IUGAAGGC	GCCTTCAC C ACCAGCGT
404	CACGCUGG CUGAUGAG X CGAA IGUGAAGG	CCTTCACC A CCAGCGTG
406	CGCACGCU CUGAUGAG X CGAA IUGGUGAA	TTCACCAC C AGCGTGCG
407	GCGCACGC CUGAUGAG X CGAA IGUGGUGA	TCACCACC A GCGTGCGC
416	CAGGUAGC CUGAUGAG X CGAA ICGCACGC	GCGTGCGC A GCTACCTG
419	GGGCAGGU CUGAUGAG X CGAA ICUGCGCA	TGCGCAGC T ACCTGCCC
422	GUUGGGCA CUGAUGAG X CGAA IUAGCUGC	GCAGCTAC C TGCCCAAC
423	UGUUGGGC CUGAUGAG X CGAA IGUAGCUG	CAGCTACC T GCCCAACA
426	CCGUGUUG CUGAUGAG X CGAA ICAGGUAG	CTACCTGC C CAACACGG
427	ACCGUGUU CUGAUGAG X CGAA IGCAGGUA	TACCTGCC C AACACGGT
428	CACCGUGU CUGAUGAG X CGAA IGGCAGGU	ACCTGCCC A ACACGGTG
431	GGUCACCG CUGAUGAG X CGAA IUUGGGCA	TGCCCAAC A CGGTGACC
439	AGUGCGUC CUGAUGAG X CGAA IUCACCGU	ACGGTGAC C GACGCACT
445	CCCCGCAG CUGAUGAG X CGAA ICGUCGGU	ACCGACGC A CTGCGGGG
447	UCCCCCGC CUGAUGAG X CGAA IUGCGUCG	CGACGCAC T GCGGGGGA GTGGGGGC T GCTGCTGC
471	GCAGCAGC CUGAUGAG X CGAA ICCCCCAC	
474	GGCGCAGC CUGAUGAG X CGAA ICAGCCCC	GGGGCTGC T GCTGCGCC GCTGCTGC T GCGCCGCG
477	CGCGCGC CUGAUGAG X CGAA ICAGCAGC	TGCTGCGC C GCGTGGGC
482	- GCCCACGC CUGAUGAG X CGAA ICGCAGCA	CGACGTGC T GGTTCACC
501	GGUGAACC CUGAUGAG X CGAA ICACGUCG	GCTGGTTC A CCTGCTGG
507	CCAGCAGG CUGAUGAG X CGAA IAACCAGC	TGGTTCAC C TGCTGGCA
509	UGCCAGCA CUGAUGAG X CGAA IUGAACCA	GGTTCACC T GCTGGCAC
510	GUGCCAGC CUGAUGAG X CGAA IGUGAACC	TCACCTGC T GCCACGCT
513	AGCGUGCC CUGAUGAG X CGAA ICAGGUGA	CTGCTGGC A CGCTGCGC
517	GCGCAGCG CUGAUGAG X CGAA ICCAGCAG	TGGCACGC T GCGCGCTC
521	GAGCGCGC CUGAUGAG X CGAA ICGUGCCA	CTGCGCGC T CTTTGTGC
528	GCACAAAG CUGAUGAG X CGAA ICGCGCAG	GCGCGCTC T TTGTGCTG
530	CAGCACAA CUGAUGAG X CGAA IAGCGCGC	CTTTGTGC T GGTGGCTC
537	GAGCCACC CUGAUGAG X CGAA ICACAAAG	CTGGTGGC T CCCAGCTG
544	CAGCUGGG CUGAUGAG X CGAA ICCACCAG	GGTGGCT C CAGCTGCG
546	CGCAGCUG CUGAUGAG X CGAA IAGCCACC	GGTGGCTC C CAGCTGCG

Table 14

	GCGCAGCU CUGAUGAG X CGAA IGAGCCAC	GTGGCTCC C AGCTGCGC
547	GGCGCAGC CUGAUGAG X CGAA IGGAGCCA	TGGCTCCC A GCTGCGCC
	GUAGGCGC CUGAUGAG X CGAA ICUGGGAG	CTCCCAGC T GCGCCTAC
551	ACCUGGUA CUGAUGAG X CGAA ICGCAGCU	AGCTGCGC C TACCAGGT
556	CACCUGGU CUGAUGAG X CGAA IGCGCAGC	GCTGCGCC T ACCAGGTG
557	GCACACCU CUGAUGAG X CGAA IUAGGCGC	GCGCCTAC C AGGTGTGC
560	CGCACACC CUGAUGAG X CGAA IGUAGGCG	CGCCTACC A GGTGTGCG
561	ACAGCGGC CUGAUGAG X CGAA ICCCGCAC	GTGCGGGC C GCCGCTGT
573	GGUACAGC CUGAUGAG X CGAA ICGGCCCG	CGGGCCGC C GCTGTACC
576 579	GCUGGUAC CUGAUGAG X CGAA ICGGCGGC	GCCGCCGC T GTACCAGC
	GCCGAGCU CUGAUGAG X CGAA IUACAGCG	CGCTGTAC C AGCTCGGC
584	CGCCGAGC CUGAUGAG X CGAA IGUACAGC	GCTGTACC A GCTCGGCG
585	CAGCGCCG CUGAUGAG X CGAA ICUGGUAC	GTACCAGC T CGGCGCTG
588	UGAGUGGC CUGAUGAG X CGAA ICGCCGAG	CTCGGCGC T GCCACTCA
595	GCCUGAGU CUGAUGAG X CGAA ICAGCGCC	GGCGCTGC C ACTCAGGC
598	GGCCUGAG CUGAUGAG X CGAA IGCAGCGC	GCGCTGCC A CTCAGGCC
599 601	CGGGCCUG CUGAUGAG X CGAA IUGGCAGC	GCTGCCAC T CAGGCCCG
603	GCCGGCC CUGAUGAG X CGAA IAGUGGCA	TGCCACTC A GGCCCGGC
607	GGGGGCCG CUGAUGAG X CGAA ICCUGAGU	ACTCAGGC C CGGCCCCC
608	CGGGGGCC CUGAUGAG X CGAA IGCCUGAG	CTCAGGCC C GGCCCCCG
612	GUGGCGGG CUGAUGAG X CGAA ICCGGGCC	GGCCCGGC C CCCGCCAC
613	UGUGGCGG CUGAUGAG X CGAA IGCCGGGC	GCCCGGCC C CCGCCACA
614	GUGUGGCG CUGAUGAG X CGAA IGGCCGGG	CCCGGCCC C CGCCACAC
615	CGUGUGGC CUGAUGAG X CGAA IGGGCCGG	CCGGCCCC C GCCACACG
618	UAGCGUGU CUGAUGAG X CGAA ICGGGGGC	GCCCCCGC C ACACGCTA
619	CUAGCGUG CUGAUGAG X CGAA IGCGGGGG	CCCCCGCC A CACGCTAG
621	CACUAGCG CUGAUGAG X CGAA IUGGCGGG	CCCGCCAC A CGCTAGTG
625	GGUCCACU CUGAUGAG X CGAA ICGUGUGG	CCACACGC T AGTGGACC
633	GCCUUCGG CUGAUGAG X CGAA IUCCACUA	TAGTGGAC C CCGAAGGC
634	CGCCUUCG CUGAUGAG X CGAA IGUCCACU	AGTGGACC C CGAAGGCG
635	ACGCCUUC CUGAUGAG X CGAA IGGUCCAC	GTGGACCC C GAAGGCGT
645	CGCAUCCC CUGAUGAG X CGAA IACGCCUU	AAGGCGTC T GGGATGCG
661	UGGUUCCA CUGAUGAG X CGAA ICCCGUUC	GAACGGGC C TGGAACCA
662	AUGGUUCC CUGAUGAG X CGAA IGCCCGUU	AACGGGCC T GGAACCAT
668	GACGCUAU CUGAUGAG X CGAA IUUCCAGG	CCTGGAAC C ATAGCGTC
669	UGACGCUA CUGAUGAG X CGAA IGUUCCAG	CTGGAACC A TAGCGTCA
677	GGCCUCCC CUGAUGAG X CGAA IACGCUAU	ATAGCGTC A GGGAGGCC
685	GGGACCCC CUGAUGAG X CGAA ICCUCCCU	AGGGAGGC C GGGGTCCC CCGGGGTC C CCCTGGGC
692	GCCCAGGG CUGAUGAG X CGAA IACCCCGG	CGGGGTC C CCTGGGCC
693	GGCCCAGG CUGAUGAG X CGAA IGACCCCG	GGGGTCC C CTGGGCCT
694	AGGCCCAG CUGAUGAG X CGAA IGGACCCC	GGGTCCC C TGGGCCT
695	CAGGCCCA CUGAUGAG X CGAA IGGGACCC	GGTCCCC C TGGGCCTGC
696	GCAGGCCC CUGAUGAG X CGAA IGGGGACC	CCCTGGGC C TGCCAGCC
701	GGCUGGCA CUGAUGAG X CGAA ICCCAGGG	CCTGGGC T GCCAGCC
702	GGGCUGGC CUGAUGAG X CGAA IGCCCAGG	GGGCCTGC C AGCCCCGG
705	CCGGGGCU CUGAUGAG X CGAA ICAGGCCC	GGCCTGCC A GCCCCGGG
706	CCCGGGGC CUGAUGAG X CGAA IGCAGGCC	GGCCIGCC A GCCCCGGC

Table 14

		CTGCCAGC C CCGGGTGC
709	GCACCCGG CUGAUGAG X CGAA ICUGGCAG	TGCCAGCC C CGGGTGCG
710	CGCACCCG CUGAUGAG X CGAA IGCUGGCA	GCCAGCC C GGGTGCGA
711	UCGCACCC CUGAUGAG X CGAA IGGCUGGC	GCCAGCCC C GGGTGCGA
734	GCUGGCAC CUGAUGAG X CGAA ICCCCCGC	
739	CUUCGGCU CUGAUGAG X CGAA ICACUGCC	GGCAGTGC C AGCCGAAG
740	ACUUCGGC CUGAUGAG X CGAA IGCACUGC	GCAGTGCC A GCCGAAGT
743	CAGACUUC CUGAUGAG X CGAA ICUGGCAC	GTGCCAGC C GAAGTCTG
750	GCAACGGC CUGAUGAG X CGAA IACUUCGG	CCGAAGTC T GCCGTTGC
753	UGGGCAAC CUGAUGAG X CGAA ICAGACUU	AAGTCTGC C GTTGCCCA
759	GCCUCUUG CUGAUGAG X CGAA ICAACGGC	GCCGTTGC C CAAGAGGC
760	GGCCUCUU CUGAUGAG X CGAA IGCAACGG	CCGTTGCC C AAGAGGCC
761	GGGCCUCU CUGAUGAG X CGAA IGGCAACG	CGTTGCCC A AGAGGCCC
768	CACGCCUG CUGAUGAG X CGAA ICCUCUUG	CAAGAGGC C CAGGCGTG
	CCACGCCU CUGAUGAG X CGAA IGCCUCUU	AAGAGGCC C AGGCGTGG
769	GCACGCC CUGAUGAG X CGAA IGGCCUCU	AGAGGCCC A GGCGTGGC
770	UCAGGGGC CUGAUGAG X CGAA ICGCCACG	CGTGGCGC T GCCCCTGA
781	GGCUCAGG CUGAUGAG X CGAA ICAGCGCC	GGCGCTGC C CCTGAGCC
784	CGGCUCAG CUGAUGAG X CGAA IGCAGCGC	GCGCTGCC C CTGAGCCG
785	CCGGCUCA CUGAUGAG X CGAA IGCAGCG	CGCTGCCC C TGAGCCGG
786	UCCGGCUCA CUGAUGAG X CGAA IGGGCAGC	GCTGCCCC T GAGCCGGA
787		CCCTGAGC C GGAGCGGA
792	UCCGCUCC CUGAUGAG X CGAA ICUCAGGG	GCGGACGC C CGTTGGGC
804	GCCCAACG CUGAUGAG X CGAA ICGUCCGC	CGGACGCC C GTTGGGCA
805	UGCCCAAC CUGAUGAG X CGAA IGCGUCCG	CGTTGGGC A GGGGTCCT
813	AGGACCCC CUGAUGAG X CGAA ICCCAACG	CAGGGGTC C TGGGCCCA
820	UGGGCCCA CUGAUGAG X CGAA IACCCCUG	AGGGGTCC T GGGCCCAC
821	GUGGGCCC CUGAUGAG X CGAA IGACCCCU	TCCTGGGC C CACCCGGG
826	CCCGGGUG CUGAUGAG X CGAA ICCCAGGA	CCTGGGCC C ACCCGGCC
827	GCCCGGGU CUGAUGAG X CGAA IGCCCAGG	CTGGGCCC A CCCGGGCA
828	UGCCCGGG CUGAUGAG X CGAA IGGCCCAG	GGGCCCAC C CGGGCAGG
830	CCUGCCCG CUGAUGAG X CGAA IUGGGCCC	GGCCCAC C GGGCAGGA
831	UCCUGCCC CUGAUGAG X CGAA IGUGGGCC	ACCCGGC A GGACGCGT
836	ACGCGUCC CUGAUGAG X CGAA ICCCGGGU	GCGTGGAC C GAGTGACC
849	GGUCACUC CUGAUGAG X CGAA IUCCACGC	GGGTGGAC C GAGTGACC
857	GAAACCAC CUGAUGAG X CGAA IUCACUCG	GTGGTTTC T GTGTGGTG
866	CACCACAC CUGAUGAG X CGAA IAAACCAC	
877	CUGGCAGG CUGAUGAG X CGAA IACACCAC	GTGGTGTC A CCTGCCAG
879	GUCUGGCA CUGAUGAG X CGAA IUGACACC	GGTGTCAC C TGCCAGAC
880	GGUCUGGC CUGAUGAG X CGAA IGUGACAC	GTGTCACC T GCCAGACC
883	GCGGGUCU CUGAUGAG X CGAA ICAGGUGA	TCACCTGC C AGACCCGC
884	GGCGGGUC CUGAUGAG X CGAA IGCAGGUG	CACCTGCC A GACCCGCC
888	CUUCGGCG CUGAUGAG X CGAA IUCUGGCA	TGCCAGAC C CGCCGAAG
889	UCUUCGGC CUGAUGAG X CGAA IGUCUGGC	GCCAGACC C GCCGAAGA
892	GCUUCUUC CUGAUGAG X CGAA ICGGGUCU	AGACCCGC C GAAGAAGC
901	AAAGAGGU CUGAUGAG X. CGAA ICUUCUUC	GAAGAAGC C ACCTCTTT
902	CAAAGAGG CUGAUGAG X CGAA IGCUUCUU	AAGAAGCC A CCTCTTTG
902	UCCAAAGA CUGAUGAG X CGAA IUGGCUUC	GAAGCCAC C TCTTTGGA
905	CUCCAAAG CUGAUGAG X CGAA IGUGGCUU	AAGCCACC T CTTTGGAG
905	COCCOMING COCKCOTO IL TOTAL I TOTAL	

Table 14

907	CCCUCCAA CUGAUGAG X CGAA IAGGUGGC	GCCACCTC T TTGGAGGG
921	UGCCAGAG CUGAUGAG X CGAA ICGCACCC	GGGTGCGC T CTCTGGCA
923	CGUGCCAG CUGAUGAG X CGAA IAGCGCAC	GTGCGCTC T CTGGCACG
925	CGCGUGCC CUGAUGAG X CGAA IAGAGCGC	GCGCTCTC T GGCACGCG
929	GUGGCGCG CUGAUGAG X CGAA ICCAGAGA	TCTCTGGC A CGCGCCAC
935	GUGGGAGU CUGAUGAG X CGAA ICGCGUGC	GCACGCGC C ACTCCCAC
936	GGUGGGAG CUGAUGAG X CGAA IGCGCGUG	CACGCGCC A CTCCCACC
938	UGGGUGGG CUGAUGAG X CGAA IUGGCGCG	CGCGCCAC T CCCACCCA
940	GAUGGGUG CUGAUGAG X CGAA IAGUGGCG	CGCCACTC C CACCCATC
941	GGAUGGGU CUGAUGAG X CGAA IGAGUGGC	GCCACTCC C ACCCATCC
942	CGGAUGGG CUGAUGAG X CGAA IGGAGUGG	CCACTCCC A CCCATCCG
944	CACGGAUG CUGAUGAG X CGAA IUGGGAGU	ACTCCCAC C CATCCGTG
945	CCACGGAU CUGAUGAG X CGAA IGUGGGAG	CTCCCACC C ATCCGTGG
946	CCCACGGA CUGAUGAG X CGAA IGGUGGGA	TCCCACCC A TCCGTGGG
949	CGGCCCAC CUGAUGAG X CGAA TAUGGGUG	CACCCATC C GTGGGCCG
956	GUGCUGGC CUGAUGAG X CGAA ICCCACGG	CCGTGGGC C GCCAGCAC
959	GUGGUGCU CUGAUGAG X CGAA ICGGCCCA	TGGGCCGC C AGCACCAC
960	CGUGGUGC CUGAUGAG X CGAA IGCGGCCC	GGGCCGCC A GCACCACG
963	CCGCGUGG CUGAUGAG X CGAA ICUGGCGG	CCGCCAGC A CCACGCGG
965	GCCCGCGU CUGAUGAG X CGAA IUGCUGGC	GCCAGCAC C ACGCGGGC
966	GGCCCGCG CUGAUGAG X CGAA IGUGCUGG	CCAGCACC A CGCGGGCC
974	GGAUGGGG CUGAUGAG X CGAA ICCCGCGU	ACGCGGGC C CCCCATCC
975	UGGAUGGG CUGAUGAG X CGAA IGCCCGCG	CGCGGGCC C CCCATCCA
976	GUGGAUGG CUGAUGAG X CGAA IGGCCCGC	GCGGGCCC C CCATCCAC
977	UGUGGAUG CUGAUGAG X CGAA IGGGCCCG	CGGGCCCC C CATCCACA
978	AUGUGGAU CUGAUGAG X CGAA IGGGGCCC	GGGCCCCC C ATCCACAT
979	GAUGUGGA CUGAUGAG X CGAA IGGGGGCC	GGCCCCCC A TCCACATC
982	CGCGAUGU CUGAUGAG X CGAA IAUGGGGG	CCCCCATC C ACATCGCG
983	CCGCGAUG CUGAUGAG X CGAA IGAUGGGG	CCCCATCC A CATCGCGG
985	GGCCGCGA CUGAUGAG X CGAA IUGGAUGG	CCATCCAC A TCGCGGCC
993	GACGUGGU CUGAUGAG X CGAA ICCGCGAU	ATCGCGGC C ACCACGTC TCGCGGCC A CCACGTCC
994	GGACGUGG CUGAUGAG X CGAA IGCCGCGA	
996	AGGGACGU CUGAUGAG X CGAA IUGGCCGC	GCGGCCAC C ACGTCCCT CGGCCACC A CGTCCCTG
997	CAGGGACG CUGAUGAG X CGAA IGUGGCCG	ACCACGTC C CTGGGACA
1002	UGUCCCAG CUGAUGAG X CGAA IACGUGGU	CCACGTCC C TGGGACAC
1003	GUGUCCCA CUGAUGAG X CGAA IGACGUGG	CACGTCC C IGGGACAC
1004	CGUGUCCC CUGAUGAG X CGAA IGGACGUG	CCTGGGAC A CGCCTTGT
1010	ACAAGGCG CUGAUGAG X CGAA IUCCCAGG	GGACACGC C TTGTCCCC
1014	GGGGACAA CUGAUGAG X CGAA ICGUGUCC	GACACGC C TIGTCCCC
1015	GGGGGACA CUGAUGAG X CGAA IGCGUGUC	GCCTTGTC C CCCGGTGT
1020	ACACCGGG CUGAUGAG X CGAA IACAAGGC	CCTTGTCC C CCGGTGTA
1021	UACACCGG CUGAUGAG X CGAA IGACAAGG	CTTGTCCC C CGGTGTAC
1022	GUACACCG CUGAUGAG X CGAA IGGACAAG	TIGTCCCC C GGTGTACG
1023	CGUACACC CUGAUGAG X CGAA IGGGACAA	GTGTACGC C GAGACCAA
1033	UUGGUCUC CUGAUGAG X CGAA ICGUACAC	GCCGAGAC C AAGCACTT
1039	AAGUGCUU CUGAUGAG X CGAA IUCUCGGC	CCGAGACC A AGCACTTC
1040	GAAGUGCU CUGAUGAG X CGAA IGUCUCGG	CCGACAGE A ADEACTTE

Table 14

1044	AGAGGAAG CUGAUGAG X CGAA ICUUGGUC	GACCAAGC A CTTCCTCT
1046	GUAGAGGA CUGAUGAG X CGAA IUGCUUGG	CCAAGCAC T TCCTCTAC
1049	GGAGUAGA CUGAUGAG X CGAA IAAGUGCU	AGCACTTC C TCTACTCC
1050	AGGAGUAG CUGAUGAG X CGAA IGAAGUGC	GCACTTCC T CTACTCCT
1052	UGAGGAGU CUGAUGAG X CGAA IAGGAAGU	ACTTCCTC T ACTCCTCA
1055	GCCUGAGG CUGAUGAG X CGAA IUAGAGGA	TCCTCTAC T CCTCAGGC
1057	UCGCCUGA CUGAUGAG X CGAA IAGUAGAG	CTCTACTC C TCAGGCGA
1058	GUCGCCUG CUGAUGAG X CGAA IGAGUAGA	TCTACTCC T CAGGCGAC
1060	UUGUCGCC CUGAUGAG X CGAA IAGGAGUA	TACTCCTC A GGCGACAA
1067	CUGCUCCU CUGAUGAG X CGAA IUCGCCUG	CAGGCGAC A AGGAGCAG
1074	GCCGCAGC CUGAUGAG X CGAA ICUCCUUG	CAAGGAGC A GCTGCGGC
1077	AGGGCCGC CUGAUGAG X CGAA ICUGCUCC	GGAGCAGC T GCGGCCCT
1083	GGAAGGAG CUGAUGAG X CGAA ICCGCAGC	GCTGCGGC C CTCCTTCC
1084	AGGAAGGA CUGAUGAG X CGAA IGCCGCAG	CTGCGGCC C TCCTTCCT
1085	UAGGAAGG CUGAUGAG X CGAA IGGCCGCA	TGCGGCCC T CCTTCCTA
1087	AGUAGGAA CUGAUGAG X CGAA IAGGGCCG	CGGCCCTC C TTCCTACT
1088	GAGUAGGA CUGAUGAG X CGAA IGAGGGCC	GGCCCTCC T TCCTACTC
1091	GCUGAGUA CUGAUGAG X CGAA IAAGGAGG	CCTCCTTC C TACTCAGC
1092	AGCUGAGU CUGAUGAG X CGAA IGAAGGAG	CTCCTTCC T ACTCAGCT
1095	GAGAGCUG CUGAUGAG X CGAA IUAGGAAG	CTTCCTAC T CAGCTCTC
1097	CAGAGAGC CUGAUGAG X CGAA IAGUAGGA	TCCTACTC A GCTCTCTG
1100	CCUCAGAG CUGAUGAG X CGAA ICUGAGUA	TACTCAGC T CTCTGAGG
1102	GGCCUCAG CUGAUGAG X CGAA IAGCUGAG	CTCAGCTC T CTGAGGCC
1104	UGGGCCUC CUGAUGAG X CGAA IAGAGCUG	CAGCTCTC T GAGGCCCA
1110	UCAGGCUG CUGAUGAG X CGAA ICCUCAGA	TCTGAGGC C CAGCCTGA
1111	GUCAGGCU CUGAUGAG X CGAA IGCCUCAG	CTGAGGCC C AGCCTGAC TGAGGCCC A GCCTGACT
1112	AGUCAGGC CUGAUGAG X CGAA IGGCCUCA	GGCCCAGC C TGACTGGC
1115	GCCAGUCA CUGAUGAG X CGAA ICUGGGCC	GCCCAGCC T GACTGGCG
1116	CGCCAGUC CUGAUGAG X CGAA IGCUGGGC	AGCCTGAC T GGCGCTCG
1120	CGAGCGCC CUGAUGAG X CGAA IUCAGGCU	ACTGGCGC T CGGAGGCT
1126	AGCCUCCG CUGAUGAG X CGAA ICGCCAGU UCUCCACG CUGAUGAG X CGAA ICCUCCGA	TCGGAGGC T CGTGGAGA
1134	AGAAAGAU CUGAUGAG X CGAA ICCUCCAC	GTGGAGAC C ATCITTCT
1144	CAGAAAGA CUGAUGAG X CGAA IGUCUCCA	TGGAGACC A TCTTTCTG
1145	ACCCAGAA CUGAUGAG X CGAA IAUGGUCU	AGACCATC T TTCTGGGT
	UGGAACCC CUGAUGAG X CGAA IAAAGAUG	CATCTITC T GGGTTCCA
1152	CAGGGCCU CUGAUGAG X CGAA IAACCCAG	CTGGGTTC C AGGCCCTG
1160	CCAGGGCC CUGAUGAG X CGAA IGAACCCA	TGGGTTCC A GGCCCTGG
1164	GCAUCCAG CUGAUGAG X CGAA ICCUGGAA	TTCCAGGC C CTGGATGC
1165	GCAUCCA CUGAUGAG X CGAA IGCCUGGA	TCCAGGCC C TGGATGCC
1166	UGGCAUCC CUGAUGAG X CGAA IGGCCUGG	CCAGGCCC T GGATGCCA
1173	GAGUCCCU CUGAUGAG X CGAA ICAUCCAG	CTGGATGC C AGGGACTC
1174	GGAGUCCC CUGAUGAG X CGAA IGCAUCCA	TGGATGCC A GGGACTCC
1180	CUGCGGGG CUGAUGAG X CGAA IUCCCUGG	CCAGGGAC T CCCCGCAG
1182	ACCUGCGG CUGAUGAG X CGAA IAGUCCCU	AGGGACTC C CCGCAGGT
1183	AACCUGCG CUGAUGAG X CGAA IGAGUCCC	GGGACTCC C CGCAGGTT
1184	CAACCUGC CUGAUGAG X CGAA IGGAGUCC	GGACTCCC C GCAGGTTG
L		

Table 14

	GGGCAACC CUGAUGAG X CGAA ICGGGGAG	CTCCCCGC A GGTTGCCC
1187	GCAGGCGG CUGAUGAG X CGAA ICAACCUG	CAGGTTGC C CCGCCTGC
1194	GGCAGGCG CUGAUGAG X CGAA ICAACCU	AGGTTGCC C CGCCTGCC
1195		GGTTGCCC C GCCTGCCC
1196	GGGCAGGC CUGAUGAG X CGAA IGGCAACC	TGCCCCGC C TGCCCCAG
1199	CUGGGGCA CUGAUGAG X CGAA ICGGGGCA	GCCCGCC T GCCCCAGC
1200	GCUGGGGC CUGAUGAG X CGAA IGCGGGGC	
1203	AGCGCUGG CUGAUGAG X CGAA ICAGGCGG	CCGCCTGC C CCAGCGCT
1204	UAGCGCUG CUGAUGAG X CGAA IGCAGGCG	CGCCTGCC C CAGCGCTA
1205	GUAGCGCU CUGAUGAG X CGAA IGGCAGGC	GCCTGCCC C AGCGCTAC
1206	AGUAGOGC CUGAUGAG X CGAA IGGGCAGG	CCTGCCCC A GCGCTACT
1211	UUGCCAGU CUGAUGAG X CGAA ICGCUGGG	CCCAGCGC T ACTGGCAA
1214	CAUUUGCC CUGAUGAG X CGAA IUAGCGCU	AGCGCTAC T GGCAAATG
1218	GCCGCAUU CUGAUGAG X CGAA ICCAGUAG	CTACTGGC A AATGCGGC
1227	GAAACAGG CUGAUGAG X CGAA ICCGCAUU	AATGCGGC C CCTGTTTC
1228	AGAAACAG CUGAUGAG X CGAA IGCCGCAU	ATGCGGCC C CTGTTTCT
1229	CAGAAACA CUGAUGAG X CGAA IGGCCGCA	TGCGGCCC C TGTTTCTG
1230	CCAGAAAC CUGAUGAG X CGAA IGGGCCGC	GCGGCCCC T GTTTCTGG
1236	GCAGCUCC CUGAUGAG X CGAA IAAACAGG	CCTGTTTC T GGAGCTGC
1242	UCCCAAGC CUGAUGAG X CGAA ICUCCAGA	TCTGGAGC T GCTTGGGA
1245	GGUUCCCA CUGAUGAG X CGAA ICAGCUCC	GGAGCTGC T TGGGAACC
1253	CUGCGCGU CUGAUGAG X CGAA IUUCCCAA	TTGGGAAC C ACGCGCAG
1254	ACUGCGCG CUGAUGAG X CGAA IGUUCCCA	TGGGAACC A CGCGCAGT
1260	AGGGGCAC CUGAUGAG X CGAA ICGCGUGG	CCACGCGC A GTGCCCCT
1265	CCCGUAGG CUGAUGAG X CGAA ICACUGCG	CGCAGTGC C CCTACGGG
1266	CCCCGUAG CUGAUGAG X CGAA IGCACUGC	GCAGTGCC C CTACGGGG
1267	ACCCCGUA CUGAUGAG X CGAA IGGCACUG	CAGTGCCC C TACGGGGT
1268	CACCCCGU CUGAUGAG X CGAA IGGGCACU	AGTGCCCC T ACGGGGTG
1278	UCUUGAGG CUGAUGAG X CGAA ICACCCCG	CGGGGTGC T CCTCAAGA
1280	CGUCUUGA CUGAUGAG X CGAA IAGCACCC	GGGTGCTC C TCAAGACG
1281	GCGUCUUG CUGAUGAG X CGAA IGAGCACC	GGTGCTCC T CAAGACGC
1283	GUGCGUCU CUGAUGAG X CGAA IAGGAGCA	TGCTCCTC A AGACGCAC
1290	GCGGGCAG CUGAUGAG X CGAA ICGUCUUG	CAAGACGC A CTGCCCGC
1292	CAGCGGC CUGAUGAG X CGAA IUGCGUCU	AGACGCAC T GCCCGCTG
1295	UCGCAGCG CUGAUGAG X CGAA ICAGUGCG	CGCACTGC C CGCTGCGA
1296	CUCGCAGC CUGAUGAG X CGAA IGCAGUGC	GCACTGCC C GCTGCGAG
1299	CAGCUCGC CUGAUGAG X CGAA ICGGGCAG	CTGCCCGC T GCGAGCTG
1306	GUGACCGC CUGAUGAG X CGAA ICUCGCAG	CTGCGAGC T GCGGTCAC
1313	UGCUGGGG CUGAUGAG X CGAA IACCGCAG	CTGCGGTC A CCCCAGCA
1315	GCUGCUGG CUGAUGAG X CGAA TUGACCGC	GCGGTCAC C CCAGCAGC
1316	GGCUGCUG CUGAUGAG X CGAA IGUGACCG	CGGTCACC C CAGCAGCC
1317	CGGCUGCU CUGAUGAG X CGAA IGGUGACC	GGTCACCC C AGCAGCCG
1317	CCGGCUGC CUGAUGAG X CGAA IGGGUGAC	GTCACCCC A GCAGCCGG
1318	ACACCGGC CUGAUGAG X CGAA ICUGGGGU	ACCCCAGC A GCCGGTGT
	CAGACACC CUGAUGAG X CGAA ICUGCUGG	CCAGCAGC C GGTGTCTG
1324	CCGGGCAC CUGAUGAG X CGAA IACACCGG	CCGGTGTC T GTGCCCGG
1331	UUCUCCCG CUGAUGAG X CGAA TACACCGG	GTCTGTGC C CGGGAGAA
1336		TCTGTGCC C GGGAGAAG
1337	CUUCUCCC CUGAUGAG X CGAA IGCACAGA	TCTGTGCC C GGGAGAAG

Table 14

1347	AGCCCUGG CUGAUGAG X CGAA ICUUCUCC	GGAGAAGC C CCAGGGCT
1348	GAGCCCUG CUGAUGAG X CGAA IGCUUCUC	GAGAAGCC C CAGGGCTC
1349	AGAGCCCU CUGAUGAG X CGAA IGGCUUCU	AGAAGCCC C AGGGCTCT
1350	CAGAGCCC CUGAUGAG X CGAA IGGGCUUC	GAAGCCCC A GGGCTCTG
1355	CGCCACAG CUGAUGAG X CGAA ICCCUGGG	CCCAGGGC T CTGTGGCG
1357	GCCGCCAC CUGAUGAG X CGAA IAGCCCUG	CAGGGCTC T GTGGCGGC
1366	UCCUCGGG CUGAUGAG X CGAA ICCGCCAC	GTGGCGGC C CCCGAGGA
1367	CUCCUCGG CUGAUGAG X CGAA IGCCGCCA	TGGCGGCC C CCGAGGAG
1368	CCUCCUCG CUGAUGAG X CGAA IGGCCGCC	GGCGGCCC C CGAGGAGG
1369	UCCUCCUC CUGAUGAG X CGAA IGGGCCGC	GCGGCCCC C GAGGAGGA
1382	GGGGUCUG CUGAUGAG X CGAA IUCCUCCU	AGGAGGAC A CAGACCCC
1384	CGGGGGUC CUGAUGAG X CGAA IUGUCCUC	GAGGACAC A GACCCCCG
1388	GCGACGGG CUGAUGAG X CGAA IUCUGUGU	ACACAGAC C CCCGTCGC
1389	GGCGACGG CUGAUGAG X CGAA IGUCUGUG	CACAGACC C CCGTCGCC
1390	AGGCGACG CUGAUGAG X CGAA IGGUCUGU	ACAGACCC C CGTCGCCT
1391	CAGGOGAC CUGAUGAG X CGAA IGGGUCUG	CAGACCCC C GTCGCCTG
1397	CUGCACCA CUGAUGAG X CGAA ICGACGGG	CCCGTCGC C TGGTGCAG
1398	GCUGCACC CUGAUGAG X CGAA IGCGACGG	CCGTCGCC T GGTGCAGC
1404	GGAGCAGC CUGAUGAG X CGAA ICACCAGG	CCTGGTGC A GCTGCTCC
1407	GGCGGAGC CUGAUGAG X CGAA ICUGCACC	GGTGCAGC T GCTCCGCC
1410	GCUGGCGG CUGAUGAG X CGAA ICAGCUGC	GCAGCTGC T CCGCCAGC
1412	GUGCUGGC CUGAUGAG X CGAA IAGCAGCU	AGCTGCTC C GCCAGCAC
1415	GCUGUGCU CUGAUGAG X CGAA ICGGAGCA	TGCTCCGC C AGCACAGC
1416	UGCUGUGC CUGAUGAG X CGAA IGCGGAGC	GCTCCGCC A GCACAGCA
1419	GGCUGCUG CUGAUGAG X CGAA ICUGGCGG	CCGCCAGC A CAGCAGCC
1421	GGGGCUGC CUGAUGAG X CGAA IUGCUGGC	GCCAGCAC A GCAGCCCC
1424	CCAGGGC CUGAUGAG X CGAA ICUGUGCU	AGCACAGC A GCCCCTGG
1427	CUGCCAGG CUGAUGAG X CGAA ICUGCUGU	ACAGCAGC C CCTGGCAG
1428	CCUGCCAG CUGAUGAG X CGAA IGCUGCUG	CAGCAGCC C CTGGCAGG
1429	ACCUGCCA CUGAUGAG X CGAA IGGCUGCU	AGCAGCCC C TGGCAGGT
1430	CACCUGCC CUGAUGAG X CGAA IGGGCUGC	GCAGCCCC T GGCAGGTG CCCCTGGC A GGTGTACG
1434	CGUACACC CUGAUGAG X CGAA ICCAGGGG	TGTACGGC T TCGTGCGG
1445	CCGCACGA CUGAUGAG X CGAA ICCGUACA	GTGCGGC C TGCCTGCG
1456	CGCAGGCA CUGAUGAG X CGAA ICCCGCAC	TGCGGGCC T GCCTGCGC
1457	GCGCAGGC CUGAUGAG X CGAA IGCCCGCA	GGGCCTGC C TGCGCCGG
1460	CCGGCGCA CUGAUGAG X CGAA ICAGGCCC	GGCCTGCC T GCGCCGGC
1461	GCCGGCGC CUGAUGAG X CGAA IGCAGGCC	GCCTGCGC C GGCTGGTG
1466	CACCAGCC CUGAUGAG X CGAA ICGCAGGC	GCGCCGGC T GGTGCCCC
1470	GGGGCACC CUGAUGAG X CGAA ICCGGCGC	GCTGGTGC C CCCAGGCC
1476	GGCCUGGG CUGAUGAG X CGAA ICACCAGC	CTGGTGCC C CCAGGCCT
1477	AGGCCUGG CUGAUGAG X CGAA IGCACCAG GAGGCCUG CUGAUGAG X CGAA IGGCACCA	TGGTGCCC C CAGGCCTC
1478	AGAGGCCU CUGAUGAG X CGAA IGGCACC	GGTGCCCC C AGGCCTCT
1479	CAGAGGCCU CUGAUGAG X CGAA IGGGCACC	GTGCCCCC A GGCCTCTG
1480	GCCCCAGA CUGAUGAG X CGAA ICCUGGGG	CCCCAGGC C TCTGGGGC
1484	AGCCCCAGA CUGAUGAG X CGAA ICCUGGG	CCCAGGCC T CTGGGGCT
1485	GGAGCCCC CUGAUGAG X CGAA IAGGCCUG	CAGGCCTC T GGGGCTCC
1487	GGAGCCCC CUGAGGAG A CGAR INGGCCGG	

Table 14

1493			
1496	1493	GUGCCUGG CUGAUGAG X CGAA ICCCCAGA	TCTGGGGC T CCAGGCAC
1590	1495		
1502 GOGUNICUI CUGANDAD X CGAA TUGCCUGG	1496		
1910 GARGARAGE CUGARIGAN X COMA TOSUNCOU AGGARGOS C GETTECTE	1500		
1514 CCCGARGGA CUGAUGAG X CGAA LAGGGGGUU	1502	GCGUUCGU CUGAUGAG X CGAA IUGCCUGG	
1517 GUUCCUGA CUGAUDAGA X CGAA TAAGCOGC GCCGCTTC C TCAGGAAC 1518 UGUUCCUG CUGAUDAGA X CGAA TAAGCOGC GCCGCTTC C TCAGGAACA 1528 GUUCCUGG CUGAUDAGA X CGAA TAGGAAGC GCTTCCTC A GGAACACC 1528 GUUCCUGG CUGAUDAGA X CGAA TAGGAAGC GCTTCCTC A GGAACACC 1528 AACUUCUU CUGAUGAGA X CGAA TUUCCUGA TCAGGAACA C ACAAGAAG 1528 AACUUCUU CUGAUGAGA X CGAA TUUUCCUC AGGAACAC C AAGAAGTT 1529 GAACTUCU CUGAUGAGA X CGAA TUGUUCCU AGGAACAC C AAGAAGTT 1529 GAACTUCU CUGAUGAGA X CGAA TAGGUUCC GGAACACC A AGAAGTT 1539 CAGGAGAGA CUGAUDAGA X CGAA TAGGUUCC AGGAACAC C AAGAAGTT 1541 CCCCCAGGG CUGAUDAGA X CGAA TAGGUUCC AGGAACAC C AAGAAGTT 1541 CUCCCCCA CUGAUDAGA X CGAA TAGGUUCC AGGAACAC C TAGGAGAG 1543 UUCCCCAG CUGAUDAGA X CGAA TAGGUUGA ATTCATCT C CTGGGGAAA 1544 CUUCCCCA CUGAUDAGA X CGAA TAGGUUGA TTCATCTC C TGGGGAAA 1545 GUUUGCCC CUGAUDAGA X CGAA TAGGUUGA TCATCTCC C TGGGGAAA 1546 GCUUGCCC CUGAUDAGA X CGAA TAGGUUGA AGGATCT C C TGGGGAAG 1557 GGAGGCU CUGAUDAGA X CGAA TAGGUUGA AAGACTTC C AGGCTCT 1559 CGAGGCU CUGAUGAGA X CGAA TAGGUUGA AAGACTTC C AGGCTCT 1559 CGAGAGCU CUGAUGAGA X CGAA TAGGUUGA AAGACTTC C AGCTCTC 1560 GCCUCUGC CUGAUGAGA X CGAA TAGGUUGGA AAGACTTC C AGCTCTC 1561 GCCACGC CUGAUGAGA X CGAA TAGGUUGGA AGCATCC C AGCTCTC 1563 GCCACGC CUGAUGAGA X CGAA TAGGUUGGA CCCACGC C COCACGC 1564 GCUCCUGC CUGAUGAG X CGAA TAGCUUGGA CCCACGC T CTCCCTC C COCACGC 1565 GCUCCUGC CUGAUGAG X CGAA TAGCUUGG CCCACGC C CAGGACC C C	1511	GAGGAAGC CUGAUGAG X CGAA ICGUUCGU	
1518 GUIUCCUC CUGANINA X CORA TIANAGOG	1514	CCUGAGGA CUGAUGAG X CGAA ICGGCGUU	AACGCCGC T TCCTCAGG
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1556 GCNGACGG CUGAUGAG X CGAA ICUCUUGCG CGCAGAGC A CCGTCTCC 1558 ACGCAGAC CUGAUGAG X CGAA IUUCUCUG CAGAGGCA C CGTCTGCGT 1558 ACGCAGAC CUGAUGAG X CGAA IACGUUGC CGCACGGC CUGAUGAG X CGAA IACGUUGC GCACGGT T GCGTGAGG 1676 CUUGGCC CUGAUGAG X CGAA IALCUCCU AGGAGATC C TGGCCAAG 1677 ACUUGGCC CUGAUGAG X CGAA IGAUCUCC GGMASTCC T GGCCAAGT 1681 AGGACUU CUGAUGAG X CGAA ICACGGGAU ATCCTGGC C AAGTTCCT 1682 CAGGAACU CUGAUGAG X CGAA ICACGGGA TCCTGGC C AAGTTCCT 1683 CCAGUUGC CUGAUGAG X CGAA ICACCUGG CCAAGTTC C TGCACTGG 1689 CCAGUUGC CUGAUGAG X CGAA ICACCUGG CCAAGTTC C TGCACTGG 1689 CCAGUUGC CUGAUGAG X CGAA ICACCUUG CAAGTTC C TGCACTGG 1689 CCCAGUGC CUGAUGAG X CGAA ICACCUUG CAAGTTC C TGCACTGG 1689 CCCAGUGC CUGAUGAG X CGAA IGAACTUG CAAGTTC C TGCACTGG	1648	UGCUCUGC CUGAUGAG X CGAA ICCGGAAC	
1658	1651	CGGUGCUC CUGAUGAG X CGAA ICGGCCGG	
1692 CCUCACGC CUCAUGAG X CGAA IACCGUGC GCACCGTC T GCGTGAGG 1676 CUUGACCA CUGAUGAG X CGAA IAUCUCCU AGGAGATC C TGGCCAAG 1677 ACUUGGCC CUGAUGAG X CGAA IGAUCUCC GGAGAATC C TGGCCAAG 1681 AGGAACUU CUCAUGAG X CGAA ICACGGAU ATCCTGGC C AAGTTCCT 1682 CACGAACU CUCAUGAG X CGAA IGCACGGAU ATCCTGGC C AAGTTCCT 1682 CACGAACU CUCAUGAG X CGAA IGCACGGA TCCTGGCC A AGTTCCT 1683 CCAGUGC CUCAUGAG X CGAA ICACCUGG CCAGCTTC C TGCACTGG 1689 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGG 1689 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGG 1689 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGG 1689 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1689 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 CCAGUGC CUCAUGAG X CGAA IGAACUUG CAAGTTC T GCACTGGC 1680	1656		
1696 CUUGGCCA CUGAUGAG X CGAA IAUCUCCU AGGAGATC C TGGCCAAG 1677	1658		
1677 ACUUGGCC CUGAUGAG X GGAA IGAUCUCC GGAGATCC T GGCCANGT 1681 AGGAACUU CUGAUGAG X GGAA ICACGGAU ATCOTGGC C AAGTTCCT 1682 CAGGAACU CUGAUGAG X GGAA IGCCAGGA TACTGGCC A AGTTCCTG 1688 CCAGUGCA CUGAUGAG X CGAA IAACUUGG CCAAGTTC C TGCACTGG 1689 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CCAAGTTC T GCACTGG 1689 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1689 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1689 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1689 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC 1680 GCCAGUGC CUGAUGAG	1662	CCUCACGC CUGAUGAG X CGAA IACGGUGC	
1691 AGGARCHU CUGAUGAG X CGAA ICCAGGAU	1676	CUUGGCCA CUGAUGAG X CGAA IAUCUCCU	
1682 CAGGAACU CUGAUGAG X CGAA IGCCAGGA TCCTGGCC A AGTTCCTG	1677	ACUUGGCC CUGAUGAG X CGAA IGAUCUCC	
1689 CCAGUGCA CUGAUGAG X CGAA TAACUUGG CCAAGTTC C TGCACTGG 1689 GCCAGUGC CUGAUGAG X CGAA TGAACUUG CAAGTTCC T GCACTGGC	1681	AGGAACUU CUGAUGAG X CGAA ICCAGGAU	
1689 GCCAGUGC CUGAUGAG X CGAA IGAACUUG CAAGTTCC T GCACTGGC	1682	CAGGAACU CUGAUGAG X CGAA IGCCAGGA	
1889 GCCAGGC CCGARGAR A COLL TOLLAR	1688	CCAGUGCA CUGAUGAG X CGAA IAACUUGG	
1692 UCAGCCAG CUGAUGAG X CGAA ICAGGAAC GTTCCTGC A CTGGCTGA	1689	GCCAGUGC CUGAUGAG X CGAA IGAACUUG	
	1692	UCAGCCAG CUGAUGAG X CGAA ICAGGAAC	GTTCCTGC A CTGGCTGA

Table 14

1694	CAUCAGCC CUGAUGAG X CGAA IUGCAGGA	TCCTGCAC T GGCTGATG
1698	CACUCAUC CUGAUGAG X CGAA ICCAGUGC	GCACTGGC T GATGAGTG
1722	ACCUGAGC CUGAUGAG X CGAA ICUCGACG	CGTCGAGC T GCTCAGGT
1725	AAGACCUG CUGAUGAG X CGAA ICAGCUCG	CGAGCTGC T CAGGTCTT
1727	GAAAGACC CUGAUGAG X CGAA IAGCAGCU	AGCTGCTC A GGTCTTTC
1732	UANAAGAA CUGAUGAG X CGAA IACCUGAG	CTCAGGTC T TTCTTTTA
1736	GACAUAAA CUGAUGAG X CGAA IAAAGACC	GGTCTTTC T TTTATGTC
1745	GGUCUCCG CUGAUGAG X CGAA IACAUAAA	TTTATGTC A CGGAGACC
1753	UGAAACGU CUGAUGAG X CGAA IUCUCCGU	ACGGAGAC C ACGTTTCA
1754	UUGAAACG CUGAUGAG X CGAA IGUCUCCG	CGGAGACC A CGTTTCAA
1761	UGUUCUUU CUGAUGAG X CGAA IAAACGUG	CACGITIC A AAAGAACA
1769	AAAGAGCC CUGAUGAG X CGAA IUUCUUUU	AAAAGAAC A GGCTCTTT
1773	AGAAAAAG CUGAUGAG X CGAA ICCUGUUC	GAACAGGC T CTTTTCT
1775	GUAGAAAA CUGAUGAG X CGAA IAGCCUGU	ACAGGCTC T TTTTCTAC
1781	CUUCCGGU CUGAUGAG X CGAA IAAAAAGA	TCTTTTC T ACCGGAAG
1784	ACUCUUCC CUGAUGAG X CGAA IUAGAAAA	TTTTCTAC C GGAAGAGT
1796	CUUGCUCC CUGAUGAG X CGAA IACACUCU	AGAGTGTC T GGAGCAAG
1802	UUGCAACU CUGAUGAG X CGAA ICUCCAGA	TCTGGAGC A AGTTGCAA
1809	CAAUGCUU CUGAUGAG X CGAA ICAACUUG	CAAGTTGC A AAGCATTG
1814	GAUUCCAA CUGAUGAG X CGAA ICUUUGCA	TGCAAAGC A TTGGAATC
1823	GUGCUGUC CUGAUGAG X CGAA IAUUCCAA	TTGGAATC A GACAGCAC
1827	UCAAGUGC CUGAUGAG X CGAA IUCUGAUU	AATCAGAC A GCACTTGA
1830	UCUUCAAG CUGAUGAG X CGAA ICUGUCUG	CAGACAGC A CTTGAAGA
1832	CCUCUUCA CUGAUGAG X CGAA IUGCUGUC	GACAGCAC T TGAAGAGG
1845	CCCGCAGC CUGAUGAG X CGAA ICACCCUC	GAGGGTGC A GCTGCGGG
1848	GCUCCCGC CUGAUGAG X CGAA ICUGCACC	GGTGCAGC T. GCGGGAGC
1857	CUUCCGAC CUGAUGAG X CGAA ICUCCCGC	GCGGGAGC T GTCGGAAG
1867	CUGACCUC CUGAUGAG X CGAA ICUUCCGA	TCGGAAGC A GAGGTCAG
1874	AUGCUGCC CUGAUGAG X CGAA IACCUCUG	CAGAGGTC A GGCAGCAT
1878	CCCGAUGC CUGAUGAG X CGAA ICCUGACC	GGTCAGGC A GCATCGGG
1881	CUUCCCGA CUGAUGAG X CGAA ICUGCCUG	CAGGCAGC A TCGGGAAG
1891	GCGGGCCU CUGAUGAG X CGAA ICUUCCCG	CGGGAAGC C AGGCCCGC
1892	GGCGGGCC CUGAUGAG X CGAA IGCUUCCC	GGGAAGCC A GGCCCGCC
1896	GCAGGGCG CUGAUGAG X CGAA ICCUGGCU	AGCCAGGC C CGCCCTGC
1897	AGCAGGGC CUGAUGAG X CGAA IGCCUGGC	GCCAGGCC C GCCCTGCT
1900	GUCAGCAG CUGAUGAG X CGAA ICGGGCCU	AGGCCCGC C CTGCTGAC
1901	CGUCAGCA CUGAUGAG X CGAA IGCGGGCC	GGCCCGCC C TGCTGACG
1902	ACGUCAGC CUGAUGAG X CGAA IGGCGGGC	GCCCGCCC T GCTGACGT
1905	UGGACGUC CUGAUGAG X CGAA ICAGGGCG	CGCCCTGC T GACGTCCA
1912	CGGAGUCU CUGAUGAG X CGAA IACGUCAG	CTGACGTC C AGACTCCG
1913	GCGGAGUC CUGAUGAG X CGAA IGACGUCA	TGACGTCC A GACTCCGC
1917	UGAAGCGG CUGAUGAG X CGAA IUCUGGAC	GTCCAGAC T CCGCTTCA
1919	GAUGAAGC CUGAUGAG X CGAA IAGUCUGG	CCAGACTC C GCTTCATC
1922	GGGGAUGA CUGAUGAG X CGAA ICGGAGUC	GACTCCGC T TCATCCCC
1925	CUUGGGGA CUGAUGAG X CGAA IAAGCGGA	TCCGCTTC A TCCCCAAG
1928	AGGCUUGG CUGAUGAG X CGAA IAUGAAGC	GCTTCATC C CCAAGCCT
1929	TONION NO.	CTTCATCC C CAAGCCTG

Table 14

1930	UCAGGCUU CUGAUGAG X CGAA IGGAUGAA	TTCATCCC C AAGCCTGA
1931	GUCAGGCU CUGAUGAG X CGAA IGGGAUGA	TCATCCCC A AGCCTGAC
1935	GCCCGUCA CUGAUGAG X CGAA ICUUGGGG	CCCCAAGC C TGACGGGC
1936	AGCCCGUC CUGAUGAG X CGAA IGCUUGGG	CCCAAGCC T GACGGGCT
1944	UCGGCCGC CUGAUGAG X CGAA ICCCGUCA	TGACGGGC T GCGGCCGA
1950	UCACAAUC CUGAUGAG X CGAA ICCGCAGC	GCTGCGGC C GATTGTGA
1961	GUAGUCCA CUGAUGAG X CGAA IUUCACAA	TTGTGAAC A TGGACTAC
1967	CACGACGU CUGAUGAG X CGAA IUCCAUGU	ACATGGAC T ACGTCGTG
1981	AACGUUCU CUGAUGAG X CGAA ICUCCCAC	GTGGGAGC C AGAACGTT
1982	GAACGUUC CUGAUGAG X CGAA IGCUCCCA	TGGGAGCC A GAACGTTC
1991	UUCUCUGC CUGAUGAG X CGAA IAACGUUC	GAACGTTC C GCAGAGAA
1994	CUUUUCUC CUGAUGAG X CGAA ICGGAACG	CGTTCCGC A GAGAAAAG
2008	AGACGCUC CUGAUGAG X CGAA ICCCUCUU	AAGAGGGC C GAGCGTCT
2016	UCGAGGUG CUGAUGAG X CGAA IACGCUCG	CGAGCGTC T CACCTCGA
2018	CCUCGAGG CUGAUGAG X CGAA IAGACGCU	AGCGTCTC A CCTCGAGG
2020	ACCCUCGA CUGAUGAG X CGAA IUGAGACG	CGTCTCAC C TCGAGGGT
2021	CACCCUCG CUGAUGAG X CGAA IGUGAGAC	GTCTCACC T CGAGGGTG
2035	CUGAACAG CUGAUGAG X CGAA ICCUUCAC	GTGAAGGC A CTGTTCAG
2037	CGCUGAAC CUGAUGAG X CGAA IUGCCUUC	GAAGGCAC T GTTCAGCG
2042	GAGCACGC CUGAUGAG X CGAA IAACAGUG	CACTGTTC A GCGTGCTC
2049	CGUAGUUG CUGAUGAG X CGAA ICACGCUG	CAGCGTGC T CAACTACG
2051	CUCGUAGU CUGAUGAG X CGAA IAGCACGC	GCGTGCTC A ACTACGAG
2054	CCGCUCGU CUGAUGAG X CGAA IUUGAGCA	TGCTCAAC T ACGAGCGG
2072	GAGGCCGG CUGAUGAG X CGAA ICGCCGCG	CGCGGCGC C CCGGCCTC
2073	GGAGGCCG CUGAUGAG X CGAA IGCGCCGC	GCGGCGCC C CGGCCTCC
2074	AGGAGGCC CUGAUGAG X CGAA IGGCGCCG	CGGCGCCC C GGCCTCCT
2078	GCCCAGGA CUGAUGAG X CGAA ICCGGGGC	GCCCCGGC C TCCTGGGC
2079	CGCCCAGG CUGAUGAG X CGAA IGCCGGGG	CCCCGGCC T CCTGGGCG
2081	GGCGCCCA CUGAUGAG X CGAA IAGGCCGG	CCGGCCTC C TGGGCGCC
2082	AGGCGCCC CUGAUGAG X CGAA IGAGGCCG	CGGCCTCC T GGGCGCCT
2089	AGCACAGA CUGAUGAG X CGAA ICGCCCAG	CTGGGCGC C TCTGTGCT
2090	CAGCACAG CUGAUGAG X CGAA IGCGCCCA	TGGGCGCC T CTGTGCTG
2092	CCCAGCAC CUGAUGAG X CGAA IAGGCGCC	GGCGCCTC T GTGCTGGG
2097	CCAGGCCC CUGAUGAG X CGAA ICACAGAG	CTCTGTGC T GGGCCTGG
2102	AUCGUCCA CUGAUGAG X CGAA ICCCAGCA	TGCTGGGC C TGGACGAT
2103	UAUCGUCC CUGAUGAG X CGAA IGCCCAGC	GCTGGGCC T GGACGATA
2114	GGCCCUGU CUGAUGAG X CGAA IAUAUCGU	ACGATATC C ACAGGGCC
2115	AGGCCCUG CUGAUGAG X CGAA IGAUAUCG	CGATATCC A CAGGGCCT
2117	CCAGGCCC CUGAUGAG X CGAA IUGGAUAU	ATATCCAC A GGGCCTGG
2122	GUGCGCCA CUGAUGAG X CGAA ICCCUGUG	CACAGGGC C TGGCGCAC
2123	GGUGCGCC CUGAUGAG X CGAA IGCCCUGU	ACAGGGCC T GGCGCACC
2129	CACGAAGG CUGAUGAG X CGAA ICGCCAGG	CCTGGCGC A CCTTCGTG
2131	AGCACGAA CUGAUGAG X CGAA IUGCGCCA	TGGCGCAC C TTCGTGCT
2132	CAGCACGA CUGAUGAG X CGAA IGUGCGCC	GGCGCACC T TCGTGCTG
2139	GCACACGC CUGAUGAG X CGAA ICACGAAG	CTTCGTGC T GCGTGTGC
2152	GGGUCCUG CUGAUGAG X CGAA ICCCGCAC	GTGCGGGC C CAGGACCC
2153	CGGGUCCU CUGAUGAG X CGAA IGCCCGCA	TGCGGGCC C AGGACCCG

Table 14

2154	GCGGGUCC CUGAUGAG X CGAA IGGCCCGC	GCGGGCCC A GGACCCGC
2159	AGGCGGCG CUGAUGAG X CGAA IUCCUGGG	CCCAGGAC C CGCCGCCT
2160	CAGGCGGC CUGAUGAG X CGAA IGUCCUGG	CCAGGACC C GCCGCCTG
2163	GCUCAGGC CUGAUGAG X CGAA ICGGGUCC	GGACCCGC C GCCTGAGC
2166	ACAGCUCA CUGAUGAG X CGAA ICGGCGGG	CCCGCCGC C TGAGCTGT
2167	UACAGCUC CUGAUGAG X CGAA IGCGGCGG	CCGCCGCC T GAGCTGTA
2172	CAAAGUAC CUGAUGAG X CGAA ICUCAGGC	GCCTGAGC T GTACTTTG
2177	CUUGACAA CUGAUGAG X CGAA IUACAGCU	AGCTGTAC T TTGTCAAG
2183	AUCCACCU CUGAUGAG X CGAA IACAAAGU	ACTITGIC A AGGIGGAT
2210	GGGGAUGG CUGAUGAG X CGAA IUCGUACG	CGTACGAC A CCATCCCC
2212	UGGGGGAU CUGAUGAG X CGAA IUGUCGUA	TACGACAC C ATCCCCCA
2213	CUGGGGGA CUGAUGAG X CGAA IGUGUCGU	ACGACACC A TCCCCCAG
2216	GUCCUGGG CUGAUGAG X CGAA IAUGGUGU	ACACCATC C CCCAGGAC
2217	UGUCCUGG CUGAUGAG X CGAA IGAUGGUG	CACCATCC C CCAGGACA
2218	CUGUCCUG CUGAUGAG X CGAA IGGAUGGU	ACCATCCC C CAGGACAG
2219	CCUGUCCU CUGAUGAG X CGAA IGGGAUGG	CCATCCCC C AGGACAGG
2220	GCCUGUCC CUGAUGAG X CGAA IGGGGAUG	CATCCCCC A GGACAGGC
2225	CGUGAGCC CUGAUGAG X CGAA IUCCUGGG	CCCAGGAC A GGCTCACG
2229	CCUCCGUG CUGAUGAG X CGAA ICCUGUCC	GGACAGGC T CACGGAGG
2231	GACCUCCG CUGAUGAG X CGAA IAGCCUGU	ACAGGCTC A CGGAGGTC
2240	GCUGGCGA CUGAUGAG X CGAA IACCUCCG	CGGAGGTC A TCGCCAGC
2245	AUGAUGCU CUGAUGAG X CGAA ICGAUGAC	GTCATCGC C AGCATCAT
2246	GAUGAUGC CUGAUGAG X CGAA IGCGAUGA	TCATCGCC A GCATCATC
2249	UUUGAUGA CUGAUGAG X CGAA ICUGGCGA	TCGCCAGC A TCATCAAA
2252	GGGUUUGA CUGAUGAG X CGAA IAUGCUGG	CCAGCATC A TCAAACCC
2255	CUGGGGUU CUGAUGAG X CGAA IAUGAUGC	GCATCATC A AACCCCAG
2259	UGUUCUGG CUGAUGAG X CGAA IUUUGAUG	CATCAAAC C CCAGAACA
2260	GUGUUCUG CUGAUGAG X CGAA IGUUUGAU	ATCAAACC C CAGAACAC
2261	CGUGUUCU CUGAUGAG X CGAA IGGUUUGA	TCAAACCC C AGAACACG
2262	ACGUGUUC CUGAUGAG X CGAA IGGGUUUG	CAAACCCC A GAACACGT
2267	GCAGUACG CUGAUGAG X CGAA IUUCUGGG	CCCAGAAC A CGTACTGC
2273	ACGCACGC CUGAUGAG X CGAA IUACGUGU	ACACGTAC T GCGTGCGT
2290	UGGACCAC CUGAUGAG X CGAA ICAUACCG	CGGTATGC C GTGGTCCA
2297	GGCCUUCU CUGAUGAG X CGAA IACCACGG	CCGTGGTC C AGAAGGCC
2298	CGGCCUUC CUGAUGAG X CGAA IGACCACG	CGTGGTCC A GAAGGCCG
2305	CCAUGGGC CUGAUGAG X CGAA ICCUUCUG	CAGAAGGC C GCCCATGG
2308	UGCCCAUG CUGAUGAG X CGAA ICGGCCUU	AAGGCCGC C CATGGGCA
2309	GUGCCCAU CUGAUGAG X CGAA IGCGGCCU	AGGCCGCC C ATGGGCAC
2310	CGUGCCCA CUGAUGAG X CGAA IGGCGGCC	GGCCGCCC A TGGGCACG
2316	UGCGGACG CUGAUGAG X CGAA ICCCAUGG	CCATGGGC A CGTCCGCA
2321	GGCCUUGC CUGAUGAG X CGAA IACGUGCC	GGCACGTC C GCAAGGCC
2324	GAAGGCCU CUGAUGAG X CGAA ICGGACGU	ACGTCCGC A AGGCCTTC
2329	CUCUUGAA CUGAUGAG X CGAA ICCUUGCG	CGCAAGGC C TTCAAGAG
2330	GCUCUUGA CUGAUGAG X CGAA IGCCUUGC	GCAAGGCC T TCAAGAGC
2333	GUGGCUCU CUGAUGAG X CGAA IAAGGCCU	AGGCCTTC A AGAGCCAC
2339	AGAGACGU CUGAUGAG X CGAA ICUCUUGA	TCAAGAGC C ACGTCTCT
2340	UAGAGACG CUGAUGAG X CGAA IGCUCUUG	CAAGAGCC A CGTCTCTA

Table 14

2345	CAAGGUAG CUGAUGAG X CGAA IACGUGGC	GCCACGTC T CTACCTTG
2345	GUCAAGGU CUGAUGAG X CGAA IAGACGUG	CACGTCTC T ACCTTGAC
2347	UCUGUCAA CUGAUGAG X CGAA IUAGAGAC	GTCTCTAC C TTGACAGA
2350	GUCUGUCA CUGAUGAG X CGAA IGUAGAGA	TCTCTACC T TGACAGAC
2351	UGGAGGUC CUGAUGAG X CGAA IUCAAGGU	ACCTTGAC A GACCTCCA
	CGGCUGGA CUGAUGAG X CGAA IUCUGUCA	TGACAGAC C TCCAGCCG
2360	ACGCUGGA CUGAUGAG X CGAA IGUCUGUC	GACAGACC T CCAGCCGT
2361	GUACGGCU CUGAUGAG X CGAA IAGGUCUG	CAGACCTC C AGCCGTAC
2363	UGUACGGC CUGAUGAG X CGAA IGAGGUCU	AGACCTCC A GCCGTACA
2364	GCAUGUAC CUGAUGAG X CGAA ICUGGAGG	CCTCCAGC C GTACATGC
2367	CUGUCGCA CUGAUGAG X CGAA IUACGGCU	AGCCGTAC A TGCGACAG
2372	CCACGAAC CUGAUGAG X CGAA IUCGCAUG	CATGCGAC A GTTCGTGG
2379	UGCAGGUG CUGAUGAG X CGAA ICCACGAA	TTCGTGGC T CACCTGCA
	CCUGCAGG CUGAUGAG X CGAA IAGCCACG	CGTGGCTC A CCTGCAGG
2391	CUCCUGCA CUGAUGAG X CGAA IUGAGCCA	TGGCTCAC C TGCAGGAG
2393	UCUCCUGC CUGAUGAG X CGAA IGUGAGCC	GGCTCACC T GCAGGAGA
2394	UGGUCUCC CUGAUGAG X CGAA ICAGGUGA	TCACCTGC A GGAGACCA
2404	AGCGGGCU CUGAUGAG X CGAA IUCUCCUG	. CAGGAGAC C AGCCCGCT
2405	CAGCGGGC CUGAUGAG X CGAA IGUCUCCU	AGGAGACC A GCCCGCTG
2408	CCUCAGCG CUGAUGAG X CGAA ICUGGUCU	AGACCAGC C CGCTGAGG
2409	CCCUCAGC CUGAUGAG X CGAA IGCUGGUC	GACCAGCC C GCTGAGGG
2412	CAUCCCUC CUGAUGAG X CGAA ICGGGCUG	CAGCCCGC T GAGGGATG
2422	AUGACGAC CUGAUGAG X CGAA ICAUCCCU	AGGGATGC C GTCGTCAT
2429	CUGCUCGA CUGAUGAG X CGAA IACGACGG	CCGTCGTC A TCGAGCAG
2436	AGGAGCUC CUGAUGAG X CGAA ICUCGAUG	CATCGAGC A GAGCTCCT
2441	CAGGGAGG CUGAUGAG X CGAA ICUCUGCU	AGCAGAGC T CCTCCCTG
2443	UUCAGGGA CUGAUGAG X CGAA IAGCUCUG	CAGAGCTC C TCCCTGAA
2444	AUUCAGGG CUGAUGAG X CGAA IGAGCUCU	AGAGCTCC T CCCTGAAT
2445	UCAUUCAG CUGAUGAG X CGAA IAGGAGCU	AGCTCCTC C CTGAATGA
2447	CUCAUUCA CUGAUGAG X CGAA IGAGGAGC	GCTCCTCC C TGAATGAG
2448	CCUCAUUC CUGAUGAG X CGAA IGGAGGAG	CTCCTCCC T GAATGAGG
2458	CCACUGCU CUGAUGAG X CGAA ICCUCAUU	AATGAGGC C AGCAGTGG
2459	GCCACUGC CUGAUGAG X CGAA IGCCUCAU	ATGAGGCC A GCAGTGGC AGGCCAGC A GTGGCCTC
2462	GAGGCCAC CUGAUGAG X CGAA ICUGGCCU	GCAGTGGC C TCTTCGAC
2468	GUCGAAGA CUGAUGAG X CGAA ICCACUGC	CAGTGGC T CTTCGACG
2469	CGUCGAAG CUGAUGAG X CGAA IGCCACUG	GTGGCCT T TCGACGTC
2471	GACGUCGA CUGAUGAG X CGAA IAGGCCAC	TCGACGTC T TCCTACGC
2480	GCGUAGGA CUGAUGAG X CGAA TACGUCGA	ACGTCTTC C TACGCTTC
2483	GAAGCGUA CUGAUGAG X CGAA IAAGACGU	CGTCTTCC T ACGCTTCA
2484	UGAAGCGU CUGAUGAG X CGAA IGAAGACG	TCCTACGC T TCATGTGC
2489	GCACAUGA CUGAUGAG X CGAA ICGUAGGA	TACGCTTC A TGTGCCAC
2492	GUGGCACA CUGAUGAG X CGAA IAAGCGUA	TCATGTGC C ACCACGCC
2498	GGCGUGGU CUGAUGAG X CGAA ICACAUGA	CATGTGCC A CCACGCCG
2499	CGGCGUGG CUGAUGAG X CGAA IGCACAUG	TGTGCCAC C ACGCCGTG
2501	CACGGCGU CUGAUGAG X CGAA IUGGCACA	GTGCCACC A CGCCGTGC
2502	GCACGGCG CUGAUGAG X CGAA IGUGGCAC	CACCACGC C GTGCGCAT
2506	AUGCGCAC CUGAUGAG X CGAA ICGUGGUG	CACCACGO C GIGOGOTI

Table 14

2513	GCCCCUGA CUGAUGAG X CGAA ICGCACGG	CCGTGCGC A TCAGGGGC
2516	CUUGCCCC CUGAUGAG X CGAA IAUGCGCA	TGCGCATC A GGGGCAAG
2522	GUAGGACU CUGAUGAG X CGAA ICCCCUGA	TCAGGGGC A AGTCCTAC
2527	UGGACGUA CUGAUGAG X CGAA IACUUGCC	GGCAAGTC C TACGTCCA
2528	CUGGACGU CUGAUGAG X CGAA IGACUUGC	GCAAGTCC T ACGTCCAG
2534	CUGGCACU CUGAUGAG X CGAA IACGUAGG	CCTACGTC C AGTGCCAG
2535	CCUGGCAC CUGAUGAG X CGAA IGACGUAG	CTACGTCC A GTGCCAGG
2540	GAUCCCCU CUGAUGAG X CGAA ICACUGGA	TCCAGTGC C AGGGGATC
2541	GGAUCCCC CUGAUGAG X CGAA IGCACUGG	CCAGTGCC A GGGGATCC
2549	GCCCUGCG CUGAUGAG X CGAA IAUCCCCU	AGGGGATC C CGCAGGGC
2550	AGCCCUGC CUGAUGAG X CGAA IGAUCCCC	GGGGATCC C GCAGGGCT
2553	UGGAGCCC CUGAUGAG X CGAA ICGGGAUC	GATCCCGC A GGGCTCCA
2558	GAGGAUGG CUGAUGAG X CGAA ICCCUGCG	CGCAGGGC T CCATCCTC
2560	GAGAGGAU CUGAUGAG X CGAA IAGCCCUG	CAGGGCTC C ATCCTCTC
2561	GGAGAGGA CUGAUGAG X CGAA IGAGCCCU	AGGGCTCC A TCCTCTCC
2564	CGUGGAGA CUGAUGAG X CGAA IAUGGAGC	GCTCCATC C TCTCCACG CTCCATCC T CTCCACGC
2565	GCGUGGAG CUGAUGAG X CGAA IGAUGGAG	CCATCCTC T CCACGCTG
2567	CAGCGUGG CUGAUGAG X CGAA IAGGAUGG	ATCCTCTC C ACGCTGCT
2569	AGCAGCGU CUGAUGAG X CGAA IAGAGGAU	TCCTCTCC A CGCTGCTC
2570	GAGCAGCG CUGAUGAG X CGAA IGAGAGGA	CTCCACGC T GCTCTGCA
2574	UGCAGAGC CUGAUGAG X CGAA ICGUGGAG	CACGCTGC T CTGCAGCC
2577	GGCUGCAG CUGAUGAG X CGAA ICAGCGUG	CGCTGCTC T GCAGCCTG
2579	CAGGCUGC CUGAUGAG X CGAA IAGCAGCG	TGCTCTGC A GCCTGTGC
2582	GCACAGGC CUGAUGAG X CGAA ICAGAGCA	TCTGCAGC C TGTGCTAC
2585	GUAGCACA CUGAUGAG X CGAA ICUGCAGA	CTGCAGCC T GTGCTACG
2586	CGUAGCAC CUGAUGAG X CGAA IGCUGCAG GUCGCCGU CUGAUGAG X CGAA ICACAGGC	GCCTGTGC T ACGCCGAC
2591	GUCGCCGU CUGAUGAG X CGAA ICACAGGC GUUCUCCA CUGAUGAG X CGAA IUCGCCGU	ACGCCAC A TGGAGAAC
2600	AAACAGCU CUGAUGAG X CGAA IUUCUCCA	TGGAGAAC A AGCTGTTT
2609	CCGCAAAC CUGAUGAG X CGAA ICUUGUUC	GAACAAGC T GTTTGCGG
2613	GCAGGAGC CUGAUGAG X CGAA ICCCGUCC	GGACGGGC T GCTCCTGC
2643	AACGCAGG CUGAUGAG X CGAA ICAGCCCG	CGGGCTGC T CCTGCGTT
2645	CAAACGCA CUGAUGAG X CGAA IAGCAGCC	GGCTGCTC C TGCGTTTG
2646	CCAAACGC CUGAUGAG X CGAA IGAGCAGC	GCTGCTCC T GCGTTTGG
2666	CACCAACA CUGAUGAG X CGAA IAAAUCAU	ATGATTTC T TGTTGGTG
2677	AGGUGAGG CUGAUGAG X CGAA IUCACCAA	TTGGTGAC A CCTCACCT
2679	UGAGGUGA CUGAUGAG X CGAA IUGUCACC	GGTGACAC C TCACCTCA
2680	GUGAGGUG CUGAUGAG X CGAA IGUGUCAC	GTGACACC T CACCTCAC
2682	GGGUGAGG CUGAUGAG X CGAA IAGGUGUC	GACACCTC A CCTCACCC
2684	GUGGGUGA CUGAUGAG X CGAA IUGAGGUG	CACCTCAC C TCACCCAC
2685	CGUGGGUG CUGAUGAG X CGAA IGUGAGGU	ACCTCACC T CACCCACG
2687	CGCGUGGG CUGAUGAG X CGAA IAGGUGAG	CTCACCTC A CCCACGCG
2689	UUCGCGUG CUGAUGAG X CGAA IUGAGGUG	CACCTCAC C CACGCGAA
2690	UUUCGCGU CUGAUGAG X CGAA IGUGAGGU	ACCTCACC C ACGCGAAA
2691	UUUUCGCG CUGAUGAG X CGAA IGGUGAGG	CCTCACCC A CGCGAAAA
2701	CUGAGGAA CUGAUGAG X CGAA IUUUUCGC	GCGAAAAC C TTCCTCAG
2702	CCUGAGGA CUGAUGAG X CGAA IGUUUUCG	CGAAAACC T TCCTCAGG

Table 14

2705	GGUCCUGA CUGAUGAG X CGAA IAAGGUUU	AAACCTTC C TCAGGACC
	GGGUCCUG CUGAUGAG X CGAA IGAAGGUU	AACCTTCC T CAGGACCC
2706	CAGGGUCC CUGAUGAG X CGAA IAGGAAGG	CCTTCCTC A GGACCCTG
2708	CGGACCAG CUGAUGAG X CGAA IUCCUGAG	CTCAGGAC C CTGGTCCG
2713	UCGGACCA CUGAUGAG X CGAA IGUCCUGA	TCAGGACC C TGGTCCGA
2714	CUCGGACCA CUGAUGAG X CGAA IGGUCCUG	CAGGACCC T GGTCCGAG
2715	GACACCUC CUGAUGAG X CGAA IACCAGGG	CCCTGGTC C GAGGTGTC
2720		GAGGTGTC C CTGAGTAT
2729	AUACUCAG CUGAUGAG X CGAA IACACCUC	AGGTGTCC C TGAGTATG
2730	CAUACUCA CUGAUGAG X CGAA IGACACCU	GGTGTCCC T GAGTATGG
2731	CCAUACUC CUGAUGAG X CGAA IGGACACC	AGTATGGC T GCGTGGTG
2741	CACCACGC CUGAUGAG X CGAA ICCAUACU	TGGTGAAC T TGCGGAAG
2753	CUUCCGCA CUGAUGAG X CGAA IUUCACCA	CGGAAGAC A GTGGTGAA
2764	UUCACCAC CUGAUGAG X CGAA IUCUUCCG	TGGTGAAC T TCCCTGTA
2774	UACAGGGA CUGAUGAG X CGAA IUUCACCA	TGAACTTC C CTGTAGAA
2777	UUCUACAG CUGAUGAG X CGAA IAAGUUCA	
2778	CUUCUACA CUGAUGAG X CGAA IGAAGUUC	GAACTTCC C TGTAGAAG
2779	UCUUCUAC CUGAUGAG X CGAA IGGAAGUU	AACTTCCC T GTAGAAGA
2794	CCACCCAG CUGAUGAG X CGAA ICCUCGUC	GACGAGGC C CTGGGTGG
2795	GCCACCCA CUGAUGAG X CGAA IGCCUCGU	ACGAGGCC C TGGGTGGC
2796	UGCCACCC CUGAUGAG X CGAA IGGCCUCG	CGAGGCCC T GGGTGGCA
2804	AAAAGCCG CUGAUGAG X CGAA ICCACCCA	TGGGTGGC A CGGCTTTT
2809	UGAACAAA CUGAUGAG X CGAA ICCGUGCC	GGCACGGC T TTTGTTCA
2817	CCGGCAUC CUGAUGAG X CGAA IAACAAAA	TTTTGTTC A GATGCCGG
2823	CGUGGGCC CUGAUGAG X CGAA ICAUCUGA	TCAGATGC C GGCCCACG
2827	AGGCCGUG CUGAUGAG X CGAA ICCGGCAU	ATGCCGGC C CACGGCCT
2828	UAGGCCGU CUGAUGAG X CGAA IGCCGGCA	TGCCGGCC C ACGGCCTA
2829	AUAGGCCG CUGAUGAG X CGAA IGGCCGGC	GCCGGCCC A CGGCCTAT
2834	GGGGAAUA CUGAUGAG X CGAA ICCGUGGG	CCCACGGC C TATTCCCC
2835	AGGGGAAU CUGAUGAG X CGAA IGCCGUGG	CCACGGCC T ATTCCCCT
2840	GCACCAGG CUGAUGAG X CGAA IAAUAGGC	GCCTATTC C CCTGGTGC
2841	CGCACCAG CUGAUGAG X CGAA IGAAUAGG	CCTATTCC C CTGGTGCG
2842	CCGCACCA CUGAUGAG X CGAA IGGAAUAG	CTATTCCC C TGGTGCGG
2843	GCCGCACC CUGAUGAG X CGAA IGGGAAUA	TATTCCCC T GGTGCGGC
2852	CAGCAGCA CUGAUGAG X CGAA ICCGCACC	GGTGCGGC C TGCTGCTG
2853	CCAGCAGC CUGAUGAG X CGAA IGCCGCAC	GTGCGGCC T GCTGCTGG
2856	UAUCCAGC CUGAUGAG X CGAA ICAGGCCG	CGGCCTGC T GCTGGATA
2859	GGGUAUCC CUGAUGAG X CGAA ICAGCAGG	CCTGCTGC T GGATACCC
2866	AGGGUCCG CUGAUGAG X CGAA IUAUCCAG	CTGGATAC C CGGACCCT
2867		TGGATACC C GGACCCTG
2872	THE PROPERTY OF THE PROPERTY O	ACCCGGAC C CTGGAGGT
2872	TOUCCOOL	CCCGGACC C TGGAGGTG
2873	Tara vaguaga	CCGGACCC T GGAGGTGC
	TOTAL CONTRACTOR	GGAGGTGC A GAGCGACT
2883		AGAGCGAC T ACTCCAGC
2891	THE THE PART OF TH	GCGACTAC T CCAGCTAT
2894	TACULACIEC CONTROL OF THE CONTROL OF	GACTACTC C AGCTATGC
2896		ACTACTCC A GCTATGCC
2897	GGCAUAGC CUGAUGAG X CGAA TGAGOAGO	

Table 14

	CCGGGCAU CUGAUGAG X CGAA ICUGGAGU	ACTCCAGC T ATGCCCGG
2900	GAGGUCCG CUGAUGAG X CGAA ICAUAGCU	AGCTATGC C CGGACCTC
2905	GAGGUCC CUGAUGAG X CGAA ICADAGC	GCTATGCC C GGACCTCC
2906	CUGAUGGA CUGAUGAG X CGAA IUCCGGGC	GCCCGGAC C TCCATCAG
2911	UCUGAUGGA CUGAUGAG X CGAA IGUCCGGG	CCCGGACC T CCATCAGA
2912		CGGACCTC C ATCAGAGC
2914	GCUCUGAU CUGAUGAG X CGAA IAGGUCCG	GGACCTCC A TCAGAGCC
2915	GGCUCUGA CUGAUGAG X CGAA IGAGGUCC	CCTCCATC A GAGCCAGT
2918	ACUGGCUC CUGAUGAG X CGAA IAUGGAGG	ATCAGAGC C AGTCTCAC
2923	GUGAGACU CUGAUGAG X CGAA ICUCUGAU	TCAGAGCC A GTCTCACC
2924	GGUGAGAC CUGAUGAG X CGAA IGCUCUGA	AGCCAGTC T CACCTTCA
2928	UGAAGGUG CUGAUGAG X CGAA IACUGGCU	CCAGTCTC A CCTTCAAC
2930	GUUGAAGG CUGAUGAG X CGAA TAGACUGG	AGTCTCAC C TTCAACCG
2932	CGGUUGAA CUGAUGAG X CGAA IUGAGACU	GTCTCACC T TCAACCGC
2933	GCGGUUGA CUGAUGAG X CGAA IGUGAGAC	TCACCTTC A ACCGCGGC
2936	GCCGCGGU CUGAUGAG X CGAA IAAGGUGA	CCTTCAAC C GCGGCTTC
2939	GAAGCCGC CUGAUGAG X CGAA IUUGAAGG	ACCGCGGC T TCAAGGCT
2945	AGCCUUGA CUGAUGAG X CGAA ICCGCGGU	GCGCTTC A AGGCTGGG
2948	CCCAGCCU CUGAUGAG X CGAA IAAGCCGC	TTCAAGGC T GGGAGGAA
2953	UUCCUCCC CUGAUGAG X CGAA ICCUUGAA	GGAGGAAC A TGCGTCGC
2963	GCGACGCA CUGAUGAG X CGAA IUUCCUCC	TGCGTCGC A AACTCTTT
2972	AAAGAGUU CUGAUGAG X CGAA ICGACGCA	TCGCAAAC T CTTTGGGG
2976	CCCCAAAG CUGAUGAG X CGAA IUUUGCGA	GCAAACTC T TTGGGGTC
2978	GACCCCAA CUGAUGAG X CGAA IAGUUUGC	TTGGGGTC T TGCGGCTG
2987	CAGCCGCA CUGAUGAG X CGAA IACCCCAA	CTTGCGGC T GAAGTGTC
2994	GACACUUC CUGAUGAG X CGAA ICCGCAAG	GAAGTGTC A CAGCCTGT
3003	ACAGGCUG CUGAUGAG X CGAA IACACUUC	AGTGTCAC A GCCTGTTT
3005	AAACAGGC CUGAUGAG X CGAA IUGACACU	GTCACAGC C TGTTTCTG
3008	CAGAAACA CUGAUGAG X CGAA ICUGUGAC	TCACAGCC T GTTTCTGG
3009	CCAGAAAC CUGAUGAG X CGAA IGCUGUGA	CCTGTTTC T GGATTTGC
3015	GCAAAUCC CUGAUGAG X CGAA IAAACAGG	GGATTTGC A GGTGAACA
3024	UGUUCACC CUGAUGAG X CGAA ICAAAUCC	AGGTGAAC A GCCTCCAG
3032	CUGGAGGC CUGAUGAG X CGAA IUUCACCU	TGAACAGC C TCCAGACG
3035	CGUCUGGA CUGAUGAG X CGAA ICUGUUCA	GAACAGC T CCAGACGG
3036	CCGUCUGG CUGAUGAG X CGAA IGCUGUUC	ACAGCCTC C AGACGGTG
3038	CACCGUCU CUGAUGAG X CGAA TAGGCUGU	CAGCCTCC A GACGGTGT
3039	ACACCGUC CUGAUGAG X CGAA IGAGGCUG	CGGTGTGC A CCAACATC
3050	GAUGUUGG CUGAUGAG X CGAA ICACACCG	GTGTGCAC C AACATCTA
3052	UAGAUGUU CUGAUGAG X CGAA IUGCACAC	TGTGCACC A ACATCTAC
3053	GUAGAUGU CUGAUGAG X CGAA IGUGCACA	GCACCAAC A TCTACAAG
3056	CUUGUAGA CUGAUGAG X CGAA IUUGGUGC	CCAACATC T ACAAGATC
3059	GAUCUUGU CUGAUGAG X CGAA IAUGUUGG	ACATCTAC A AGATCCTC
3062	GAGGAUCU CUGAUGAG X CGAA IUAGAUGU	ACAGATC C TCCTGCTG
3068	CAGCAGGA CUGAUGAG X CGAA IAUCUUGU	CAAGATCC T CCTGCTGC
3069	GCAGCAGG CUGAUGAG X CGAA IGAUCUUG	AGATCCTC C TGCTGCAG
3071	CUGCAGCA CUGAUGAG X CGAA IAGGAUCU	GATCCTCC T GCTGCAGG
3072	CCUGCAGC CUGAUGAG X CGAA IGAGGAUC	CCTCCTGC T GCTGCAGG
3075	ACGCCUGC CUGAUGAG X CGAA ICAGGAGG	CCTCCTGC T GCAGGCGT

Table 14

3078 UGUACGCC CUGAUGAG X CGAA ICAGCAGG CCTGCTGC A GGCGTACA 3086 GUGAAACC CUGAUGAG X CGAA IUACGCCU AGGCGTAC A GGTTTCAC	
3093 CACAUGCG CUGAUGAG X CGAA LAAACCUG CAGGTTTC A CGCATGTG	
TTTCACGC A TGTGTGCT	
3097 AGCACACA CUGAUGAG X CGAA ICGUGAAA ITTCACCC X TOTAL COMMON TOTAL C	
TOTAL	_
3108 ADGGGAGC COGACOAC II COCATTEC	
TGCAGCTC C CATTTCAT	
GCAGCTCC C ATTTCATC	
CACCTCCC A TITCATCA	
3115 UGAGGAA COGAGGA I COGATTO A TOAGCAAG	
3120 COUGLOSA COGAGGAS A COM 112100 ATTENDED A GOAGGETT	_
3123 AARCOUGE COGROUND A CONTRACTOR TOTAL TOTAL ACTUAGE A ACTUAGE	
3126 OCCARGO COMOMO A COMPANION COMMONO C CONCATT	-
3140 AAROSOG COSROGAS & CONTINUE CARGARCE C CACATTIT	
3141 ARANGOG COGROGAG A COM TONION AND AND AND AND AND AND AND AND AND AN	_
3142 ADDANGS COGROSAS A CONTINUE ACADECOC A CAPITITIC	_
AACCCCAC A TITTTCCT	
3145 AGGARARA COGROGIO A COLL TANDANIO CATTETTO C TGCGCGTC	
ATTITUC T GCGCGTCA	_
3153 UGACGCC COGROSAG A CONTINUE A TOTOTGAC	
3161 GOCAGAGA COGAGGAGA COGAGGAGA COGAGGAGA CAGAGAGAGA CAGAGAGAGA CAGAGAGAGA	
3164 CGGGGCAG CGGAGGAG A COLUMNIA COLUMNIA CATCATCATC T. GACACGGC	
3166 GCCGUGUC CUGAUGAG X CGAA TAGAUGAC GTCATCT T CHICAGOS 3170 GGAGGCCG CUGAUGAG X CGAA TUCAGAGA TCTCTGAC A CGGCCTCC	-
3175 CAGAGGGA CUGAUGAG X CGAA ICCGUGUC GACACGGC C TCCCTCTG	
3175 CAGAGGG CUGAUGAG X COAA IGCCGUGU ACACGGCC T CCCTCTGC	
3178 UAGCAGAG CUGAUGAG X CGAA TAGGCCGU ACGGCCTC C CTCTGCTA	
3179 GUAGCAGA CUGAUGAG X CGAA IGAGGCCG CGGCCTCC C TCTGCTAC	
3180 AGUAGCAG CUGAUGAG X CGAA IGGAGGCC GGCCTCCC T CTGCTACT	
3182 GGAGUAGC CUGAUGAG X CGAA LAGGGAGG CCTCCCTC T GCTACTCC	
3185 GAUGGAGU CUGAUGAG X CGAA ICAGAGGG CCCTCTGC T ACTCCATC	
3188 CAGGAUGG CUGAUGAG X CGAA IUAGCAGA TCTGCTAC T CCATCCTG	
3190 UUCAGGAU CUGAUGAG X CGAA IAGUAGCA TGCTACTC C ATCCTGAA	
3191 UUUCAGGA CUGAUGAG X CGAA IGAGUAGC GCTACTCC A TCCTGAAA	
3194 GGCUUUCA CUGAUGAG X CGAA IAUGGAGU ACTCCATC C TGAAAGCC	
3195 UGGCUUUC CUGAUGAG X CGAA IGAUGGAG CTCCATCC T GAAAGCCA	
3202 GCGUUCUU CUGAUGAG X CGAA ICUUUCAG CTGAAAGC C AAGAACGC	
3203 UGCGUUCU CUGAUGAG X CGAA IGCUUUCA TGAAAGCC A AGAACGCA	
3211 GACAUCCC CUGAUGAG X CGAA ICGUUCUU AAGAACGC A GGGATGTC	
3222 UGGCCCCC CUGAUGAG X CGAA ICGACAUC GATGTCGC T GGGGGCCA	
3229 GCGCCCUU CUGAUGAG X CGAA ICCCCCAG CTGGGGGC C AAGGGCGG	
3230 GGCGCCCU CUGAUGAG X CGAA IGCCCCCA TGGGGGCC A AGGGCGCC	
3238 GGGCCGGC CUGAUGAG X CGAA ICGCCCUU AAGGGCGC C GCCGGCCC	
3241 AGAGGGCC CUGAUGAG X CGAA ICGGCGCCC GGCCCCCCC	
3245 GGGCAGAG CUGAUGAG X CGAA ICCGGCGG CCGCCGGC CCTCTGCCC	
3246 AGGGCAGA CUGAUGAG X CGAA IGCCGGCG CGCCGGCC C TCTGCCCT	
3247 GAGGGCAG CUGAUGAG X CGAA IGGCCGGC GCCGGCCC T CTGCCCTC	

Table 14

3249	CGGAGGGC CUGAUGAG X CGAA IAGGGCCG	COGCCCTC T GCCCTCCG
3252	CCUCGGAG CUGAUGAG X CGAA ICAGAGGG	CCCTCTGC C CTCCGAGG
3252	GCCUCGGA CUGAUGAG X CGAA IGCAGAGG	CCTCTGCC C TCCGAGGC
3254	GGCCUCGG CUGAUGAG X CGAA IGGCAGAG	CTCTGCCC T CCGAGGCC
3256	ACGGCCUC CUGAUGAG X CGAA IAGGGCAG	CTGCCCTC C GAGGCCGT
3262	CACUGCAC CUGAUGAG X CGAA ICCUCGGA	TCCGAGGC C GTGCAGTG
3267	ACAGCCAC CUGAUGAG X CGAA ICACGGCC	GGCCGTGC A GTGGCTGT
3277	GGUGGCAC CUGAUGAG X CGAA ICCACUGC	GCAGTGGC T GTGCCACC
3278	UGCUUGGU CUGAUGAG X CGAA ICACAGCC	GGCTGTGC C ACCAAGCA
3279	AUGCUUGG CUGAUGAG X CGAA IGCACAGC	GCTGTGCC A CCAAGCAT
3281	GAAUGCUU CUGAUGAG X CGAA IUGGCACA	TGTGCCAC C AAGCATTC
3282	GGAAUGCU CUGAUGAG X CGAA IGUGGCAC	GTGCCACC A AGCATTCC
3282	AGCAGGAA CUGAUGAG X CGAA ICUUGGUG	CACCAAGC A TTCCTGCT
3290	CUUGAGCA CUGAUGAG X CGAA IAAUGCUU	AAGCATTC C TGCTCAAG
3290	GCUUGAGC CUGAUGAG X CGAA IGAAUGCU	AGCATTCC T GCTCAAGC
3291	UCAGCUUG CUGAUGAG X CGAA ICAGGAAU	ATTCCTGC T CAAGCTGA
3294	AGUCAGCU CUGAUGAG X CGAA IAGCAGGA	TCCTGCTC A AGCTGACT
3300	GUCGAGUC CUGAUGAG X CGAA ICUUGAGC	GCTCAAGC T GACTCGAC
3304	CGGUGUCG CUGAUGAG X CGAA IUCAGCUU	AAGCTGAC T CGACACCG
3309	UGACACGG CUGAUGAG X CGAA IUCGAGUC	GACTOGAC A COGTGTCA
3311	GGUGACAC CUGAUGAG X CGAA IUGUCGAG	CTCGACAC C GTGTCACC
3317	CACGUAGG CUGAUGAG X CGAA IACACGGU	ACCGTGTC A CCTACGTG
3319	GGCACGUA CUGAUGAG X CGAA IUGACACG	CGTGTCAC C TACGTGCC
3320	UGGCACGU CUGAUGAG X CGAA IGUGACAC	GTGTCACC T ACGTGCCA
3327	CCAGGAGU CUGAUGAG X CGAA ICACGUAG	CTACGTGC C ACTCCTGG
3328	CCCAGGAG CUGAUGAG X CGAA IGCACGUA	TACGTGCC A CTCCTGGG
3330	ACCCCAGG CUGAUGAG X CGAA IUGGCACG	CGTGCCAC T CCTGGGGT
3332	UGACCCCA CUGAUGAG X CGAA IAGUGGCA	TGCCACTC C TGGGGTCA
3333	GUGACCCC CUGAUGAG X CGAA IGAGUGGC	GCCACTCC T GGGGTCAC
3340	GUCCUGAG CUGAUGAG X CGAA IACCCCAG	CTGGGGTC A CTCAGGAC
3342	CUGUCCUG CUGAUGAG X CGAA IUGACCCC	GGGGTCAC T CAGGACAG
3344	GGCUGUCC CUGAUGAG X CGAA IAGUGACC	GGTCACTC A GGACAGCC
3349	GUCUGGGC CUGAUGAG X CGAA IUCCUGAG	CTCAGGAC A GCCCAGAC
3352	UGCGUCUG CUGAUGAG X CGAA ICUGUCCU	AGGACAGC C CAGACGCA
3353	CUGCGUCU CUGAUGAG X CGAA IGCUGUCC	GGACAGCC C AGACGCAG
3354	GCUGCGUC CUGAUGAG X CGAA IGGCUGUC	GACAGCCC A GACGCAGC
3360	TOTAL TOTAL TOTAL	CCAGACGC A GCTGAGTC
3363	TOUCCOLC	GACGCAGC T GAGTCGGA
3375	UCCCCGGG CUGAUGAG X CGAA ICUUCCGA	TCGGAAGC T CCCGGGGA
3377		GGAAGCTC C CGGGGACG
3378	UCGUCCCC CUGAUGAG X CGAA IGAGCUUC	GAAGCTCC C GGGGACGA
3390		GACGACGC T GACTGCCC
3394		ACGCTGAC T GCCCTGGA
3397	GCCUCCAG CUGAUGAG X CGAA ICAGUCAG	CTGACTGC C CTGGAGGC
3398		TGACTGCC C TGGAGGCC
3399		GACTGCCC T GGAGGCCG
3406	UUGGCUGC CUGAUGAG X CGAA ICCUCCAG	CTGGAGGC C GCAGCCAA

Table 14

3409	GGGUUGGC CUGAUGAG X CGAA ICGGCCUC	GAGGCCGC A GCCAACCC
3412	GCCGGGUU CUGAUGAG X CGAA ICUGCGGC	GCCGCAGC C AACCCGGC
3413	UGCCGGGU CUGAUGAG X CGAA IGCUGCGG	CCGCAGCC A ACCCGGCA
3416	CAGUGCCG CUGAUGAG X CGAA IUUGGCUG	CAGCCAAC C CGGCACTG
3417	GCAGUGCC CUGAUGAG X CGAA IGUUGGCU	AGCCAACC C GGCACTGC
3421	GAGGGCAG CUGAUGAG X CGAA ICCGGGUU	AACCCGGC A CTGCCCTC
3423	CUGAGGGC CUGAUGAG X CGAA IUGCCGGG	CCCGGCAC T GCCCTCAG
3425	AGUCUGAG CUGAUGAG X CGAA ICAGUGCC	GGCACTGC C CTCAGACT
3427	AAGUCUGA CUGAUGAG X CGAA IGCAGUGC	GCACTGCC C TCAGACTT
3428	GAAGUCUG CUGAUGAG X CGAA IGGCAGUG	CACTGCCC T CAGACTTC
3430	UUGAAGUC CUGAUGAG X CGAA IAGGGCAG	CTGCCCTC A GACTTCAA
3434	GGUCUUGA CUGAUGAG X CGAA IUCUGAGG	CCTCAGAC T TCAAGACC
3437	GAUGGUCU CUGAUGAG X CGAA IAAGUCUG	CAGACTTC A AGACCATC
3442	UCCAGGAU CUGAUGAG X CGAA IUCUUGAA	TTCAAGAC C ATCCTGGA
3443	GUCCAGGA CUGAUGAG X CGAA IGUCUUGA	TCAAGACC A TCCTGGAC
3445	UCAGUCCA CUGAUGAG X CGAA IAUGGUCU	AGACCATC C TGGACTGA
3447	AUCAGUCC CUGAUGAG X CGAA IGAUGGUC	GACCATCC T GGACTGAT
3452	UGGCCAUC CUGAUGAG X CGAA IUCCAGGA	TCCTGGAC T GATGGCCA
3459	GGGCGGGU CUGAUGAG X CGAA ICCAUCAG	CTGATGGC C ACCCGCCC
3460	UGGGCGGG CUGAUGAG X CGAA IGCCAUCA	TGATGGCC A CCCGCCCA
3462	UGUGGGCG CUGAUGAG X CGAA IUGGCCAU	ATGGCCAC C CGCCCACA
3463	CUGUGGGC CUGAUGAG X CGAA IGUGGCCA	TGGCCACC C GCCCACAG
3466	UGGCUGUG CUGAUGAG X CGAA ICGGGUGG	CCACCCGC C CACAGCCA
3467	CUGGCUGU CUGAUGAG X CGAA IGCGGGUG	CACCCGCC C ACAGCCAG
3468	CCUGGCUG CUGAUGAG X CGAA IGGCGGGU	ACCCGCCC A CAGCCAGG
3470	GGCCUGGC CUGAUGAG X CGAA IUGGGCGG	CCGCCCAC A GCCAGGCC
3473	CUCGGCCU CUGAUGAG X CGAA ICUGUGGG	CCCACAGC C AGGCCGAG
3474	UCUCGGCC CUGAUGAG X CGAA IGCUGUGG	CCACAGCC A GGCCGAGA
3478	CUGCUCUC CUGAUGAG X CGAA ICCUGGCU	AGCCAGGC C GAGAGCAG
3485	CUGGUGUC CUGAUGAG X CGAA ICUCUCGG	CCGAGAGC A GACACCAG
3489	GCUGCUGG CUGAUGAG X CGAA IUCUGCUC	GAGCAGAC A CCAGCAGC
3491	GGGCUGCU CUGAUGAG X CGAA IUGUCUGC	GCAGACAC C AGCAGCCC
3492	AGGGCUGC CUGAUGAG X CGAA IGUGUCUG	CAGACACC A GCAGCCCT
3495	GACAGGGC CUGAUGAG X CGAA ICUGGUGU	ACACCAGC A GCCCTGTC
3498	CGUGACAG CUGAUGAG X CGAA ICUGCUGG	CCAGCAGC C CTGTCACG
3499	GCGUGACA CUGAUGAG X CGAA IGCUGCUG	CAGCAGCC C TGTCACGC
3500	GGCGUGAC CUGAUGAG X CGAA IGGCUGCU	AGCAGCCC T GTCACGCC
3504	GCCCGGCG CUGAUGAG X CGAA IACAGGGC	GCCCTGTC A CGCCGGGC
3508	UAGAGCCC CUGAUGAG X CGAA ICGUGACA	TGTCACGC C GGGCTCTA
3513	GGACGUAG CUGAUGAG X CGAA ICCCGGCG	CGCCGGGC T CTACGTCC
3515	UGGGACGU CUGAUGAG X CGAA IAGCCCGG	CCGGGCTC T ACGTCCCA TCTACGTC C CAGGGAGG
3521	CCUCCCUG CUGAUGAG X CGAA TACGUAGA	CTACGTC C CAGGGAGG
3522	CCCUCCCU CUGAUGAG X CGAA IGACGUAG	
3523	UCCCUCCC CUGAUGAG X CGAA IGGACGUA	TACGTCCC A GGGAGGGA
3540	UGGGUGUG CUGAUGAG X CGAA ICCGCCCC	GGGCGGC C ACACCCA GGGCGGCC C ACACCCAG
3541	CUGGGUGU CUGAUGAG X CGAA IGCCGCCC	GGGGGGCC A CACCCAGG
3542	CCUGGGUG CUGAUGAG X CGAA IGGCCGCC	GGCGGCCC A CACCCAGG

Table 14

3544	GGCCUGGG CUGAUGAG X CGAA IUGGGCCG	CGGCCCAC A CCCAGGCC
3544	CGGGCCUG CUGAUGAG X CGAA IUGUGGGC	GCCCACAC C CAGGCCCG
3546	GCGGGCCU CUGAUGAG X CGAA IGUGUGGG	CCCACACC C AGGCCCGC
3547	UGCGGGCC CUGAUGAG X CGAA IGGUGUGG	CCACACCC A GGCCCGCA
3548		ACCCAGGC C CGCACCGC
3552	GCGGUGCG CUGAUGAG X CGAA ICCUGGGU	CCCAGGCC C GCACCGCT
3553	AGCGGUGC CUGAUGAG X CGAA IGCCUGGG	AGGCCCGC A CCGCTGGG
3556	CCCAGCGG CUGAUGAG X CGAA ICGGGCCU	GCCCGCAC C GCTGGGAG
3558	CUCCCAGC CUGAUGAG X CGAA IUGCGGGC	CGCACCGC T GGGAGTCT
3561	AGACUCCC CUGAUGAG X CGAA ICGGUGCG	TGGGAGTC T GAGGCCTG
3569	CAGGCCUC CUGAUGAG X CGAA IACUCCCA	TCTGAGGC C TGAGTGAG
3575	CUCACUCA CUGAUGAG X CGAA ICCUCAGA	CTGAGGC C TGAGTGAGT
3576	ACUCACUC CUGAUGAG X CGAA IGCCUCAG	
3592	CAGGCCUC CUGAUGAG X CGAA ICCAAACA	TGTTTGGC C GAGGCCTG
3598	GACAUGCA CUGAUGAG X CGAA ICCUCGGC	GCCGAGGC C TGCATGTC
3599	GGACAUGC CUGAUGAG X CGAA IGCCUCGG	CCGAGGCC T GCATGTCC
3502	GCCGGACA CUGAUGAG X CGAA ICAGGCCU	AGGCCTGC A TGTCCGGC
3607	CUUCAGCC CUGAUGAG X CGAA IACAUGCA	TGCATGTC C GGCTGAAG
3611	CAGCCUUC CUGAUGAG X CGAA ICCGGACA	TGTCCGGC T GAAGGCTG
3618	GGACACUC CUGAUGAG X CGAA ICCUUCAG	CTGAAGGC T GAGTGTCC
3626	CCUCAGCC CUGAUGAG X CGAA IACACUCA	TGAGTGTC C GGCTGAGG
3630	CAGGCCUC CUGAUGAG X CGAA ICCGGACA	TGTCCGGC T GAGGCCTG
3636	CUCGCUCA CUGAUGAG X CGAA ICCUCAGC	GCTGAGGC C TGAGCGAG
3637	ACUCGCUC CUGAUGAG X CGAA IGCCUCAG	CTGAGGCC T GAGCGAGT
3649	CCUUGGCU CUGAUGAG X CGAA IACACUCG	CGAGTGTC C AGCCAAGG
3650	CCCUUGGC CUGAUGAG X CGAA IGACACUC	GAGTGTCC A GCCAAGGG
3653	CAGCCCUU CUGAUGAG X CGAA ICUGGACA	TGTCCAGC C AAGGGCTG
3654	UCAGCCCU CUGAUGAG X CGAA IGCUGGAC	GTCCAGCC A AGGGCTGA
3660	GGACACUC CUGAUGAG X CGAA ICCCUUGG	CCAAGGGC T GAGTGTCC
366B	GGUGUGCU CUGAUGAG X CGAA IACACUCA	TGAGTGTC C AGCACACC
3669	AGGUGUGC CUGAUGAG X CGAA IGACACUC	GAGTGTCC A GCACACCT
3672	GGCAGGUG CUGAUGAG X CGAA ICUGGACA	TGTCCAGC A CACCTGCC
3674	ACGGCAGG CUGAUGAG X CGAA IUGCUGGA	TCCAGCAC A CCTGCCGT
3676	AGACGGCA CUGAUGAG X CGAA IUGUGCUG	CAGCACAC C TGCCGTCT
3677	AAGACGGC CUGAUGAG X CGAA IGUGUGCU	AGCACACC T GCCGTCTT
3680	GUGAAGAC CUGAUGAG X CGAA ICAGGUGU	ACACCTGC C GTCTTCAC
3684	GGAAGUGA CUGAUGAG X CGAA IACGGCAG	CTGCCGTC T TCACTTCC
3687	UGGGGAAG CUGAUGAG X CGAA IAAGACGG	CCGTCTTC A CTTCCCCA
3689	UGUGGGGA CUGAUGAG X CGAA IUGAAGAC	GTCTTCAC T TCCCCACA
3692	GCCUGUGG CUGAUGAG X CGAA IAAGUGAA	TTCACTTC C CCACAGGC
3693	AGCCUGUG CUGAUGAG X CGAA IGAAGUGA	TCACTTCC C CACAGGCT
3694	CAGCCUGU CUGAUGAG X CGAA IGGAAGUG	CACTTCCC C ACAGGCTG
3695	CCAGCCUG CUGAUGAG X CGAA IGGGAAGU	ACTTCCCC A CAGGCTGG
3697	CGCCAGCC CUGAUGAG X CGAA IUGGGGAA	TTCCCCAC A GGCTGGCG
3701	CGAGCGCC CUGAUGAG X CGAA ICCUGUGG	CCACAGGC T GGCGCTCG
3707	UGGAGCCG CUGAUGAG X CGAA ICGCCAGC	GCTGGCGC T CGGCTCCA
3712	UGGGGUGG CUGAUGAG X CGAA ICCGAGCG	CGCTCGGC T CCACCCCA
3714	CCUGGGGU CUGAUGAG X CGAA IAGCCGAG	CTCGGCTC C ACCCCAGG
3/14		

Table 14

A 73.5	CCCUGGGG CUGAUGAG X CGAA IGAGCCGA	TCGGCTCC A CCCCAGGG
3715	GCCCUGG CUGAUGAG X CGAA IUGGAGCC	GGCTCCAC C CCAGGGCC
3717	UGGCCCUG CUGAUGAG X CGAA IGUGGAGC	GCTCCACC C CAGGGCCA
3718	CUGGCCCU CUGAUGAG X CGAA IGGUGGAG	CTCCACCC C AGGGCCAG
3719	GCUGGCCC CUGAUGAG X CGAA IGGGUGGA	TCCACCCC A GGGCCAGC
3720	GAAAAGCU CUGAUGAG X CGAA ICCCUGGG	CCCAGGGC C AGCTTTTC
3725	GGAAAAGC CUGAUGAG X CGAA IGCCCUGG	CCAGGGCC A GCTTTTCC
3726	UGAGGAAA CUGAUGAG X CGAA ICUGGCCC	GGGCCAGC T TITCCTCA
3729	CCUGGUGA CUGAUGAG X CGAA IAAAAGCU	AGCTTTTC C TCACCAGG
3734	UCCUGGUG CUGAUGAG X CGAA IGAAAAGC	GCTTTTCC T CACCAGGA
3737	GCUCCUGG CUGAUGAG X CGAA IAGGAAAA	TTTTCCTC A CCAGGAGC
3739	GGGCUCCU CUGAUGAG X CGAA IUGAGGAA	TTCCTCAC C AGGAGCCC
3740	CGGCUCC CUGAUGAG X CGAA IGUGAGGA	TCCTCACC A GGAGCCCG
3746	GGAAGCCG CUGAUGAG X CGAA ICUCCUGG	CCAGGAGC C CGGCTTCC
3747	UGGAAGCC CUGAUGAG X CGAA IGCUCCUG	CAGGAGCC C GGCTTCCA
3751	GGAGUGGA CUGAUGAG X CGAA ICCGGGCU	AGCCCGGC T TCCACTCC
3754	UGGGGAGU CUGAUGAG X CGAA IAAGCCGG	CCGGCTTC C ACTCCCCA
3755	GUGGGGAG CUGAUGAG X CGAA IGAAGCCG	CGGCTTCC A CTCCCCAC
3757	AUGUGGGG CUGAUGAG X CGAA IUGGAAGC	GCTTCCAC T CCCCACAT
3759	CUAUGUGG CUGAUGAG X CGAA IAGUGGAA	TTCCACTC C CCACATAG
3760	CCUAUGUG CUGAUGAG X CGAA IGAGUGGA	TCCACTCC C CACATAGG
3761	UCCUAUGU CUGAUGAG X CGAA IGGAGUGG	CCACTCCC C ACATAGGA
3762	UUCCUAUG CUGAUGAG X CGAA IGGGAGUG	CACTCCCC A CATAGGAA
3764	UAUUCCUA CUGAUGAG X CGAA IUGGGGAG	CTCCCCAC A TAGGAATA
3776	CUGGGGAU CUGAUGAG X CGAA IACUAUUC	GAATAGTC C ATCCCCAG
3777	UCUGGGGA CUGAUGAG X CGAA IGACUAUU	AATAGTCC A TCCCCAGA
3780	GAAUCUGG CUGAUGAG X CGAA IAUGGACU	AGTCCATC C CCAGATTC
3781	CGAAUCUG CUGAUGAG X CGAA IGAUGGAC	GTCCATCC C CAGATTCG
3782	GCGAAUCU CUGAUGAG X CGAA IGGAUGGA	TCCATCCC C AGATTCGC CCATCCCC A GATTCGCC
3783	GGCGAAUC CUGAUGAG X CGAA IGGGAUGG	AGATTOGC C ATTGTTCA
3791	UGAACAAU CUGAUGAG X CGAA ICGAAUCU	GATTCGC C ATTGTTCAC
3792		CATTGTTC A CCCCTCGC
3799	GCGAGGGG CUGAUGAG X CGAA IAACAAUG	TTGTTCAC C CCTCGCCC
3801	GGGCGAGG CUGAUGAG X CGAA IUGAACAA	TGTTCACC C CTCGCCCT
3802	AGGGCGAG CUGAUGAG X CGAA IGUGAACA	GTTCACCC C TCGCCCTG
3803	CAGGGCGA CUGAUGAG X CGAA IGGUGAAC	TTCACCCC T CGCCCTGC
3804	GCAGGGCG CUGAUGAG X CGAA IGGGUGAA	CCCCTCGC C CTGCCCTC
3808	GAGGGCAG CUGAUGAG X CGAA ICGAGGGG	CCCTCGCC C TGCCCTCC
3809	GGAGGGCA CUGAUGAG X CGAA IGCGAGGG	CCTCGCCC T GCCCTCCT
3810	AGGAGGGC CUGAUGAG X CGAA IGGCGAGG	CGCCCTGC C CTCCTTTG
3813	CAAAGGAG CUGAUGAG X CGAA ICAGGGCG	GCCTGCC C TCCTTTGC
3814	GCAAAGGA CUGAUGAG X CGAA IGCAGGGC	CCCTGCCC T CCTTTGCC
3819	GGCAAAGG CUGAUGAG X CGAA IGCCAGGG	CTGCCCTC C TTTGCCTT
381	AAGGCAAA CUGAUGAG X CGAA IAGGGCAG	TGCCCTCC T TTGCCTTC
381	GAAGGCAA CÚGAUGAG X CGAA IGAGGGCA	TCCTTTGC C TTCCACCC
382	GGGUGGAA CUGAUGAG X CGAA ICAAAGGA	CCTTTGCC T TCCACCCC
382	4 GGGGUGGA CUGAUGAG X CGAA IGCAAAGG	3311333

Table 14

3827	GUGGGGGU CUGAUGAG X CGAA IAAGGCAA	TTGCCTTC C ACCCCCAC
3828	GGUGGGGG CUGAUGAG X CGAA IGAAGGCA	TGCCTTCC A CCCCCACC
3830	AUGGUGGG CUGAUGAG X CGAA IUGGAAGG	CCTTCCAC C CCCACCAT
3831	GAUGGUGG CUGAUGAG X CGAA IGUGGAAG	CTTCCACC C CCACCATC
	GGAUGGUG CUGAUGAG X CGAA IGGUGGAA	TTCCACCC C CACCATCC
3832	UGGAUGGU CUGAUGAG X CGAA IGGGUGGA	TCCACCCC C ACCATCCA
3834	CUGGAUGG CUGAUGAG X CGAA IGGGGUGG	CCACCCCC A CCATCCAG
3836	ACCUGGAU CUGAUGAG X CGAA IUGGGGGU	ACCCCCAC C ATCCAGGT
3837	CACCUGGA CUGAUGAG X CGAA IGUGGGGG	CCCCCACC A TCCAGGTG
3840	CUCCACCU CUGAUGAG X CGAA IAUGGUGG	CCACCATC C AGGTGGAG
3840	UCUCCACC CUGAUGAG X CGAA IGAUGGUG	CACCATCC A GGTGGAGA
	CUUCUCAG CUGAUGAG X CGAA IUCUCCAC	GTGGAGAC C CTGAGAAG
3851	CCUUCUCA CUGAUGAG X CGAA IGUCUCCA	TGGAGACC C TGAGAAGG
3853	UCCUUCUC CUGAUGAG X CGAA IGGUCUCC	GGAGACCC T GAGAAGGA
3863	GCUCCCAG CUGAUGAG X CGAA IUCCUUCU	AGAAGGAC C CTGGGAGC
3864	AGCUCCCA CUGAUGAG X CGAA IGUCCUUC	GAAGGACC C TGGGAGCT
3865	GAGCUCCC CUGAUGAG X CGAA IGGUCCUU	AAGGACCC T GGGAGCTC
3872	AUUCCCAG CUGAUGAG X CGAA ICUCCCAG	CTGGGAGC T CTGGGAAT
3874	AAAUUCCC CUGAUGAG X CGAA IAGCUCCC	GGGAGCTC T GGGAATTT
3891	ACACCUUU CUGAUGAG X CGAA IUCACUCC	GGAGTGAC C AAAGGTGT
3892	CACACCUU CUGAUGAG X CGAA IGUCACUC	GAGTGACC A AAGGTGTG
3902	GUGUAÇAG CUGAUGAG X CGAA ICACACCU	AGGTGTGC C CTGTACAC
3903	UGUGUACA CUGAUGAG X CGAA IGCACACC	GGTGTGCC C TGTACACA
3904	CUGUGUAC CUGAUGAG X CGAA IGGCACAC	GTGTGCCC T GTACACAG
3909	CUCGCCUG CUGAUGAG X CGAA IUACAGGG	CCCTGTAC A CAGGCGAG
3911	UCCUCGCC CUGAUGAG X CGAA IUGUACAG	CTGTACAC A GGCGAGGA
3921	AGGUGCAG CUGAUGAG X CGAA IUCCUCGC	GCGAGGAC C CTGCACCT
3922	CAGGUGCA CUGAUGAG X CGAA IGUCCUCG .	CGAGGACC C TGCACCTG
3923	CCAGGUGC CUGAUGAG X CGAA IGGUCCUC	GAGGACCC T GCACCTGG .
3926	CAUCCAGG CUGAUGAG X CGAA ICAGGGUC	GACCCTGC A CCTGGATG
3928	CCCAUCCA CUGAUGAG X CGAA IUGCAGGG	CCCTGCAC C TGGATGGG
3929	CCCCAUCC CUGAUGAG X CGAA IGUGCAGG	CCTGCACC T GGATGGGG
3941	ACCCACAG CUGAUGAG X CGAA IACCCCCA	TGGGGGTC C CTGTGGGT
3942	GACCCACA CUGAUGAG X CGAA IGACCCCC	GGGGTCC C TGTGGGTC
3943	UGACCCAC CUGAUGAG X CGAA IGGACCCC	GGGGTCCC T GTGGGTCA
3951	CCCCAAUU CUGAUGAG X CGAA IACCCACA	TGTGGGTC A AATTGGGG
3968	ACUCCCAC CUGAUGAG X CGAA ICACCUCC	GGAGGTGC T GTGGGAGT
3984	AUAUAUUC CUGAUGAG X CGAA IUAUUUUA	TAAAATAC T GAATATAT
4002	UUCAAAAC CUGAUGAG X CGAA IAAAAACU	AGTTTTC A GTTTTGAA

Stem Length = 8. Core Sequence = CUGAUGAG X CGAA (X = GCCGUUAGGC or other stem II sequence and length (greater than or equal to 2 base-pairs)). I = Inosine nucleotide

Seq1 = TERT (Homo sapiens telomerase reverse transcriptase (TERT) mRNA, 4015 bp); Nakamura et al., Science 277 (5328), 955-959 (1997)

Table 15: Human telomerase reverse transcriptase (TERT) G-Cleaver Ribozyme and Target Sequence

1:	Substrate Sequence	Seq ID	Ribozyme Sequence	Seq ID Nos
rosidon	gondocancon a codece	311	CGCAG UGAUGGCAUGCACUAUGCGCG AGGACGCAGC	
2	GCGUCCUGCU G CGCAC		GUGCG UGAUGGCAUGCACUAUGCGCG AGCAGGACGC	
1 5	GUCCUGCUGC G CACGU		ACGUG UGAUGGCAUGCACUAUGCGCG GCAGCAGGAC	
1 6	GGCCACCCC G CGAUG		CAUCG UGAUGGCAUGCACUAUGCGCG GGGGGUGGCC	
3 5	CCACCCCGC G AUGCC		GGCAU UGAUGGCAUGCACUAUGCGCG GCGGGGGUGG	
5.8	CCCCGCGAU G CCGCG		CGCGG UGAUGGCAUGCACUAUGCGCG AUCGCGGGGG	
19	CCGCGAUGCC G CGCGC		GCGCG UGAUGGCAUGCACUAUGCGCG GGCAUCGCGG	
63	GCGAUGCCGC G CGCUC		GAGCG UGAUGGCAUGCACUAUGCGCG GCGGCAUCGC	
65	CAUGCCGCGC G CUCCC		GGGAG UGAUGGCAUGCACUAUGCGCG GCGCGGCAUC	-
72	CGCGCUCCCC G CUGCC		GGCAG UGAUGGCAUGCACUAUGCGCG GGGGAGCGCG	
75	GCUCCCCCCU G CCGAG		CUCGG UGAUGGCAUGCACUAUGCGCG AGCGGGGAGC	
38	CCCCGCUGCC G AGCCG		CGGCU UGAUGGCAUGCACUAUGCGCG GGCAGCGGGG	
92	GCCGAGCCGU G CGCUC		GAGCG UGAUGGCAUGCACUAUGCGCG ACGCCUCGGC	
87	CGAGCCGUGC G CUCCC		GGGAG UGAUGGCAUGCACUAUGCGCG GCACGGCUCG	1
70	DOCUCCOCO G CUGCG		CGCAG UGAUGGCAUGCACUAUGCGCG AGGGAGCGCA	4
0.1	GUNCOURCE G CGCAG		CUGCG UGAUGGCAUGCACUAUGCGCG AGCAGGGAGC	
. 0	UCCURCUSE G CAGC		GGCUG UGAUGGCAUGCACUAUGCGCG GCAGCAGGGA	
;	POCESTIAN OF COAGO		CCUCG UGAUGGCAUGCACUAUGCGCG GGUAGUGGCU	
	STORY OF THE PROPERTY OF THE P		CACCU UGAUGGCAUGCACUAUGCGCG GCGGUAGUGG	
110	ACCORDAGED G CUGCC		GGCAG UGAUGGCAUGCACUAUGCGCG ACCUCGCGGU	
122	GCGAGGUGCU G CCGCU		AGCGG UGAUGCAUGCACUAUGCGCG AGCACCUCGC	
124	AGGUGCUGCC G CUGGC		GCCAG UGAUGGCAUGCACUAUGCGCG GGCAGCACCU	
130	CCACGUUCGU G CGGCG		CGCCG UGAUGGCAUGCACUAUGCGCG ACGAACGUGG	
144	SENSO B CONGRETARIO		CCAGG UGAUGGCAUGCACUAUGCGCG GCCGCACGAA	-
172	GGCGGCUGGU G CAGCG		CGCUG UGAUGGCAUGCACUAUGCGCG ACCAGCCGCC	-
177	CUGGUGCAGC G CGGGG		CCCCG UGAUGGCAUGCACUAUGCGCG GCUGCACCAG	-
198	GCGGCUUUCC G CGCGC		GCGCG UGAUGGCAUGCACUAUGCGCG GGAAAGCCGC	
1	1000		CONTRACT TO THE PROPERTY OF TH	_

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ACCAG UGAUGGCAUGCACUAUGCGCG GCGCGGAAAG	CCAGG UGAUGGCAUGCACUAUGCGCG ACUGGGCCAC	ACGCA UGAUGGCAUGCACUAUGCGCG ACCAGGCACU	GCACG UGAUGGCAUGCACUAUGCGCG ACACCAGGCA	CAGGS UGAUGGCAUGCACUAUGCGCG ACGCACACCA	CCGUG UGAUGGCAUGCACUAUGCGCG GUCCCAGGGC	GGGGG UGAUGGCAUGCACUAUGCGCG GGCCGUGCGU	GGCGG UGAUGGCAUGCACUAUGCGCG GGGGGGCGGC	GGGGG UGAUGGCAUDAUGCGCG GGCGGGGGGC	CCUSG UGAUGGCAUGCACUAUGCGCG GGAAGGAGGG	CAGGA UGAUGGCAUGCACUAUGCGCG ACCUGGCGGA	UCAGG UGAUGGCAUGCACUAUGCGCG AGGACACCUG	UCCUU UGAUGGCAUGCACUAUGCGCG AGGCAGGACA	GCACU UGAUGGCAUGCACUAUGCGCG GGGCCACCAG	UGCAG UGAUGGCAUGCACUAUGCGCG ACUCGGGCCA	CUCUG UGAUGGCAUGCACUAUGCGCG AGCACUCGGG	UCGCA UGAUGGCAUGCACUAUGCGCG AGCCUCUGCA	GCUCG UGAUGGCAUGCACUAUGCGCG ACAGCCUCUG	GCGCU UGAUGGCAUGCACUAUGCGCG GCACAGCCUC	CGCCG UGAUGGCAUGCACUAUGCGCG GCUCGCACAG	CUUCS UGAUGGCAUGCACUAUGCGCG GCCGCGCUCG	UUCUU UGAUGGCAUGCACUAUGCGCG GCGCCGCGCU	GCCAG UGAUGGCAUGCACUAUGCGCG ACGUUCUUCG	CAGCG UGAUGGCAUNAUGCGCG GAAGCCGAAG	AGCAG UGAUGGCAUGCACUAUGCGCG GCGAAGCCGA	UCCAG UGAUGGCAUGCACUAUGCGCG AGCGCGAAGC	CCCCG UGAUGGCAUGCACUAUGCGCG GGGCCCCGUC	GGCCU UGAUGGCAUGCACUAUGCGCG GGGGGGGCCC	CHIRCG HGAUGGCAUGCACVAUGCGCG ACGCUGGUGG	ARCHIG LIGAUGGCAUGCACUAUGCGCG GCACGCUGGU	THE STATE OF THE PROPERTY OF T	
CUUUCCGCGC G CUGGU	GIGGCCCAGU G CCUGG	AGUGCCUGGU G UGCGU	ugcondende a cenac	neenenacen e coone	GCCTIGGGAC G CACGG	20000 9 335500000	222222222222222	2222 8 22822222	CCCUCCUUCC G CCAGG	UCCGCCAGGU G UCCUG	CAGGUGUCCU G CCUGA	UGUCCUGCCU G AAGGA	CUGGUGGCCC G AGUGC	UGGCCCGAGU G CUGCA	CCCGAGUGCU G CAGAG	UGCAGAGGCU G UGCGA	CAGAGGCUGU G CGAGC	CARGOTTOTICS G AGCGC	Cardinate a Cardinate	COCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOC	date of the control o	General G CUGGC	CHICGGCUUC G CGCUG	urgeconcec e cuecu	CONTROPORTI G CUGGA	50550 5000000000	COOCA C COCCOCCOCC	מפרונינים אפפים	CCACCAGGGG G CGCAG	ACCAGGGGG G CAGCG	
202	216	223	225	229	000	223	254	257	270	277	282	286	303	307	310	3.19	122		323	25	355	334	0 40	36		500	0/0	392	412	414	

436	CCAACACGGU G ACCGA	UCGGU UGAUGGCAUGCACUAUGCGCG ACCGUGUUGG
440	CACGGUGACC G ACGCA	UGCGU UGAUGGCAUGCACUAUGCGCG GGUCACCGUG
443	GGUGACCGAC G CACUG	CAGUG UGAUGCAUGCACUAUGCGCG GUCGGUCACC
448	CCGACGCACU G CGGGG	CCCCG UGAUGSCAUGCACUAUGCGCG AGUGCGUCGG
472	CGUGGGGGCU G CUGCU	AGCAG UGAUGGCAUGCACUAUGCGCG AGCCCCCACG
475	gaggangen a chaca	CGCAG UGAUGGCAUGCACUAUGCGCG AGCAGCCCCC
478	accuacuacu a cacca	CSGCG UGAUGGCAUGCACUAUGCGCG AGCAGCAGCC
480	coccoccoc a ccaca	CGCGG UGAUGGCAUGCACUAUGCGCG GCAGCAGCAG
483	cuecuececc e ceuee	CCACG UGAUGGCAUGCACUAUGCGCG GGCGCAGCAG
491	CCGCGUGGGC G ACGAC	GUCGU UGAUGGCAUGCACUAUGCGCG GCCCACGCGG
494	CGUGGGCGAC G ACGUG	CACGU UGAUGCCAUGCACUAUGCGCG GUCGCCCACG
499	GCGACGACGU G CUGGU	ACCAG USAUGGCAUGCACUAUGCGCG ACGUCGUCGC
511	UGGUUCACCU G CUGGC	GCCAG UGAUGGCAUGCACUAUGCGCG AGGUGAACCA
519	CUGCUGGCAC G CUGCG	CGCAG UGAUGGCACGAUGCGCG GUGCCAGCAG
522	CUGGCACGCU G CGCGC	GCGCG UGAUGGCACUAUGCGCG AGCGUGCCAG
524	GSCACGCUGC G CGCUC	GAGCG UGAUGGCAUGCACUAUGCGCG GCAGCGUGCC
526	CACGCUGCGC G CUCUU	AAGAG UGAUGGCAUGCACUAUGCGCG GCGCAGCGUG
533	cacacucum a nacua	CAGCA UGAUGCAUCCACUAUGCGCG AAAGAGCGCG
535	cacucunuan a cuadu	ACCAG UGAUGGCAUGCACUAUGCGCG ACAAAGAGCG
552	GCUCCCAGCU G CGCCU	AGGCG UGAUGCCAUGCACUAUGCGCG AGCUGGGAGC
554	UCCCAGCUGC G CCUAC	GUAGG UGAUGGCAUGCACG GCAGCUGGGA
565	CCUACCAGGU G UGCGG	CCGCA USAUGGCAUGCACUAUGCGCG ACCUGGUAGG
267	UACCAGGUGU G CGGGC	GCCCG UGAUGGCAUGCACGACG ACACCUGGUA
574	uguacaaacc a ccacu	AGCGG UGAUGGCAUGCACUAUGCGCG GGCCCGCACA
577	GCGGGCCGCC G CUGUA	UACAG UGAUGGCAUGCACUAUGCGCG GGCGGCCCGC
580	GGCCGCCGCU G UACCA	UGGUA UGAUGCANGCACUAUGCGCG AGCGGCGGCC
593	CCAGCUCGGC G CUGCC	GGCAG UGAUGGCAUGCACUAUGCGCG GCCGAGCUGG
965	GCUCGGCGCU G CCACU	AGUGG UGAUGCAUGCACUAUGCGCG AGCGCCGAGC
919	cccggcccc g ccACA	UGUGG UGANGGCAUGCACUAUGCGCG GGGGGCCGGG
623	CCCGCCACAC G CUAGU	ACUAG UGAUGCAUGCACUAUGCGCG GUGUGGCGGG
636	AGUGGACCCC G AAGGC	GCCUU UGAUGGCAUGCACUAUGCGCG GGGGUCCACU

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GUUCG UGAUGGCAUGCACUAUGCGCG MUCCCAGAGG	CCGUU UGAUGGCAUGCACUAUGCGCG GCAUCCCAGA	GCUGG UGAUGGCAUGCACUAUGCGCG AGGCCCAGGG	CCUCG UGAUGGCAUGCACUAUGCGCG ACCCGGGGCO	CUCCU UGAUGGCAUGCACUAUGCGCG GCACCCGGGG	CCCCG UGAUGGCAUGCACUAUGCGCG GCCUCCUCGC	GCUGG UGAUGGCACUAUGCGCG ACUGCCCCCG	GACUU UGAUGGCAUGCACUAUGCGCG GGCUGGCACU	AACGG UGAUGGCAUGCACUAUGCGCG AGACUUCGGC	UUGGG UGAUGGCAUGCACUAUGCGCG AACGGCAGAC	GGCAG UGAUGGCAUGCACUAUGCGCG GCCACGCCUG	AGGGG UGAUGGCAUGCACUAUGCGCG AGCGCCACGC	CGGCU UGAUGGCAUGCACUAUGCGCG AGGGGCAGCG	ACGGG UGAUGCAUGCACUAUGCGCG GUCCGCUCCG	CCACG UGAUGGCAUGCACUAUGCGCG GUCCUGCCCG	UCACU UGAUGGCAUGCACUAUGCGCG GGUCCACGCG	ACGGU UGAUGGCAUGCACUAUGCGCG ACUCGGUCCA	CCACA UGAUGGCAUGCACUAUGCGCG AGAAACCACG	CACCA UGAUGGCAUGCACUAUGCGCG ACAGAAACCA	GGUGA UGAUGGCAUGCACUAUGCGCG ACCACACAGA	INTIRG INALIGGCAUGCACUAUGCGCG AGGUGACACC	HITCH HEADEGCAUGCACUAUGCGCG GGGUCUGGCA	INTERNIT LIGADISGCAUGCACUAUGCGCG GGCGGGUCUG	GAGCG UGAUGGCAUGCACUAUGCGCG ACCCUCCAAA	CALCAR TRATIGGCATIGCACUAUGCGCG GCACCCUCCA	GAGAG CANCECATICACITATION GUGCCAGAGA	GGGG CONTROLLER CONTROLLER GCGTGCCAGA	AGUGG UGANGGCANGCANTAIRCOCC GGCCCANGGA	GCUGG UGAUGGANGCACCACCACCACCACCACCACCACCACCACCACCACCAC	GCCCG UGAUGGCAUGCACOAGGCGCG COCCCCGGAIG	GGCCG UGAUGGCAUGCACUAGGCG GAGGGGGGGG	CAAGG UGAUGGCAUGCACUAUGCGCG GUGUCCAAGG
CGUCUGGGAU G CGAAC	UCUGGGAUGC G AACGG	CCCUGGGCCU G CCAGC	AGCCCCGGGU G CGAGG	CCCCGGGUGC G AGGAG	GCGAGGAGGC G CGGGG	COGGGGGAGU G CCAGC	ACTION OF ANGUE	COCCEPACITOR C CCGUU	CITATION GIRLS G CCCAA	Casescrates a cueco	Goottagonerii a ccccu	CONTROLL G AGGG	CROBACTISCAL G CCCGU	COCCERGEAC G CGUGG	COCCUSED C AGIGA	MODERATE O MODELL	COLOR O COMPANION	Section of the sectio	00000 0 00000000	OCUGUGUSEO G OCACC	GGUGUCACCU G CCASA	UGCCAGACCC G CCGAA	CAGACCUGCC & AMANA	UUUGGAGGGU G CGCGC	uggAgggugc g cucuc	UCUCUGGCAC G CGCCA	UCUGGCACGC G CCACU	UCCGUGGGCC G CCAGC	CCAGCACCAC G CGGGC	CAUCCACAUC G CGGCC	CONTRACTAC G CCUUG
651	653	703	716	21.8	250	727	121	761	10,1	120	200	200	007	200	1,0	820	824	867	869	874	881	890	893	917	919	931	933	957	896	886	0.00

1031	CANADA COLLEGE OF DECECO	GGGGA UGAUGGCAUGCACUAUACGCA AAGACGGGG
1031	GUCCCCGGU G UACGC	GCGUA UGAUGGCAUGCACUAUGCGCG ACCGGGGGAC
1034	CCCGGIGUAC G CCGAG	CUCGG UGAUGGCAUGCACUAUGCGCG GUACACCGGG
	GGUGUACGCC G AGACC	GGUCU UGAUGGCAUGCACUAUGCGCG GGCGUACACC
1064	CUCCUCAGGC G ACAAG	CUUGU UGAUGGCAUGCACUAUGCGCG GCCUGAGGAG
1078	AGGAGCAGCU G CGGCC	GGCCG UGAUGGCAUGCACUAUGCGCG AGCUGCUCCU
1105	UCAGCUCUCU G AGGCC	GGCCU UGAUGGCAUGCACUAUGCGCG AGAGAGCUGA
1117	GGCCCAGCCU G ACUGG	CCAGU UGAUGGCAUGCACUAUGCGCG AGGCUGGGCC
1124	CCUGACUGGC G CUCGG	CCGAG UGAUGGCAUGUGCGCG GCCAGUCAGG
1111	GGCCCUGGAU G CCAGG	CCUGG UGAUGGCAUGCACUAUGCGCG AUCCAGGGCC
1185	GGGACUCCCC G CAGGU	ACCUG UGAUGGCAUGCACUAUGCGCG GGGGAGUCCC
1192	cccecaeguu e cccce	CGGGG UGAUGGCAUGCACUAUGCGCG AACCUGCGGG
1197	AGGUUGCCCC G CCUGC	GCAGG UGAUGGCAUGCACUAUGCGCG GGGGAACCU
1201	UGCCCCGCCU G CCCCA	UGGGG UGAUGGCAUGCACUAUGCGCG AGGCGGGCA
1209	CUGCCCCAGC G CUACU	AGUAG UGAUGGCAUGCACUAUGCGCG GCUGGGGCAG
1222	ACUGGCAAAU G CGGCC	GGCCG UGAUGGCAUGCACUAUGCGCG AUUUGCCAGU
1231	UGCGCCCCU G UUUCU	AGNAA UGAUGGCAUGCACUAUGCGCG AGGGGCCGCA
1243	UNCUGGAGCU G CUUGG	CCAAG UGAUGGCAUGCACUAUGCGCG AGCUCCAGAA
1256	UGGGAACCAC G CGCAG	CUGCG UGAUGGCAUGCACUAUGCGCG GUGGUUCCCA
1258	GGAACCACGC G CAGUG	CACUG UGAUGGCAUGCACUAUGCGCG GCGUGGUUCC
1263	CACGCGCAGU G CCCCU	AGGG UGAUGCAUGCACUAUGCGCG ACUGCGCGUG
1276	CCIACGGGGU G CUCCU	AGGAG UGAUGGCAUGCACUAUGCGCG ACCCCGUAGG
1288	UCCUCAAGAC G CACUG	CAGUG UGAUGGCAUGCACUAUGCGCG GUCUUGAGGA
1293	AAGACGCACU G CCCGC	GCGGG UGAUGGCAUGCACUAUGCGCG AGUGCGUCUU
1297	CGCACUGCCC G CUGCG	CGCAG UGAUGGCAUGCACUAUGCGCG GGGCAGUGCG
1300	ACUGCCCGCU G CGAGC	GCUCG UGAUGGCAUGCACUAUGCGCG AGCGGGCAGU
1302	UGCCCGCUGC G AGCUG	CAGCU UGAUGGCAUGCACUAUGCGCG GCAGCGGGCA
1307	GCUGCGAGCU G CGGUC	GACCG UGAUGGCAUGUGCGCG AGCUCGCAGC
1328	AGCAGCCGGU G UCUGU	ACAGA UGAUGGCAUGCACUAUGCGCG ACCGGCUGCU
1332	accedence e neccc	GGGCA UGAUGGCAUGCACUAUGCGCG AGACACCGGC
1334	CEGUGICUGU & CCCGG	CCGGG UGAUGGCAUGCACUAUGCGCG ACAGACACCG

1358	CCAGGGCUCU G UGGCG	CGCCA UGAUGGCAUGCACUAUGCGCG AGAGCCCOOG
1370	GGCGGCCCC G AGGAG	CUCCU UGAUGGCAUGCACUAUGCGCG GGGGGCCGCC
1395	GACCCCGUC G CCUGG	CCAGG UGAUGGCAUANGCGCG GACGGGGUC
1402	GUCGCCUGGU G CAGCU	AGCUG UGAUGGCAUGCACUAUGCGCG ACCAGGCGAC
1408	UGGUGCAGCU G CUCCG	CGGAG UGAUGCAUGCACUAUGCGCG AGCUGCACCA
1413	CAGCUGCUCC G CCAGC	GCUGG UGAUGGCAUGCACUAUGCGCG GCAGCAGCUG
1438	CCUGGCAGGU G UACGG	CCGUA UGAUGGCAUGCACUAUGCGCG ACCUGCCAGG
1450	ACGGCUUCGU G CGGGC	GCCCG UGAUGGCAUGCACUAUGCGCG ACGAAGCCGU
1458	discassecti s ceuse	GCAGG UGAUGGCAUGCACUAUGCGCG AGGCCCGCAC
1462	eggeengeen e ceeeg	CGGCG UGAUGGCAUGCACUAUGCGCG AGGCAGGCCC
1464	accuercues e coese	GCCGG UGAUGGCAUGCACUAUGCGCG GCAGGCAGGC
1474	accedences a cocce	GGGGG UGAUGGCAUGCACUAUGCGCG ACCAGCCGGC
1505	CAGGCACAAC G AACGC	GCGUU UGAUGGCAUGCACUAUGCGCG GUUGUGCCUG
1509	CACAACGAAC G CCGCU	AGCGG UGAUGCAUGCACUAUGCGCG GUUCGUUGUG
1512	AACGAACGCC G CUUCC	GGAAG UGAUGGCAUGCACUAUGCGCG GGCGUUCGUU
1556	GGGGAAGCAU G CCAAG	CUUGG UGAUGGCAUGCACUAUGCGCG AUGCUUCCCC
1567	CCAAGCUCUC G CUGCA	UGCAG UGAUGGCAUGCACUAUGCGCG GAGAGCUUGG
1570	AGCUCUCGCU G CAGGA	UCCUG UGAUGGCAUGCACUAUGCGCG AGCGAGAGCU
1579	UGCAGGAGCU G ACGUG	CACGU UGAUGGCAUGCACUAUGCGCG AGCUCCUGCA
1591	CGUGGAAGAU G AGCGU	ACGCU UGAUGGCAUGCACUAUGCGCG AUCUUCCACG
1597	AGAUGAGCGU G CGGGA	UCCCG UGAUGGCAUGCCACG ACGCUCAUCU
1605	GUGCGGGACU G CGCUU	AAGCG UGAUGGCAUGCACUAUGCGCG AGUCCCGCAC
1607	GCGGGACUGC G CUUGG	CCAAG UGAUGGCAUGCACUAUGCGCG GCAGUCCOGC
1615	GCGCUUGGCU G CGCAG	CUGCG UGAUGGCAUGCACUAUGCGCG AGCCAAGCGC
1617	GCUUGGCUGC G CAGGA	UCCUG UGAUGGCAUGCACUAUGCGCG GCAGCCAAGC
1638	GGGGNUGGCU G UGNUC	GAACA UGAUGGCAUGCACUAUGCGCG AGCCAACCCC
1640	gannagangn a nacca	CGGAA UGAUGCAUGCACUAUGCGCG ACAGCCAACC
1649	UGUUCCGGCC G CAGAG	CUCUG UGAUGGCAUGCACUAUGCGCG GGCCGGAACA
1663	AGCACCGUCU G CGUGA	UCACG UGAUGGCAUGCACUAUGCGCG AGACGGUGCU
1667	CCGUCUGCGU G AGGAG	CUCCU UGAUGGCAUGCACUAUGCGCG ACGCACACGG
	DIDEO O INDIMINATION	PAGITO HGAINGCAUGCACHAUGCGCG AGGAACUUGG

CAGUGCA	CAGCCAGU	CAUCAGC	ACUCAUCA	CGACGUAC	CUCGACGA	AAAAGAAA	UCUUCCGG	CUIGCICC	GUGCUGUC	CCUCUUCA	CUGCACCC	CTCCCGCA	1100011000	0000000	AGGCGGCCC	CAGGGCGG	BAGUCUGGA	SGCUUGGGG	SCCCGUCAG	SCCGCAGCC	AUCGGCCGC	CAAUCGGCC	GAACGUUCU	eccencing.	AGGUGAGAC	CCCUCGAGG	GUGCCUUCA	CGCUCAACA	UAGUUGAGC	I COLUCIO	
TICAL UGAUGGAUGCACUAUGCGCG AGCCAGUGCA	ACACU UGAUGGCAUGCACUAUGCGCG AUCAGCCAGU	CHACA HOATIGGACHAGGGGG ACUCAUCAGC	ACRIA HARIGGEAUGCACUAUGCGCG ACACUCAUCA	CAGOTI HEALINGCAUGCACOLAUGCGCG GACGACGUAC	CHOCK HEALIGGCAUGCACUAUGCGCG AGCUCGACGA	CCUTA HEALIGGCAUGCACUAUGCGCG AUAAAAGAAA	CCACA HRAIIGGCAUGCACUAUGCGCG ACUCUUCCGG	CHILIC HOST ROCATIGGACUAUGOGGG AACUTGCUCC	CICCIII IIGAIIGGCAUGCACUAUGCGCG AAGUGCUGUC	SCORE MENINGCALINAUGCGCG ACCOUCUCA	AGCCG CONTROL OF THE PROPERTY AND THE PROPERTY OF THE PROPERTY	UCCCG SCASSCANCERISCOSCI AGCIICOGA	UCCGA UGAUGGCAUGCACACACACACACACACACACACACACACA	SAUGGCAUGCACOAOGCGCG	GUCAG UGAUGGCAUGCACUAUGCGCG AGGCCGGGCC	GACGU UGAUGCAUGCACUAUGCGCG AGCAGGCGG	UGAAG UGAUGGCAUGCACUAUGCGCG GGAGUCUGGA	CCCGU UGAUGGCAUGCACUAUGCGCG AGCCUUGGGG	GGCCG UGAUGGCAUGCACUAUGCGCG AGCCCGUCAG	ACAAU UGAUGGCAUGCACUAUGCGCG GGCCGCAGCC	GUUCA UGAUGGCAUGCACUAUGCGCG AAUCGGCCGC	ALIGHU UGAUGGCAUGCACUAUGCGCG ACAAUCGGCC	CUCUG UGAUGGCAUGCACUAUGCGCG GGAACGUUCU	ACGCU UGAUGGCAUGCACUAUGCGCG GCCCCUCUUU	ACCCU UGAUGGCAUGCACUAUGCGCG GAGGUGAGAC	GCCUU UGAUGGCAUGCACUAUGCGCG ACCCUCGAGG	CUGAA UGAUGGCAUGCACUAUGCGCG AGUGCCUUCA	THEAR DEAUGCAUGCACUAUGCGCG ACGCUGAACA	CCCCI INTRINGERALIGERACINAUGCGCG GUAGUUGAGC	USCUCIO INTERCENTING PARTIFICACION GCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	100000000000000000000000000000000000000
SU LICALI UG	ACACU UG	OIL WORLD	ACGITA IIG	OIL HOUSE	OT CAST OF	OLI WELLOW	OC ACCOUNT	OHID THE	SU CUCITI III	ACCUSE IN	MOCOO I	20000	UCCGA U	CAGGG U	GUCAG U	GACGU U	UGAAG U	n necoon n	D SCCCG U	ACAAU U	GUUCA U	AUGUU U	מתכתפ ת	ACGCU U	ACCCU 1	accun t	CUGAA I	THICAG	T TODOO	00000	
	UGCACUGGCU G AUGAG	ACUGGCUGAU & AGUSU	GCUGAGGGU G UGUAC	UGAUGAGUGU G UACGO	GUACGUCGUC G AGCUG	UCGUCGAGCU G CUCAG	UUUCUUUUAU G UCACG	CCGGAAGAGU G UCUGG	GGAGCAAGUU G CAAAG	GACAGCACUU G AAGAG	UGAAGAGGU G CAGCU	GGGUGCAGCU G CGGGA	UGCGGGAGCU G UCGGA	AGCCAGGCCC G CCCUG	GGCCCGCCCU G CUGAC	CCGCCCUGCU G ACGUC	UCCAGACUCC G CUUCA	CCCCAAGCCU G ACGGG	CHIRACGGGCU G CGGCC	THE WAY OF THE PARTY OF THE PAR	Caccoccoccin a light	THOSE CONTRACTOR	GGCCGMUGG G ANGRO	Menace of Contract	GIOTOPOLIC G AGGG	CONTRACTOR BARBOT	DADIEL O HOUSE	UGAAGGCACO G COCACO	UGUUCAGCGU G CUCAA	GCUCAACUAC G AGCGG	
	1699	1702	1706	1708	1718	1723	1742	1793	1807	1834	1843	1849	1858	1898	1903	1906	1920	1937	10/6	1343	1991	1955	1957	1992	2002	0000	2029	2038	2047	2057	

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AGAGG UGAUGGCAUGAGGGGGG GCCCAGGAGG	CAGCA HEALIGGCAUGCACUAUGCGCG AGAGGCGCCC	GCCAC TICATICGCATTCACTIATICGGGGG ACAGAGGCGC	CCCAG UGAGGGAGGGAGGGGGGGGGGGGGGGGGGGGGGG	GAUAU UGAUGGCAUGCACOACOCCC GOCCACCCC	AGGUG UGAUGGCACUAUGCGCG GCCAGGCCCC	CGCAG UGAUGGCAUGCACUAUGCGCG ACGAAGGUGC	ACACG UGAUGGCAUGCACUAUGCGCG AGCACGAAGG	CCGCA UGAUGGCAUGCACUAUGCGCG ACGCAGCACG	GCCCG UGAUGGCAUGCACUAUGCGCG ACACGCAGCA	GGCGG UGAUGCCAUGCACUAUGCGCG GGGUCCUGGG	UCAGG UGAUGGCAUGCACUAUGCGCG GGCGGGUCCU	CAGCU UGAUGGCAUDGCGCG AGGCGGCGGG	AAGUA UGAUGGCAUGCACUAUGCGCG AGCUCAGGCG	CUUGA UGAUGGCAUGCACUAUGCGCG AAAGUACAGC	CGUCA UGAUGGCAUGCACUAUGCGCG AUCCACCUUG	CCCGU UGAUGGCAUGCACUAUGCGCG ACAUCCACCU	GUACG UGAUGGCAUGCACUAUGCGCG GCCCGUCACA	GGUGU UGAUGGCAUGCACUAUGCGCG GUACGCGCCC	GCUGG UGAUGGCAUGCACUAUGCGCG GAUGACCUCC	GCACG UGAUGGCAUGCACUAUGCGCG AGUACGUGUU	CGACG UGAUGGCAUGCACUAUGCGCG ACGCAGUACG	CACGG UGAUGGCAUGCACUAUGCGCG AUACCGACGC	AUGGG UGAUGGCAUGCACUAUGCGCG GGCCUUCUGG	CCUUG UGAUGGCAUGCACUAUGCGCG GGACGUGCCC	UCUGU UGAUGGCAUGCACUAUGCGCG AAGGUAGAGA	UGUCG UGAUGGCAUGCACUAUGCGCG AUGUACGGCU	ACUGU UGAUGGCAUGCACUAUGCGCG GCAUGUACGG	UCCUG UGAUGGAUGCACUAUGCGCG AGGUGAGCCA	CUCAG UGAUGGCAUGCACUAUGCGCG GGGCUGGUCU	UCCCU UGAUGGCAUGCACUAUGCGCG AGCGGGCUGG	GACGG UGAUGGCAUAUGCGCG AUCCCUCAGC	
וייווטט ט טטטטווטטווטט	CICCIOCOCCO C COCCO	degreection is nacros	acaccucudu a cuada	GGGCCUGGAC G AUAUC	AGGGCCUGGC G CACCU	GCACCUUCGU G CUGCG	conceneer a causa	cenecuecen e necee	udcuaceueu a ceaac	CCCAGGACCC G CCGCC	AGGACCCGCC G CCUGA	CCCCCCCCC G AGCUG	CGCCUGAGCU G UACUU	GCUGUACUUU G UCAAG	CAAGGUGGAU G UGACG	AGGUGGAUGU G ACGGG	UGUGACGGGC G CGUAC	GGGCGCGUAC G ACACC	GGAGGICAUC G CCAGC	AACACGUACU G CGUGC	CHINCHECE G COUCE	GCGUCGGUAU G CCGUG	CCAGAAGGCC G CCCAU	GGGCACGUCC G CAAGG	UCUCUACCUU G ACAGA	AGCCGUACAU G CGACA	CCGIACAUGC G ACAGU	TOCOMODO CARGA	AGACCAGCCC G CUGAG	CCAGCCCGCU G AGGGA	GCUGAGGGAU G CCGUC.	
2000	7807	2093	2095	2108	2127	2137	2140	2144	2146	2161	2164	2168	2173	2180	2192	2194	2201	2207	2243	2274	227R	228B	2306	2322	2353	2374	2376	2000	2410	2413	2420	2000

AGAGG UGAUGGCAUGCACUAUGCGCG GCCCAGGAGG

2432	CRITCHICANC G AGCAG	CUGCU UGAUGGCAUGCACUAUGCGCG GAUGACGACG
35.50	CONTROLL G BAIRS	UCAUT UGAUGGCAUGCACUAUGCGCG AGGGAGGAGC
2443	CHOCCHGANI G AGGCC	GGCCU UGAUGCAUGCACUAUGCGCG AUUCAGGGAG
2474	HIGGCOCOCOO G ACGUC	GACGU UGAUGGCAUGCACUAUGCGCG GAAGAGGCCA
2487	GICUICCUAC G COUCA	UGAAG UGAUGGCAUGCACUAUGCGCG GUAGGAAGAC
2494	UACGCUUCAU G UGCCA	UGGCA UGAUGGCAUGCACUAUGCGCG AUGAAGCGUA
2496	CGCUUCAUGU G CCACC	GGUGG UGAUGGCAUGCACUAUGCGCG ACAUGAAGCG
2504	GUGCCACCAC G CCGUG	CACGG UGAUGGCAUGCACUAUGCGCG GUGGUGGCAC
2509	ACCACGCCGU G CGCAU	AUGCG UGAUGGCAUGCACUAUGCGCG ACGCCGUCGU
2511	CACGCCGUGC G CAUCA	UGAUG UGAUGSCAUGCACUAUGOGCG GCACGGCGUG
2538	UACGUCCAGU G CCAGG	CCUGG UGAUGGCAUGCACUAUGCGCG ACUGGACGUA
2551	AGGGGAUCCC G CAGGG	CCCUG UGAUGGCAUGCACUAUGCGCG GGGAUCCCCU
2572	UCCUCUCCAC G CUGCU	AGCAG UGAUGGCAUGCACUAUGCGCG GUGGAGAGGA
2575	nanacycean e anane	CAGAG UGAUGGCAUGCACUAUGCGCG AGCGUGGAGA
2580	ACGCUGCUCU G CAGCC	GGCUG UGAUGGCAUGCACUAUGCGCG AGAGCAGCGU
2587	UCUGCAGCCU G UGCUA	UAGCA UGAUGGCAUGCACUAUGCGCG AGGCUGCAGA
2589	UGCAGCCUGU G CUACG	CGUAG UGAUGGCAUGCACUAUGCGCG ACAGGCUGCA
2597	GUGCUACGGC G ACAUG	CAUGU UGAUGCCAUGCACUAGGGG GCCGUAGCAC
2614	AGAACAAGCU G UUUGC	GCAAA UGAUGGCAUGCACIAUGCGCG AGCUUGUUCU
2618	CAAGCUGUUU G CGGGG	CCCCG UGAUGGCAUGCACUAUGCGCG AAACAGCUUG
2641	GGGACGGCU G CUCCU	AGGAG UGAUGGCAUGCACUAUGCGCG AGCCCGUCCC
2647	COCOCCOCO G COOM	AAACG UGAUGGCAUGCACUAUGCGCG AGGAGCAGCC
2660	UNUGGUGGAU G AUTUC	GAAAU UGAUGGCAUGCACUAUGCGGG AUCCACCAAA
2668	AUGAUUUCUU G UUGGU	ACCAA UGAUGGCAUGCACUAUGCGCG AAGAAAUCAU
2674	UCUUGUUGGU G ACACC	GGUGU UGAUGGCAUGCACUAUGCGCG ACCAACAAGA
2693	CCUCACCCAC G CGAAA	UTUCG UGAUGGCAUGCACUAUGCGCG GUGGGUGAGG
2695	UCACCCACGC G AAAAC	GUUUU UGAUGGCAUGCACUAUGCGCG GCGUGGGUGA
2721	ACCCUGGUCC G AGGUG	CACCU UGAUGGCAUGCACUAUGCGCG GGACCAGGGU
2726	GGUCCGAGGU G UCCCU	AGGGA UGAUGCACUAUGCGCG ACCUCGGACC
2732	AGGUGUCCCU G AGUAU	AUACU UGAUGGCAUGCACUAUGCGCG AGGGACACCU
2742	GAGUAUGGCU G CGUGG	CCACG UGAUGGCAUGCACUAUGCGCG AGCCAUACUC

2749	GCUGCGUGGU G AACUU	AAGUU UGAUGGCAUGCACUAUGCGCG ACCACGCAGC
2755	UGGUGAACUU G CGGAA	UUCCG UGAUGGCAUGCACUAUGCGCG AAGUUCACCA
2770	AGACAGUGGU G AACUU	AAGUU UGAUGGCAUGCACUAUGCGCG ACCACUGUCU
2780	GAACUUCCCU G UAGAA	UUCUA UGAUGGCAUGCACUAUGCGCG AGGGAAGUUC
2789	UGUAGAAGAC G AGGCC	GOCCU UGAUGGCAUGCACUAUGCGCG GUCUUCUACA
2813	CACGGCUUUU G UUCAG	CUGAA UGAUGGCAUGCACUAUGCGCG AAAAGCCGUG
2821	UUGUUCAGAU G CCGGC	GCCGG UGAUGGCAUGCACUAUGCGCG AUCUGAACAA
2847	uncoccuden e caeco	GGCCG UGAUGGCAUGCACUAUGCGCG ACCAGGGGAA
2854	deneceecen e coeco	AGCAG UGAUGCCAUGCACUAUGCGCG AGGCCGCACC
2857	GCGGCCUGCU G CUGGA	UCCAG UGAUGGCAUGCACUAUGCGCG AGCAGGCCGC
2881	CCCUGGAGGU G CAGAG	CUCUG UGAUGGCAUGCACUAUGCGCG ACCUCCAGGG
2888	GGUGCAGAGC G ACUAC	GUAGU UGAUGGCAUGCACUAUGCGCG GCUCUGCACC
2903	CUCCAGCUAU G CCCGG	CCGGG UGAUGGCAUGCACUAUGCGCG AUAGCUGGAG
2940	ACCUUCAACC G CGGCU	AGCCG UGAUGGCAUGCACUAUGCGCG GGUUGAAGGU
2965	GGAGGAACAU G CGUCG	CGACG UGAUGGCAUGCACTIAUGCGCG AUGUUCCUCC
2970	AACAUGCGUC G CAAAC	GUUUG UGAUGGCAUGCACUAUGCGCG GACGCAUGUU
2989	unagagucun a caacu	AGCCG UGAUGGCAUGCACUAUGCGCG AAGACCCCAA
2995	UCUUGCGGCU G AAGUG	CACUU UGAUGGCAUGCACUAUGCGCG AGCCGCAAGA
3000	CGGCUGAAGU G UCACA	UGUGA UGAUGGCAUGCACUAUGCGCG ACUUCAGCCG
3010	GUCACAGCCU G UUUCU	AGAAA UGAUGCCAUGCACUAUGCGCG AGGCUGUGAC
3022	UDCUGGAUUU G CAGGU	ACCUG UGAUGGCAUGCACUAUGCGCG AAAUCCAGAA
3028	AUUUGCAGGU G AACAG	CUGUU UGAUGGCAUGCACUAUGCGCG ACCUGCAAAU
3046	UCCAGACGGU G UGCAC	GUGCA UGAUGGCAUGCACUAUGCGCG ACCGUCUGGA
3048	CAGACGGUGU G CACCA	UGGUG UGAUGGCAUAGCGCG ACACCGUCUG
3073	AGAUCCUCCU G CUGCA	UGCAG UGAUGGCAUGCACUAUGCGCG AGGAGGAUCU
3076	uccuccuacu a chaac	GCCUG UGAUGGCAUGCACUAUGCGCG AGCAGGAGGA
3095	CAGGUUUCAC G CAUGU	ACAUG UGAUGGAUGCACUAUGCGCG GUGAAACCUG
3099	UUUCACGCAU G UGUGC	GCACA UGAUGGCAUGCACUAUGCGCG AUGCGUGAAA
3101	UCACGCAUGU G UGCUG	CAGCA UGAUGGCAUGCACUAUGCGCG ACAUGCGUGA
3103	ACGCAUGUGU G CUGCA	UGCAG UGAUGGCAUGCACUAUGCGCG ACACAUGCGU
3106	CAUGUGUGU G CAGCU	AGCUG UGAUGGCAUGCACUAUGCGCG AGCACACAUG

	CGCG AGGAAAAAUG	CGCG GCAGGAAAA	CGCG AGAGAUGACG	CGCG AGAGGGAGGC	CGCG AGGAUGGAGU	cece eurcanaecu	CGCG AUCCCUGCGU	cece eacaucceue	cece eccanteecc	caca aacaccana	CCCC AGAGGCCGG	CGCG GGAGGGCAGA	CCCC ACGCCUCGG	CCCC ACCCACUGCA	SCOCG ACAGCCACUG	SCGCG AGGAAUGCUU	SCGCG AGCUUGAGCA	SCGCG GAGUCAGCUU	SCGCG ACGGUGUCGA	SCGCG ACGUAGGUGA	acece encuaeecne	acace Accudeducu	SCGCG GUCCCCGGGA	scece encencecee	acece Addeduceuce	SCGCG AGUCAGCGUC	acece eeccuccaee	acece Acuaccadau	GCGCG AGUCCAGGAU	GUGGG GGGGGGAU
MUNICOLD 6 COROLD MUNICOLD 6 MANGE MUNIC	ACGCG UGAUGGCAUGCACUAUGCGCG AGGAAAAAUG	UGACG UGAUGGCAUGCACUAUGG	CGUGU UGAUGGCAUGCACUAUG	AGUAG UGAUGGCAUGCACUAUG	GCUUU UGAUGGCAUGCACUAUG	CCCUG UGAUGGCAUGCACUAUG	AGCGA UGAUGGCAUGCACUAUG	CCCAG UGAUGGCAUGCACUAUG	GGCGG UGAUGGCAUGCACUAUG	GCCGG UGAUGGCAUGCACUAUG	GAGGG UGAUGGCAUGCACUAUG	GGCCU UGAUGGCAUGCACUAUG	CACUG UGAUGGCAUGCACUAUG	UGGCA UGAUGGCAUGCACUAUG	GGUGG UGAUGGCAUGCACUAUG	UUGAG UGAUGGCAUGCACUAUG	CGAGU UGAUGGCAUGCACUAUG	. GGUGU UGAUGGCAUGCACUAUG	GGUGA UGAUGGCAUGCACUAUC	AGUGG UGAUGGCAUGCACUAUG	AGCUG UGAUGGCAUGCACUAUG	CGACU UGAUGGCAUGCACUAUC	AGCGU UGAUGGCAUGCACUAUG	GUCAG UGAUGGCAUGCACUAUC	GCAGU UGAUGGCAUGCACUAUC	CAGGG UGAUGGCAUGCACUAUC	GGCUG UGAUGGCAUGCACUAUC	GAGGG UGAUGGCAUGCACUAUC	GCCAU UGAUGGCAUGCACUAUC	TIMITO STORES CONTROLL COCKED
	CAUDUUCCU G CGCGU	JUDIUUCCUGC G CGUCA	CGUCAUCUCU G ACACG	JCCCUCU G CUACU	ACUCCAUCCU G AAAGC	AGCCAAGAAC G CAGGG	ACGCAGGGAU G UCGCU	CAGGGAUGUC G CUGGG	Chagge g cogec	CAAGGCGCC G CCGGC	cceeccaca e cccac	UCUGCCCUCC G AGGCC	CCGAGGCCGU G CAGUG	UGCAGUGGCU G UGCCA	CAGUGGCUGU G CCACC	CAUUCCU G CUCAA	UGCUCAAGCU G ACUCG	AAGCUGACUC G ACACC	ACACCGU G UCACC	UCACCUACGU G CCACU	CCCAGAC G CAGCU	CGCAGCU G AGUCG	CCGGGGAC G ACGCU	CGGGGACGAC G CUGAC	ACGACGCU G ACUGC	GACGCUGACU G CCCUG	CCUGGAGGCC G CAGCC	CCGCACU G CCCUC	AUCCUGGACU G AUGGC	CAUCO O COCO COCOCO

3905	GGUGUGCCCU G UACAC	GUGUA UGAUGCAUGCACUAUGCGCG AGGGCACACC
3915	GUACACAGGC G AGGAC	GUCCU UGAUGGCAUGCACUAUGCGCG GCCUGUGUAC
3924	CGAGGACCCU G CACCU	AGGUG UGAUGGCAUGCACUAUGCGCG AGGGUCCUCG
3944	GGGGGGCCCU G UGGGG	ACCCA UGAUGGCAUGCACUAUGCGCG AGGGACCCCC
3966	GGGGGAGGU G CUGUG	CACAG UGAUGGCAUGCACUAUGCGCG ACCUCCCCCC
3969	GGGAGGUGCU G UGGGA	UCCCA UGAUGCAUGCACAUAGCGCG AGCACCUCCC
3985	GUAAAAUACU G AAUAU	AUAUU UGAUGGCAUGCACUAUGCGCG AGUAUUUAC
3993	CUGAAUAUAU G AGUUU	AAACU UGAUGGCAUGCACUAUGCGCG AUAUAUUCAG
4008	UUUCAGUUUU G AAAAA	UUUUU UGAUGGCAUGCACUAUGCGCG AAAACUGAAA

Seq I = TEKT (Home sapiens telemense creates tenscriptuse (TERT) mRNA, 4015 bp); Nakamuna *et al.*, Science 277 (5328), 955-959 (1997) input Sequence = TERT. Cut Site = YGM or UGU.
Stem Length = 5/10. Core Sequence = UGAUG GCAUGCACUAUGC GCG

Table 16: Human telomerase reverse transcriptase (TERT) DNAzyme and Target Sequence

1	DIAMESTIC SEQUENCE	och. ID	2000000	
Position		Nos		
o	CAGGACGC GGCTAGCTACAACGA AGCGCTGC		GCAGCGCT G GCGTCCTG	
11	AGCAGGAC GGCTAGCTACAACGA GCAGCGCT.		AGCGCIGC G GICCIGCI	
16	TGCGCAGC GGCTAGCTACAACGA AGGACGCA		TGCGTCCT G GCTGCGCA	
19	ACGIGCGC GGCIAGCIACAACGA AGCAGGAC		GICCIGCI G GCGCACGI	
21	CCACGIGC GGCIAGCIACAACGA GCAGCAGG		CCTGCTGC G GCACGTGG	
23	TCCCACGI GGCTAGCTACAACGA GCGCAGCA		TGCTGCGC A ACGTGGGA	
25	CTTCCCAC GGCTAGCTACAACGA GTGCGCAG		CIGCGCAC G GIGGGAAG	
32	GCCAGGGC GGCTAGCTACAACGA TTCCCACG		CGTGGGAA G GCCCTGGC	
38	GCCGGGGC GGCTAGCTACAACGA CAGGGCTT		AAGCCCIG G GCCCCGGC	
44	GGGGTGGC GGCTAGTACGA CGGGGCCA		TGGCCCCG G GCCACCCC	
47	GCGGGGGT GGCTAGTACGA GGCCGGGG		CCCCGGCC A ACCCCCGC	
53	GGCATCGC GGCTAGCTACAACGA GGGGGTGG		CCACCCC G GCGAIGCC	
95	CGCGGCAT GGCTAGCTACAACGA CGCGGGGG		CCCCGGG A ATGCCGCG	
58	CGCGCGGC GGCTAGCTACAACGA ATCGCGGG		CCCGCGAT G GCCGCGCG	
61	GAGCGCG GGCTACTACAACGA GGCATCGC		GCGATGCC G GCGCGCTC	
63	GGGAGCGC GGCTACTACAACGA GCGGCATC		GATGCCGC G GCGCTCCC	
99	CGGGGAGC GGCTAGTACGA GCGCGGCA		TGCCGCGC G GCTCCCCG	
72	TCGGCAGC GGCTAGCTACAACGA GGGGAGCG		COCICCCC G GCIGCCGA	
75	GGCTCGGC GGCTAGCTACAACGA AGCGGGGA		TCCCGGT G GCCGAGCC	
80	OGCACGGC GGCTAGCTACAACGA TCGGCAGC		GCTGCCGA G GCCGTGCG	0 .
83	GAGCGCAC GGCTAGCTACAACGA GGCTCGGC		GCCGAGCC G GTGCGCTC	
85	GGGAGCGC GGCTAGCTACAACGA ACGGCTCG		CGAGCCGT G GCGCTCCC	
87	CAGGGAGC GGCTAGCTACGA GCACGGCT		AGCCGIGC G GCICCCIG	
94	TGCGCAGC GGCTAGCTACAACGA AGGGAGCG		CGCTCCCT G GCTGCGCA	
16	GGCTGCGC GCCTAGCTACAACGA AGCAGGGA		TCCCTGCT G GCGCAGCC	
66	GIGGCIGC GCCIAGCIACAACGA GCAGCAGG		CCIGCIGC G GCAGCCAC	
	DOCOCOUR ADDITION OF THE PARTY		CAMPACOC C ACCOUNTS	

105	GCGGTAGT GGCTAGCTACAACGA GGCTGCGC	GCGCAGCC A ACTACCGC
108	CTCGCGGT GGCTAGCTACAACGA AGTGGCTG	CAGCCACT A ACCGCGAG
111	CACCTCGC GGCTAGCTACAACGA GGTAGTGG	CCACTACC G GCGAGGTG
116	GGCAGCAC GGCTAGCTACAACGA CTCGCGGT	ACCECGAG G GTGCTGCC
118	GCGGCAGC GGCTAGTACGA ACCTCGCG	CGCGAGGI G GCTGCCGC
121	CCAGCGGC GGCTAGCAACGA AGCACCTC	GAGGTGCT G GCCGCTGG
124	TGGCCAGC GGCTAGCTACAACGA GGCAGCAC	GTGCTGCC G GCTGGCCA
128	AACGIGGC GGCIAGCIACAACGA CAGCGGCA	TGCCGCTG G GCCACGTT
131	ACGAACGT GGCTAGCTACAACGA GGCCAGCG	CGCTGGCC A ACGTTCGT
133	GCACGAAC GGCTAGCTACAACGA GTGGCCAG	CIGGCCAC G GITCGIGC
137	CGCCGCAC GGCTAGCTACAACGA GAACGTGG	CCACGITC G GIGCGGCG
139	GGCGCCGC GGCTAGCACGA ACGAACGT	ACGITCGI G GCGCGCC
142	CCAGGCGC GGCTAGCTACGA CGCACGAA	TTCGTGCG G GCGCCTGG
144	CCCCAGGC GGCTAGCTACAACGA GCCGCACG	CGTGCGGC G GCCTGGGG
151	CCTGGGGC GCCTACCTACGA CCCAGGCG	CGCCTGGG G GCCCCAGG
159	CCGCCAGC GGCTAGCTACGA CCTGGGGC	GCCCCAGG G GCTGGCGG
163	CCAGCCGC GGCTAGCTACGA CAGCCCTG	CAGGGCTG G GCGGCTGG
166	GCACCAGC GGCTAGCTACAACGA CGCCAGCC	GGCTGGCG G GCTGGTGC
170	CGCTGCAC GGCTAGCTACGA CAGCCGCC	GGCGGCTG G GTGCAGCG
172	CGCGCTGC GGCTAGCTACGA ACCAGCCG	CGCTGCT G GCAGCGCG
175	CCCCGCGC GGCTAGCTACAACGA TGCACCAG	CTGGTGCA G GCGCGGGG
177	GTCCCCGC GGCTAGCTACAACGA GCTGCACC	GGTGCAGC G GCGGGGAC
183	CGCCGGGT GGCTAGCTACAACGA CCCCGCGC	GCGCGGGG A ACCCGGCG
188	AAAGCCGC GGCTAGCTACAACGA CGGGTCCC	GGGACCCG G GCGCTTT
191	COGRANGE GGCTAGCTACAACGA CGCCGGGT	ACCCGGCG G GCTTTCCG
198	CAGCGCGC GGCTAGCTACAACGA GGAAAGCC	GGCTTTCC G GCGCGCTG
200	ACCAGGGC GGCTAGCTACAAGGA GCGGAAAG	CITICCGC G GCGCTGGT
202	CCACCAGC GGCTAGCTACAACGA GCGCGGAA	Trecesse s serestes
206	TGGGCCAC GGCTAGCTACAACGA CAGCGCGC	GCGCGCTG G GTGGCCCA
509	CACTGGGC GGCTAGCTACAACGA CACCAGCG	CGCTGGTG G GCCCAGTG
214	CCAGGCAC GGCTAGCTACAACGA TGGGCCAC	GIGGCCCA G GIGCCIGG

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216	CACCAGGC GGCTAGCTACAACGA ACTGGGCC	GGCCCAGI G GCCIGGIG	
221	ACCCACAC GGCTAGCTACAACGA CAGGCACT	υ	
223	GCACGCAC GGCTAGCTACAACGA ACCAGGCA	recereer e erecerec	
225	GGGCACGC GGCTAGCTACAACGA ACACCAGG	cordardr a acardeec	
227	CAGGGCAC GGCTAGCTACAACGA GCACACCA	TGGTGTGC G GTGCCCTG	
229	CCCAGGGC GGCTAGCTACGA ACGCACAC	GIGIGGGI G GCCCIGGG	
237	CCGTGCGT GGCTAGCTACGACGA CCCAGGGC	GCCCTGGG A ACGCACGG	
239	GGCCGTGC GGCTAGCTACAACGA GTCCCAGG	CCTGGGAC G GCACGGCC	
241	GCGGCCGT GGCTAGCTACAACGA GCGTCCCA	TGGGACGC A ACGGCCGC	
244	GGGGCGGC GGCTAGCTACGA CGTGCGTC	GACGCACG G GCCGCCCC	
247	CGGGGGGC GGCTAGCTACAACGA GGCCGTGC	GCACGGCC G GCCCCCCG	
254	GGGGCGGC GGCTAGCTACAACGA GGGGGGCG	2222222 g 2222252	
257	GAGGGGG GGCTAGCTACAACGA GGCGGGGG	CCCCGGC G GCCCCCTC	
270	CACCTGGC GGCTAGCTACAACGA GGAAGGAG	CTCCTTCC G GCCAGGTG	
275	CAGGACAC GGCTAGCTACAACGA CTGGCGGA	TCCGCCAG G GTGTCCTG	
277	GGCAGGAC GGCTAGCTACAACGA ACCTGGCG	CGCCAGGT G GTCCTGCC	
282	CTTCAGGC GGCTACTACAACGA AGGACACC	GGTGTCCT G GCCTGAAG	
292	CCACCAGC GGCTAGCTACAACGA TCCTTCAG	CTGAAGGA G GCTGGTGG	
296	CGGGCCAC GGCTAGCTACAACGA CAGCTCCT	AGGAGCTG G GTGGCCCG	
299	ACTCGGGC GGCTAGCTACAACGA CACCAGCT	AGCTGGTG G GCCCGAGT	
305	TGCAGCAC GGCTAGCTACAACGA TCGGGCCA	TGGCCCGA G GTGCTGCA	
307	TCTGCAGC GGCTAGCTACAACGA ACTCGGGC	GCCCGAGT G GCTGCAGA	
310	GCCTCTGC GGCTAGCTACAACGA AGCACTCG	CGAGTGCT G GCAGAGGC	
316	CGCACAGC GGCTAGCTACAACGA CTCTGCAG	CTGCAGAG G GCTGTGCG	
319	GCTCGCAC GGCTAGCTACAACGA AGCCTCTG	CAGAGGCT G GTGCGAGC	
321	GUGCIUGO GGUTAGUTACAACGA ACAGUUTO	GAGGCTGT G GCGAGCGC	
325	CGCCGCGC GGCTAGCTACAACGA TCGCACAG	CTGTGCGA G GCGCGGCG	
327	CGCGCCGC GGCTAGCTACAACGA GCTCGCAC	GIGCGAGC G GCGGCGCG	-
330	CTTCGCGC GGCTAGCTACAACGA CGCGCTCG	CGAGCGCG G GCGCGAAG	
332	TTCTTCGC GGCTAGCTACGA GCCGCGCT	AGCGCGC G GCGNAGAA	
339	CAGCACGT GGCTAGCTACAACGA TCTTCGCG	CGCGAAGA A ACGTGCTG	

341	GCCAGCAC GGCTAGCTACAACGA GTTCTTCG	CGAAGAAC G GTGCTGGC
343	AGGCCAGC GGCTAGCTACAACGA ACGTTCTT	AAGAACGT G GCTGGCCT
347	CCGAAGGC GGCTAGCTACAACGA CAGCACGT	ACGIGCTG G GCCTTCGG
354	CGCGAAGC GGCTAGCTACAACGA CGAAGGCC	GGCCITCG G GCITCGCG
359	AGCAGCGC GGCTAGCTACAACGA GAAGCCGA	TOGGCTIC G GCGCIGCT
361	CCAGCAGC GGCTAGCTACAACGA GCGAAGCC	GGCTTCGC G GCTGCTGG
364	CGTCCAGC GGCTAGCTACAACGA AGCGCGAA	TTCGCGCT G GCTGGACG
369	GGCCCCGT GGCTAGCTACAACGA CCAGCAGC	GCTGCTGG A ACGGGGCC
374	CCGCGGGC GGCTACTACGACGA CCCGTCCA	TGGACGGG G GCCCGCGG
378	GCCCCCGC GGCTAGCTACAACGA GGGCCCCG	20000000 0 2220000
384	GGGGGGG GGCTAGTACGA CCCCGCGG	2222229 9 BBB2522
395	GTGAAGGC GGCTAGCTACAACGA CTCGGGGG	CCCCCGAG G GCCTTCAC
401	CTGGTGGT GGCTAGCTACAACGA GAAGGCCT	AGGCCTTC A ACCACCAG
404	ACGCTGGT GGCTAGCTACGA GGTGAAGG	CCTTCACC A ACCAGCGT
408	GCGCACGC GGCTAGCTACAACGA TGGTGGTG	CACCACCA G GCGTGCGC
410	CTGCGCAC GGCTAGCTACAACGA GCTGGTGG	CCACCAGC G GTGCGCAG
412	AGCTGCGC GGCTAGCTACGA ACGCTGGT	ACCAGGGT G GCGCAGCT
414	GTAGCTGC GGCTAGCTACAACGA GCACGCTG	CAGCGTGC G GCAGCTAC
417	CAGGIAGO GGCTAGCTACAACGA TGCGCACG	CGTGCGCA G GCTACCTG
420	GGGCAGGT GGCTAGCTACAACGA AGCTGCGC	GCGCAGCT A ACCTGCCC
424	TGTTGGGC GGCTAGCTACGA AGGTAGCT	AGCTACCT G GCCCAACA
429	CACCGTGT GGCTAGCTACAACGA TGGGCAGG	CCTGCCCA A ACACGGTG
431	GTCACCGT GGCTAGCTACAACGA GTTGGGCA	TGCCCAAC A ACGGTGAC
434	TOGGTCAC GGCTAGCTACAACGA CGTGTTGG	CCAACACG G GTGACCGA
437	GCGTCGGT GGCTAGCTACAACGA CACCGTGT	ACACGGTG A ACCGACGC
441	CAGTGCGT GGCTAGCTACAACGA CGGTCACC	GGTGACCG A ACGCACTG
443	CGCAGTGC GGCTAGCTACAACGA GTCGGTCA	TGACCGAC G GCACTGCG
445	CCCGCAGT GGCTAGCTACAACGA GCGTCGGT	ACCGACGC A ACTGCGGG
448	TCCCCCGC GGCTAGCTACAACGA AGTGCGTC	GACGCACT G GCGGGGA
456	CGCCCCGC GGCTAGCTACAACGA TCCCCCGC	GCGGGGGA G GCGGGGCG
461	CCCCACGC GGCTAGCTACAACGA CCCGCTCC	GGAGCGGG G GCGTGGGG

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		SCCCCCAC GGCTAGCTACAACGA GCCCCGCT	SCAGCAGC GGCTAGCTACAACGA CCCCACGC	SCAGCAGO GGCTAGCTACGA AGCCCCCA	SECGRAGE GGETAGETACGA AGCAGECE	PROPORTION AND AGCAGCAG	PACIFICISC GGCTAGCTACGA GCAGCAGC	SUCCACIO GOCTAGCTACAACGA GGCGCAGC	TCGCCCAC GGCTAGCTACAACGA GCGGCGCA	STCGTCGC GGCTAGCTACGA CCACGCGG	CACGICGI GGCIAGCIACAACGA CGCCCACG	CAGCACGT GGCTAGCTACAACGA CGTCGCCC	ACCAGCAC GGCTAGCTACAACGA GTCGTCGC	GAACCAGC GGCTAGCTACAACGA ACGTCGTC	AGGTGAAC GGCTAGCTACAACGA CAGCACGT	CAGCAGGT GGCTAGCTACAACGA GAACCAGC	GTGCCAGC GGCTAGCTACACGA AGGTGAAC	CAGCGTGC GGCTAGCTACGA CAGCAGGT	CHARACT GGCTAGCTACAACGA GCCAGCAG	CHURCHAR GRETAGETACAACGA GTGCCAGC	GARCIECE GOCTAGCTACAACGA AGCGTGCC	AAGAGGGC GGCTAGCTACGA GCAGCGTG	CAAAGAGC GGCTAGCTACAACGA GCGCAGCG	ACCAGGAC GGCTAGCTACAACGA AAAGAGCG	CCACCAGC GGCTAGCTACAACGA ACAAAGAG	GGAGCCAC GGCTAGCTACAACGA CAGCACAA	CTGGGAGC GGCTAGCTACGA CACCAGCA	GEORGEAGC GECTAGCTACAACGA TGGGAGCC	GENERACE AGETACHACHACGA AGCTGGGA	SECTION OF THE PROPERTY OF THE	CACCHOST GGCTAGGTACAACGA AGGCGCAG	50 cm 6m 5

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	COCGCAC GGCTAGCTACAACGA ACCTGGTA	IACCAGGI 6 GIGGOGGC
	SOCCOGO GGOTAGCTACAACGA ACACCTGG	CCAGGIGI G GCGGGCCG
	COGCOGC GGCTAGCTACAACGA CCGCACAC	GTGTGCGG G GCCGCCGC
	CAGCGGC GGCTAGCTACGA GGCCCGCA	TGCGGGCC G GCCGCTGT
	STACAGE GGCTAGETACAACGA GGCGGCCC	GGGCCGCC G GCTGTACC
	CTGGTAC GGCTAGCTACGA AGCGGCGG	CCGCCGCT G GTACCAGC
	AGCTOST GGCTAGCTACAACGA ACAGCGGC	GCGCTGT A ACCAGCTC
	SCCGAGC GGCTAGCTACAACGA TGGTACAG	CIGIACCA G GCTCGGCG
	SCAGCGC GGCTAGCTACAACGA CGAGCTGG	CCAGCTCG G GCGCTGCC
	TGGCAGC GGCTAGCTACAACGA GCCGAGCT	AGCTCGGC G GCTGCCAC
	SAGTGGC GGCTAGCTACAACGA AGCGCCGA	TOGGOGOT G GCCACTCA
	CCTGAGT GGCTAGCTACAACGA GGCAGCGC	GCGCTGCC A ACTCAGGC
	SCCGGGC GGCTAGCTACAACGA CTGAGTGG	CCACTCAG G GCCCGGCC
	CGGGGGC GGCTAGTACAACGA CGGGCCTG	CAGGCCCG G GCCCCCGC
	STGTGGC GGCTAGCTACAACGA GGGGGCCG	CGGCCCCC G GCCACACG
	AGCGTGT GGCTAGCTACAACGA GGCGGGGG	CCCCCGCC A ACACGCTA
	CTAGCGT GGCTAGCTACAACGA GTGGCGGG	CCCGCCAC A ACGCTAGT
	CACTAGC GGCTAGCTACAACGA GTGTGGCG	CGCCACAC G GCTAGTGG
	GGTCCAC GGCTAGCTACAACGA TAGCGTGT	ACACGCTA G GTGGACCC
	TCGGGGT GGCTAGCTACGA CCACTAGC	GCTAGTGG A ACCCCGAA
	CAGACGC GGCTAGCTACAACGA CTTCGGGG	CCCCGNAG G GCGTCTGG
	CCCAGAC GGCTAGCTACAACGA GCCTTCGG	CCGAAGGC G GTCTGGGA
	TICGCAT GGCTAGCTACAACGA CCCAGACG	CGTCTGGG A ATGCGAAC
	CGTTCGC GGCTACTACAACGA ATCCCAGA	TCTGGGAT G GCGAACGG
	GGCCCGT GGCTAGCTACAACGA TCGCATCC	GGATGCGA A ACGGGCCT
	TCCAGGC GGCTAGCTACAACGA CCGTTCGC	GCGAACGG G GCCTGGAA
	CTATEST GGCTAGCTACAACGA TCCAGGCC	GGCCTGGA A ACCATAGC
	ACGCTAT GGCTAGCTACAACGA GGTTCCAG	CTGGAACC A ATAGCGTC
	CTGACGC GGCTAGCTACAACGA TATGGTTC	GAACCATA G GCGTCAGG
	CCCTGAC GGCTAGCTACAACGA GCTATGGT	ACCATAGC G GTCAGGGA
ACCCCGGC GGCTAGCTACAACGA CTCCCTGA TCAGGGAG G G	CCCCGGC GGCTAGCTACAACGA CTCCCTGA	TCAGGGAG G GCCGGGGT

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689	AGGGGGAC GGCTAGCTACAACGA CCCGGCCI	שמפרכים כו מדיריירים
669	TGGCAGGC GGCTACCACGA CCAGGGGG	CCCCCTGG G GCCTGCCA
703	GGGCTGGC GGCTAGCTACGA AGGCCCAG	CTGGGCT G GCCAGCCC
707	CCCGGGGC GGCTAGCTACGA TGGCAGGC	GCCTGCCA G GCCCCGGG
714	CCTCGCAC GGCTAGCTACGA CCGGGGCT	AGCCCCGG G GTGCGAGG
716	CTCCTCGC GGCTAGCTACAACGA ACCCGGGG	CCCCGGGT G GCGAGGAG
724	CCCCGCGC GGCTAGCTACAACGA CTCCTCGC	GCGAGGAG G GCGCGGGG
726	GCCCCCG GGCTAGCTACAACGA GCCTCCTC	GAGGAGGC G GCGGGGGC
732	GGCACTGC GGCTAGCTACAACGA CCCCGCGC	GCGCGGG G GCAGTGCC
735	GCTGGCAC GGCTAGCTACAACGA TGCCCCCG	CGGGGGCA G GTGCCAGC
737	CGGCTGGC GGCTAGCTACAACGA ACTGCCCC	GGGGCAGT G GCCAGCCG
741	ACTICGGC GGCTAGCTACAACGA TGGCACTG	CAGTGCCA G GCCGAAGT
747	CGGCAGAC GGCTAGCTACAACGA TTCGGCTG	CAGCCGAA G GTCTGCCG
751	GCAACGGC GGCTAGCTACAACGA AGACTTCG	CGAAGTCT G GCCGTTGC
754	TGGGCAAC GGCTAGCTACAACGA GGCAGACT	AGTCTGCC G GTTGCCCA
757	TCTTGGGC GGCTAGCTACAACGA AACGGCAG	CTGCCGTT G GCCCAAGA
166	GCCTGGGC GGCTAGCTACAACGA CTCTTGGG	CCCAAGAG G GCCCAGGC
772	CGCCACGC GGCTAGCTACAACGA CTGGGGCCT	AGGCCCAG G GCGTGGCG
774	AGCGCCAC GGCTAGCTACAACGA GCCTGGGC	GCCCAGGC G GTGGCGCT
777	GGCAGCGC GGCTAGCTACAACGA CACGCCTG	CAGGCGTG G GCGCTGCC
779	GGGGCAGC GGCTAGCTACAACGA GCCACGCC	GGCGTGGC G GCTGCCCC
782	TCAGGGGC GGCTAGCTACAACGA AGCGCCAC	GTGGCGCT G GCCCCTGA
790	GCTCCGGC GGCTAGCTACAACGA TCAGGGGC	GCCCTGA G GCCGGAGC
796	GCGTCCGC GGCTAGCTACAACGA TCCGGCTC	GAGCCGGA G GCGGACGC
800	ACGGGCGT GGCTAGCTACAACGA CCGCTCCG	CGGAGCGG A ACGCCCGT
802	CAACGGGC GGCTAGCTACAACGA GTCCGCTC	GAGCGGAC G GCCCGTTG
806	TGCCCAAC GGCTAGCTACAACGA GGGCGTCC	GGACGCCC G GTTGGGCA
811	ACCCCTGC GGCTAGCTACAACGA CCAACGGG	CCCGTTGG G GCAGGGGT
817	CCCAGGAC GGCTAGCTACAAGGA CCCTGCCC	GGGCAGGG G GTCCTGGG
824	GGGTGGGC GGCTAGCTACGA CCAGGACC	GOTCCTGG G GCCCACCC
1	CANDOCCO KON KON MOOD MOOD MANAGEMENT	CENTRAL A MUNICIPAL

839		DOMESTICA & DOGOSOO
	CCACGCGT GGCTAGCTACGA CCTGCCCG	COCCURATE A SECULATION
841	GTCCACGC GGCTAGCTACGA GTCCTGCC	GGCAGGAC G GCGTGGAC
843	CGGTCCAC GGCTAGCTACAACGA GCGTCCTG	CAGGACGC G GTGGACCG
847	CACTCGGT GGCTACTACAACGA CCACGCGT	ACGCGTGG A ACCGAGTG
852	ACGGICAC GGCTAGCTACAACGA TCGGTCCA	TGGACCGA G GTGACCGT
855	ACCACGGT GGCTAGCTACGA CACTCGGT	ACCGAGIG A ACCGIGGT
858	GAAACCAC GGCTAGCTACAACGA GGTCACTC	GAGTGACC G GTGGTTTC
198	ACAGAAAC GGCTAGCTACAACGA CACGGTCA	TGACCGTG G STTTCTGT
867	CACCACAC GGCTAGCTACGA AGAMACCA	TGGTTTCT G STGTGGTG
869	GACACCAC GGCTAGCTACGA ACAGNAAC	GITICIGI G GIGGIGIC
872	GGTGACAC GGCTAGCTACAACGA CACACAGA	TCTGTGTG G GTGTCACC
874	CAGGIGAC GGCTAGCTACAACGA ACCACACA	TGTGTGGT G GTCACCTG
877	TGGCAGGT GGCTAGCTACGA GACACCAC	GTGGTGTC A ACCTGCCA
881	GGTCTGGC GGCTAGCTACGA AGGTGACA	TGTCACCT G GCCAGACC
988	COGCGGGT GGCTAGCTACAACGA CTGGCAGG	CCTGCCAG A ACCCGCCG
890	TCTTCGGC GGCTAGCTACAACGA GGGTCTGG	CCAGACCC G GCCGAAGA
899	GAGGIGG GGCIACCAACGA TICITCGG	CCGAAGAA G GCCACCTC
902	AAAGAGGT GGCTAGCTACAACGA GGCTTCTT	AAGAAGCC A ACCTCTT
915	GAGCGCAC GGCTAGCTACAACGA CCTCCAAA	TTTGGAGG G GTGCGCTC
917	GAGAGOGC GGCTAGCTACAACGA ACCCTCCA	TGGAGGGT G GCGCTCTC
919	CAGAGAGC GGCTAGCTACAACGA GCACCCTC	GAGGGTGC G GCTCTCTG
927	GCGCGTGC GGCTAGCTACAACGA CAGAGAGC	GCTCTCTG G GCACGCGC
929	TGGCGCGT GGCTAGCTACGA GCCAGAGA	TCTCTGGC A ACGCGCCA
931	AGTGGCGC GGCTAGCTACAACGA GTGCCAGA	TCTGGCAC G GCGCCACT
933	GGAGTGGC GGCTAGCTACAACGA GCGTGCCA	TOGCACGC G GCCACTCC
936	GTGGGAGT GGCTAGCTACAACGA GGCGCGTG	CACGCGCC A ACTCCCAC
942	GGATGGGT GGCTAGCTACAACGA GGGAGTGG	CCACTCCC A ACCCATCC
946	CCACGGAT GGCTAGCTACAACGA GGGTGGGA	TCCCACCC A ATCCGTGG
950	CGGCCCAC GGCTAGCTACAACGA GGATGGGT	ACCUATCC G GTGGGCCG
954	CTGGCGGC GGCTAGCTACAACGA CCACGGAT	ATCCGTGG G GCCGCCAG

957	GTGCTGGC GGCTAGCTACAACGA GGCCCACG	CGTGGGCC G GCCAGCAC
196	CGTGGTGC GGCTAGCTACGA TGGCGGCC	GGCCGCCA G GCACCACG
963	CGCGTGGT GGCTAGCTACGA GCTGGCGG	COGCCAGC A ACCACGOG
996	GCCCGCGT GGCTAGCTACGA GGTGCTGG	CCAGCACC A ACGCGGGC
896	GGGCCCGC GGCTAGCTACGA GTGGTGCT	AGCACCAC G GCGGGCCC
972	TGGGGGG GGCTAGCTACAACGA CCGCGTGG	CCACGCGG G GCCCCCCA
979	ATGTGGAT GGCTAGCTACAACGA GGGGGGCC	GGCCCCC A ATCCACAT
983	CGCGATGT GGCTAGCTACAACGA GGATGGGG	CCCCATCC A ACATCGCG
985	GCCGCGAT GGCTAGCTACAACGA GTGGATGG	CCATCCAC A ATCGCGGC
988	GTGGCCGC GGCTAGCTACAACGA GAIGTGGA	TCCACATC G GCGGCCAC
991	GTGGTGGC GGCTAGCTACAACGA CGCGATGT	ACATOGOG G GCCACCAC
994	GACGIGGI GGCIAGCIACAACGA GGCCGCGA	TCGCGGCC A ACCACGTC
766	AGGGACGT GGCTAGCTACAACGA GGTGGCCG	CGGCCACC A ACGTCCCT
666	CCAGGGAC GGCTAGCTACAACGA GTGGTGGC	GCCACCAC G GTCCCTGG
1008	AGGCGTGT GGCTAGCTACAACGA CCCAGGGA	TCCCTGGG A ACACGCCT
1010	CAAGGCGT GGCTAGCTACAACGA GTCCCAGG	CCTGGGAC A ACGCCTTG
1012	GACAAGGC GGCTAGCTACAACGA GTGTCCCA	TGGGACAC G GCCTTGTC
1017	CGGGGGAC GGCTAGCTACAACGA AAGGCGTG	CACGCCTT G GTCCCCCG
1025	GCGTACAC GGCTAGCTACAACGA CGGGGGAC	GTCCCCCG G GTGTACGC
1027	CGGCGTAC GGCTAGCTACAACGA ACCGGGGG	CCCCCGGT G GTACGCCG
1029	CTCGGCGT GGCTAGCTACGA ACACCGGG	CCCGGTGT A ACGCCGAG
1031	GTCTCGGC GGCTAGCTACAACGA GTACACCG	CGGTGTAC G GCCGAGAC
1037	TGCTTGGT GGCTAGCTACAACGA CTCGGCGT	ACGCCGAG A ACCAAGCA
1042	GGAAGTGC GGCTAGCTACAACGA TTGGTCTC	GAGACCAA G GCACTICC
1044	GAGGAAGT GGCTAGCTACAACGA GCTTGGTC	GACCAAGC A ACTTCCTC
1053	TGAGGAGT GGCTAGCTACAACGA AGAGGAAG	CTTCCTCT A ACTCCTCA
1062	CITGICGC GGCIAGCIACAACGA CIGAGGAG	CICCICAG G GCGACAAG
1065	CTCCTTGT GGCTAGCTACAACGA CGCCTGAG	CICAGGCG A ACAAGGAG
1072	GCAGCTGC GGCTAGCTACGA TCCTTGTC	GACAAGGA G GCAGCTGC
1075	GCCGCAGC GGCTACTACGA TGCTCCTT	AAGGAGCA G GCTGCGGC
1078	AGGCCGC GGCTAGCTACGA AGCTGCTC	GAGCAGCT G GCGGCCCT

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AGGAGGC GGCTAGCTACAACGA CGCAGCTG	AGCTGAGT GGCTAGCTACAACGA AGGAAGGA	CAGAGAGC GGCTAGCTACAACGA TGAGTAGG	GGCTGGGC GGCTAGCTACAACGA CTCAGAGA	AGTCAGGC GGCTAGCTACAACGA TGGGCCTC	GCGCCAGT GGCTAGCTACAACGA CAGGCTGG	CCGAGCGC GGCTAGCTACGACGA CAGTCAGG	CTCCGAGC GGCTAGCTACAACGA GCCAGTCA	CCACGAGC GGCTAGCTACAACGA CTCCGAGC	GTCTCCAC GGCTAGCTACAACGA GAGCCTCC	AAGATGGT GGCTAGCTACAACGA CTCCACGA	AGAMAGAT GGCTAGCTACAACGA GGTCTCCA	CCTGGAAC GGCTAGCTACAACGA CCAGAAAG	TCCAGGGC GGCTAGCTACAACGA CTGGAACC	CCTGGCAT GGCTAGCTACGA CCAGGGCC	TCCCTGGC GGCTAGCTACAACGA ATCCAGGG	CGGGGAGT GGCTACCAACGA CCCTGGCA	CAACCTGC GGCTAGCTACAACGA GGGGAGTC	GGGGCAAC GGCTAGCTACGA CTGCGGGG	GGCGGGGC GGCTAGCTACGA AACCTGCG	GGGCAGGC GGCTAGCTACGA GGGGCAAC	GCTGGGGC GGCTAGCTACGA AGGCGGGG	AGTAGCGC GGCTAGCTACAACGA TGGGGCAG	CCAGTAGC GGCTAGCTACGA GCTGGGGC	TIGCCAGT GGCTAGCTACGA AGCGCTGG	GCATITIC GGCTAGCTACAACGA CAGTAGCG	GGCCGCAT GGCTAGCTACAACGA TIGCCAGT	GGGGCCGC GGCTAGCTACAACGA ATTTGCCA	ACAGGGG GGCTAGCTACAACGA CGCATTTG	CCAGAAAC GGCTAGCTACAACGA AGGGGCCG	CANGCAGC GGCTAGCTACAACGA TCCAGAAA
1081	1093	1098	1108	1113	1118	1122	1124	1132	1136	1142	1145	1155	1162	1169	1171	1178	1185	1189	1192	1197	1201	1207	1209	1212	1216	1220	1222	1225	1231	1240

1258 1261 1269 1274 1276 1286 1288 1290 1293 1297 1300 1307 1310 1313 1319 1322 1326 1328 1345 1358 1361

1254

1380	GICTGIGI GGCTAGCTACAACGA CCTCCTCC	GGAGGAGG A ACACAGAC
1382	GGGTCTGT GGCTAGCTACAACGA GTCCTCCT	AGGAGGAC A ACAGACCC
1386	ACGGGGGT GGCTACTACAACGA CTGTGTCC	GGACACAG A ACCCCCGT
1392	CAGGCGAC GGCTAGCTACAACGA GGGGGTCT	AGACCCCC G GTCGCCTG
1395	CACCAGGC GGCTACTACAACGA GACGGGGG	CCCCGTC G GCCTGGTG
1400	AGCTGCAC GGCTAGCTACAACGA CAGGCGAC	GTCGCCTG G GTGCAGCT
1402	GCAGCTGC GGCTAGCTACGA ACCAGGCG	CGCCTGGT G GCAGCTGC
1405	GGAGCAGC GGCTAGCTACAACGA TGCACCAG	CIGGIGCA G GCTGCTCC
1408	GGCGGAGC GGCTACTACAACGA AGCTGCAC	GTGCAGCT G GCTCCGCC
1413	GIGCIGGC GGCTAGCTACGA GGAGCAGC	GCTGCTCC G GCCAGCAC
1417	TGCTGTGC GGCTAGCTACAACGA TGGCGGAG	CTCCGCCA G GCACAGCA
1419	GCTGCTGT GGCTAGCTACAACGA GCTGGCGG	CCGCCAGC A ACAGCAGC
1422	GGGGCTGC GGCTAGCTACGA TGTGCTGG	CCAGCACA G GCAGCCCC
1425	CCAGGGGC GGCTAGCAACGA TGCTGTGC	GCACAGCA G GCCCCTGG
1432	ACACCTGC GGCTAGCTACGA CAGGGGCT	AGCCCCTG G GCAGGTGT
1436	CCGTACAC GGCTAGCTACAACGA CTGCCAGG	CCTGGCAG G GTGTACGG
1438	AGCCGTAC GGCTAGCTACAACGA ACCTGCCA	TGGCAGGT G GTACGGCT
1440	GAAGCCGT GGCTAGCTACGA ACACCTGC	GCAGGTGT A ACGGCTTC
1443	CACGAAGC GGCTAGCTACAACGA CGTACACC	GGTGTACG G GCTTCGTG
1448	GCCCGCAC GGCTAGCTACGA GAAGCCGT	ACGCCTTC G GTGCGGGC
1450	AGGCCCGC GGCTAGCTACGA ACGNAGCC	GGCTTCGT G GCGGGCCT
1454	AGGCAGGC GGCTAGCTACGA CCGCACGA	TCGTGCCG G GCCTGCCT
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1464	CAGCCGGC GGCTAGCTACGA GCAGGCAG	CTGCCTGC G GCCGGCTG
1468	GCACCAGC GGCTAGCTACAACGA CGGCGCAG	CTGCGCCG G GCTGGTGC
1472	GGGGCAC GGCTACTACAACGA CAGCCGGC	GCGGCTG G GTGCCCCC
1474	CTGGGGGC GGCTAGCTACGA ACCAGCCG	CGGCTGGT G GCCCCCAG
1482	CCAGAGGC GGCTAGCTACGA CTGGGGGC	GCCCCCAG G GCCTCTGG
1491	CCTGGAGC GGCTAGCTACGA CCCAGAGG	CCTCTGGG G GCTCCAGG
1498	CGTTGTGC GGCTAGCTACAACGA CTGGAGCC	GGCTCCAG G GCACAACG

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1503	GOGITOGI GCTAGCIACAACGA TGTGCCTG	CAGGCACA A ACGAACGC
1507	AGGGGGT GGCTAGTACAACGA TCGTTGTG	CACAACGA A ACGCCGCT
1509	GAAGCGGC GGCTAGCTACAACGA GTTCGTTG	CAACGAAC G GCCGCTTC
1512	GAGGAAGC GGCTAGCTACAACGA GGCGTTCG	CGAACGCC G GCTTCCTC
1524	CTTGGTGT GGCTAGCTACGA TCCTGAGG	CCTCAGGA A ACACCAAG
1526	TTCTTGGT GGCTAGCTACAACGA GTTCCTGA	TCAGGAAC A ACCAAGAA
1534	AGATGAAC GGCTAGCTACAACGA TTCTTGGT	ACCAAGAA G GITCAICT
1538	AGGGAGAT GGCTAGCTACAACGA GAACTTCT	AGAAGTIC A ATCTCCCT
1552	TGGCATGC GGCTAGCTACGACGA TTCCCCCAG	CTGGGGAA G GCATGCCA
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1561	GCGAGAGC GGCTAGCTACAACGA TTGGCATG	CATGCCAA G GCTCTCGC
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1570	GCTCCTGC GGCTAGCTACAACGA AGCGAGAG	CTCTCGCT G GCAGGAGC
1576	ACGICAGO GGCTAGCTACAACGA TCCTGCAG	CTGCAGGA G GCTGACGT
1580	TICCACGI GCTAGCTACAACGA CAGCTCCT	AGGAGCTG A ACGTGGAA
1582	TCTTCCAC GGCTAGCTACAACGA GTCAGCTC	GAGCTGAC G GTGGAAGA
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1595	TCCCGCAC GGCTAGCTACAACGA GCTCATCT	AGATGAGC G GTGCGGGA
1597	AGTOCOGO GGOTAGCTACAACGA ACGCTCAT	ATGAGCGT G GCGGGACT
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1605	CCAAGCGC GGCTAGCTACAACGA AGTCCCGC	GCGGGACT G GCGCTTGG
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1615	TCCTGCGC GGCTAGCTACGA AGCCAAGC	GCTTGGCT G GCGCAGGA
1617	GCTCCTGC GGCTAGCTACAACGA GCAGCCAA	TTGGCTGC G GCAGGAGC
1623	CCCTGGGC GCCTACTACGA TCCTGCGC	GCGCAGGA G GCCCAGGG
1631	CAGCCAAC GGCTAGCTACAACGA CCCTGGGC	GCCCAGGG G GTTGGCTG

CGGAACAL GGL	CGGAACAC GGCTAGCTACAACGA AGCCAACC	6611661 6 6161166
CCGGAAC GGC	GCCGGAAC GCCTACAACGA ACAGCCAA	TIGGCTGT G GITCCGGC
CIGGGG GGC	TCTGCGGC GGCTAGCTACAACGA CGGAACAC	GTGTTCCG G GCCGCAGA
GCTCTGC GGC	TGCTCTGC GGCTAGCTACAACGA GGCCGGAA	TTCCGGCC G GCAGAGCA
ACGGTGC GGC	GACGGIGC GGCTAGCTACAACGA TCTGCGGC	GCCGCAGA G GCACCGTC
AGACGGT GGC	CAGACGGT GGCTAGCTACAACGA GCTCTGCG	CGCAGAGC A ACCOLUTE
CGCAGAC GG	ACGCAGAC GGCTAGCTACAACGA GGTGCTCT	AGAGGACC G GICINGGI
CTCACGC GG	CCICACGC GGCTAGCIACAACGA AGACGGIG	CACCGTCT G GCGTGAGG
CTCCTCAC GG	CICCICAC GGCTAGCTACAACGA GCAGACGG	CCGTCTGC G GTGAGGAG
SCCAGGAT GG	GCCAGGAT GGCTAGCTACAACGA CTCCTCAC	GTGAGGAG A ALCUIGEC
AACTTGGC GG	AACTIGGE GGCIAGCIACAACGA CAGGAICI	AGATCCTG G GCCAAGTT
SCAGGAAC GG	GCAGGAAC GGCTAGCTACAACGA TIGGCCAG	CTGGCCAA G GTTCCTGC
SCCAGTGC GG	GCCAGTGC GGCTAGCTACAACGA AGGAACTT	AAGTTCCT G GCACTGGC
CAGCCAGT GG	CAGCCAGT GGCTAGCTACAACGA GCAGGAAC	GITCCIGC A ACTGGCTG
PCATCAGC GG	TCATCAGC GGCTAGCTACAACGA CAGTGCAG	CTGCACTG G GCTGATGA
ACACTCAT GG	ACACTCAT GGCTAGCTACAACGA CAGCCAGT	ACTGGCTG A ATGAGTGT
STACACAC GG	GTACACAC GGCTAGCTACAACGA TCATCAGC	GCTGATGA G GTGTGTAC
ACGIACAC GG	ACGIACAC GGCTAGCTACAACGA ACTCATCA	TGATGAGT G GTGTACGT
CGACGIAC GG	CGACGIAC GGCTAGCIACACGA ACACTCAT	ATGAGTGT G GTACGTCG
GACGACGT GG	GACGACGI GGCTAGCIACAACGA ACACACIC	GAGIGIGI A ACGICGIC
TCGACGAC GG	TCGACGAC GGCTAGCTACAACGA GTACACAC	GTGTGTAC G GTCGTCGA
AGCTCGAC GG	AGCTCGAC GGCTAGCTACAACGA GACGTACA	TGTACGTC G GTCGAGCT
TGAGCAGC GG	TGAGCAGC GGCTAGCTACAACGA TCGACGAC	GTCGTCGA G GCTGCTCA
ACCTGAGG GG	ACCTGAGC GGCTAGCTACAACGA AGCTCGAC	GICGAGCT G GCTCAGGT
AGAAAGAC GC	AGNAAGAC GGCTAGCTACAACGA CTGAGCAG	CIGCICAG G GICTIFICI
CGTGACAT GC	CGTGACAT GGCTAGCTACAACGA AAAAGAAA	TTTCTTT A ATGTCACG
TCCGTGAC GK	TCCGTGAC GGCTAGCTACAACGA ATAAAAGA	TCTTTTAT G GTCACGGA
GICTCCGT GO	GICTCCGT GGCTAGCTACAACGA GACATAAA	TITATGIC A ACGGAGAC
AACGTGGT G	AACGTGGT GGCTAGCTACAACGA CTCCGTGA	TCACGGAG A ACCACGIT
TGAAACGT G	TGAAACGT GGCTAGCTACAACGA GGTCTCCG	CGGAGACC A ACGTITCA
TTTGAAAC G	TITGAAAC GGCTAGCTACAACGA GTGGTCTC	GAGACCAC G GITTCAAA

1767	GAGCCTGT GGCTAGCTACAACGA TCTTTTGA	TCARAGG A ACAGGCTC
1771	AAAAAAAC GGCTAGCTACAACGA CTGTTCTT	AAGAACAG G GCTCTTTT
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1782	CTTCGGGT GGCTAGCTACGA AGAMANA	Demonstration of the second
1791	CCAGACAC GGCTAGCTACAACGA TCTTCCGG	COORDINATE OF THE PROPERTY OF
1793	CTCCAGAC GGCTAGCTACAACGA ACTCTTCC	GGAAGAGT G GTCTGGAG
1800	CAACITIGG GGCTAGCTACAAGGA TCCAGACA	TGTCTGGA G GCAAGTTG
1804	TITGCAAC GGCTAGCTACAAGGA TIGCTCCA	TGGAGCAA G GTTGCAAA
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1825	AGTGCTGT GGCTAGCTACAACGA CTGATTCC	GGAATCAG A ACAGCACT
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1858	CITCCGAC GGCTAGCTACAACGA AGCTCCCG	CGGGAGCT G GTCGGAAG
1865	ACCTCTGC GGCTAGCTACGA TTCCGACA	TGTCGGAA G GCAGAGGT
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1903	ACGICAGO GGCTAGCTACAACGA AGGGCGGG	CCCGCCCT G GCTGACGT
1907	CTGGACGT GGCTAGCTACAACGA CAGCAGGG	CCCTGCTG A ACGTCCAG
1909	GTCTGGAC GGCTAGCTACAACGA GTCAGCAG	CIGCIGAC G GICCAGAC

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1915	AGCGGAGT GGCTAGCTACAACGA CIGGACGI	MCG1CCGC a conscious
1920	GATGAAGC GGCTAGCTACAACGA GGAGTCTG	CAGACTUC G GOLLUATO
1925	TTGGGGAT GGCTAGCTACAACGA GAAGCGGA	TCCGCTTC A ATCCCCAA
1933	CGTCAGGC GGCTAGCTACAACGA TTGGGGAT	ATCCCCAA G GCCTGACG
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1942	GCCGCAGC GGCTAGCTACAACGA CCGTCAGG	CCTGACGG G GCTGCGGC
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1948	CAATCGGC GGCTAGCTACAACGA CGCAGCCC	GGGCTGCG G GCCGATTG
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1959	GICCATGI GGCTAGCTACAACGA TCACAAIC	GATTGTGA A ACATGGAC
1961	TAGTCCAT GGCTAGCTACAACGA GTTCACAA	TIGIGAAC A AIGGACTA
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1979	GITCTGGC GGCTAGCTACAACGA TCCCACGA .	TCGTGGGA G GCCAGAAC
1985	CGGAACGT GGCTAGCTACAACGA TCTGGCTC	GAGCCAGA A ACCITCCG
1987	TGCGGAAC GGCTAGCTACAACGA GTTCTGGC	GCCAGAAC G GTTCCGCA
1992	TICTCIGC GGCTAGCTACGA GGAACGIT	AACGIICC G GCAGAGAA
2006	CGCTCGGC GGCTAGCTACAACGA CCTCTTTT	AAAAGAGG G GCCGAGCG
2011	TGAGACGC GGCTAGCTACAACGA TCGGCCCT	AGGGCCGA G GCGTCTCA
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2018	CTCGAGGT GGCTAGCTACGA GAGACGCT	AGCGTCTC A ACCTCGAG
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2000	COGCINGE GCCIACTACAACGA AGIIGAGC	GCTCAACT A ACGAGCGG
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2063	CGCCGCGC GGCIAGCIACAA CCCCCCC	CONCRETE OF CONCRE
2065	GGCGCCGC GGCTAGCTACGA GCCCGCTC	200000000000000000000000000000000000000
2068	CGGGGCGC GGCTAGCTACGA CGCGCCCG	20000000 0 0000000
2070	GCCGGGGC GGCTAGCTACAACGA GCCGCGCC	GGCGCGGC 6 GCCCCGGC
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2100	GTCCAGGC GGCTAGCTACAACGA CCAGCACA	TGTGCTGG G GCCTGGAC
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2137	CACGCAGC GGCTACTACGA ACGAAGGT	ACCITICGI G GCTGCGTG
2140	GCACACGC GGCTAGCTACAACGA AGCACGAA	Tregreer e ecenerac
2143	CCCCACAC GGCTAGCTACAACGA GCAGCACG	CGTGCTGC G GTGTGCGG
2144	GCCCCCAC GGCTACCTACGA ACGCAGCA	TGCTGCGT G GTGCGGGC
21.46	GGGCCCGC GGCTAGCTACAACGA ACACGCAG	CIGCGIGI G GCGGGCCC
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2157	CHACGGGT GGCTAGCTACAACGA CCTGGGCC	GGCCCAGG A ACCCGCCG
2161	CAGGGG GGCTAGCTACAACGA GGGTCCTG	CAGGACCC G GCCGCCTG
2010	COTOROGC GGCTAGCTACAACGA GGCGGGTC	GACCCGCC G GCCTGAGC
1017		

2170	AGTACAGC GGCTAGCTACAACGA TCAGGCGG	CCGCCTGA G GCTGTACT
2173	CAAAGTAC GGCTAGCTACAACGA AGCTCAGG	CCTGAGCT G GTACTITG
2175	GACAAAGT GGCTAGCTACAACGA ACAGCTCA	TGAGCTGT A ACTITIGIC
2180	ACCTIGAC GGCIAGCIACAACGA AAAGIACA	TGTACTIT G GTCAAGGI
2186	ACATCCAC GGCTAGCTACAACGA CTTGACAA	TIGICAAG G GIGGAIGI
2190	CGTCACAT GGCTAGCTACAACGA CCACCTTG	CAAGGIGG A AIGIGACG
2192	CCCGTCAC GGCTAGCTACAACGA ATCCACCT	AGGIGGAT G GIGACGGG
2195	GCGCCCGT GGCTAGCTACAACGA CACATCCA	TGGATGTG A ACGGGCGC
2199	GTACGCGC GGCTAGCTACAACGA CCGTCACA	TGTGACGG G GCGCGTAC
2201	TCGTACGC GGCTAGTACAACGA GCCCGTCA	TGACGGGC G GCGTACGA
2203	TGTCGTAC GGCTAGCTACAACGA GCGCCCGT	ACGGCCC G GTACGACA
2205	GGIGICGI GGCIAGCIACAACGA ACGCGCCC	GGGCGCGT A ACGACACC
2208	GATGGTGT GGCTAGCTACAACGA CGTACGCG	CGCGTACG A ACACCATC
2210	GGGATGGT GGCTAGCTACGA GTCGTACG	CGTACGAC A ACCATECE
2213	TGGGGGAT GGCTACTACAACGA GGTGTCGT	ACGACACC A ATCCCCCA
2223	GAGCCTGT GGCTAGCTACGA CCTGGGGG	CCCCCAGG A ACAGGCTC
2227	CCGTGAGC GGCTAGCTACGA CTGTCCTG	CAGGACAG G GCTCACGG
2231	ACCTCCGT GGCTAGCTACAACGA GAGCCTGT	ACAGGCTC A ACGGAGGT
2237	GCGATGAC GGCTAGCTACAACGA CTCCGTGA	TCACGGAG G GTCATCGC
2240	CTGGCGAT GGCTAGCTACGA GACCTCCG	CGGAGGTC A ATCGCCAG
2243	ATGCTGGC GGCTAGCTACAACGA GATGACCT	AGGICAIC G GCCAGCAI
2247	GATGATGC GGCTAGCTACAACGA TGGCGATG	CATCGCCA G GCATCATC
2249	TIGATGAT GGCTAGCTACAACGA GCIGGCGA	TCGCCAGC A ATCATCAA
2252	GGTTTGAT GGCTAGCTACAACGA GATGCTGG	CCAGCATC A ATCAAACC
2257	TCTGGGGT GGCTAGCTACAACGA TTGATGAT	ATCATCAA A ACCCCAGA
2265	GTACGIGT GGCTAGCTACAACGA TCTGGGGT	ACCCOAGA A ACACGIAC
2267	CAGTACGT GGCTAGCTACAACGA GTTCTGGG	CCCAGAAC A ACGTACTG
2269	CGCAGIAC GGCTAGCIACAACGA GIGITCIG	CAGAACAC G GTACTGCG
2271	CACGCAGT GGCTAGCTACGACGA ACGTGTTC	GAACACGT A ACTGCGTG
2274	ACGCACGC GGCTAGCTACAACGA AGTACGTG	CACGTACT G GCGTGCGT
2276	CGACGCAC GGCTAGCTACAACGA GCAGTACG	CGIACTÓC G GIGCGICG

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2278	ACCGACGC GGCTAGCTACAACGA ACGCAGTA	TACTGCGT & GCGTCGGT
2280	ATACCGAC GGCTAGTACAACGA GCACGCAG	CTGCGTGE G GTCGGTAI
2284	CGGCATAC GGCTAGCTACAACGA CGACGCAC	GTGCGTCG G GTATGCCG
228K	CACGGCAT GGCTAGCTACAACGA ACCGACGC	GCGTCGGT A ATGCCGTG
8000	ACCACGGC GGCTAGCTACAACGA ATACCGAC	GTCGGTAT G GCCGTGGT
2201	TOGACCAC GGCTAGCTACAACGA GGCATACC	GGTATGCC G GTGGTCCA
2204	TICTISGAC GGCTAGCTACAACGA CACGGCAT	ATGCCGTG G GTCCAGAA
2303	TEGGCGGC GGCTAGCTACAACGA CTTCTGGA	TCCAGAAG G GCCGCCCA
2306	CCATGGGC GGCTAGCTACAACGA GGCCTTCT	AGAAGGCC G GCCCATGG
2310	GTGCCCAT GGCTAGCTACAACGA GGGCGCC	GGCCGCCC A ATGGGCAC
2314	GGACGTGC GGCTAGCTACGA CCATGGGC	GCCCATGG G GCACGTCC
2316	GCGGACGT GGCTAGCTACAACGA GCCCATGG	CCATGGGC A ACGTCCGC
2318	TIGGGGAC GGCTAGCTACAACGA GIGCCCAI	ATGGGCAC G GTCCGCAA
2322	GGCCTTGC GGCTAGCTACAACGA GGACGTGC	GCACGTCC G GCAAGGCC
2227	TTGAAGGC GGCTAGCTACAACGA CTTGCGGA	TCCGCAAG G GCCTTCAA
2337	GACGIGGC GGCTAGCTACAACGA TCTTGAAG	CITCAAGA G GCCACGIC
2340	AGAGACGT GGCTAGCTACAACGA GGCTCTTG	CAAGAGCC A ACGICITCT
2000	CTAGAGAL GGCTAGCTACAACGA GTGGCTCT	AGAGCCAC G GTCTCTAC
25.52	CHOSTA COURT COURT ACAGGA AGAGACT	ACGUCTOT A ACCUTGAC
2340	ACCULTANT GOLTAGCTACAACGA CAAGGTAG	CTACCTTG A ACAGACCT
4667	CTGTCAGG CTGTCAGAGGA CTGTCAAG	CTTGACAG A ACCTCCAG
2356	TGTALGG GGCTAGCTACAACGA TGGAGGTC	GACCTCCA G GCCGTACA
8966	GCANGTAC GGCTAGCTACAACGA GGCTGGAG	CTCCAGCC G GTACATGC
02.50	TOGGATGT GGCTAGCTACAACGA ACGGCTGG	CCAGCCGT A ACATGCGA
22.50	TOTOGOAT GGCTAGCTACAACGA GTACGGCT	AGCCGTAC A ATGCGACA
2312	ACTIOTOGY GGGTAGCTACAACGA ATGTACGG	CCGTACAT G GCGACAGT
23/4	ACTOR COURSE CONTROL OF CONTROLS	TACATGCG A ACAGTICG
2377	CONTROL GOOD OF THE PROPERTY O	ATGCGACA G GTTCGTGG
2380	CCACGAAC GGCIAGCIACAACCA 101CCCC	GACAGTTC G GTGGCTCA
2384	TGAGCCAC GGCIAGCIACAACGA GAACISIC	AGTITION G GCTCACCT
2387	AGGIGAGC GGCTAGCTACAACGA CACGAACI	Secretary a promoted
2391	CTGCAGGT GGCTAGCTACAACGA GAGCCACG	COLORGE A ACCIONA

	COMPOUNDED ACCOUNTS ACCOUNTS	GCTCACCT G GCAGGAGA
2395	TCTCCTGC GGCIAGCIACAACGA AGGIGAGC	CONCROS & CACADOM
2402	GGGCTGGT GGCTAGCTACAACGA CTCCTGCA	Tochrong a promoced
2406	CAGCGGGC GGCTAGCTACAACGA TGGTCTCC	GGAGACCA G GCCCGCTG
2410	CCCTCAGC GGCTAGCTACGA GGGCTGGT	ACCAGCCC G GCTGAGGG
2418	GACGGCAT GGCTAGCTACAACGA CCCTCAGC	GCTGAGGG A ATGCCGTC
2420	ACGACGGC GGCTAGCTACAACGA ATCCCTCA	TGAGGGAT G GCCGTCGT
2423	ATGACGAC GGCTAGCTACAACGA GGCATCCC	GGGATGCC G GTCGTCAT
2426	TCGATGAC GGCTAGCTACAACGA GACGGCAT	ATGCCGTC G GTCATCGA
2429	TGCTCGAT GGCTAGCTACAACGA GACGACGG	CCGTCGTC A ATCGAGCA
2434	AGCTCTGC GGCTAGCTACGA TCGATGAC	GICATCGA G GCAGAGCT
2439	GGAGGAGC GGCTAGCTACAACGA TCTGCTCG	CGAGCAGA G GCTCCTCC
2451	GGCCTCAT GGCTAGCTACAACGA TCAGGGAG	CTCCCTGA A ATGAGGCC
2456	CIGCIGGC GGCTAGCTACAACGA CICATICA	TGAATGAG G GCCAGCAG
2460	GCCACTGC GGCTAGCTACAACGA TGGCCTCA	TGAGGCCA G GCAGTGGC
2463	GAGGCCAC GGCTAGTACAACGA TGCTGGCC	GGCCAGCA G GTGGCCTC
2466	GAAGAGGC GGCTAGCTACAACGA CACTGCTG	CAGCAGIG G GCCTCTIC
2475	GAAGACGT GGCTAGCTACAACGA CGAAGAGG	CCTCTTCG A ACGTCTTC
2477	AGGAAGAC GGCTAGCTACAACGA GTCGAAGA	TCTTCGAC G GTCTTCCT
2485	TGAAGCGT GGCTAGCTACAACGA AGGAAGAC	GTCTTCCT A ACGCTTCA
2487	CATGAAGC GGCTAGCTACAACGA GTAGGAAG	CTTCCTAC G GCTTCATG
2492	TGGCACAT GGCTAGCTACAACGA GAAGCGTA	TACGCTTC A ATGTGCCA
2494	GGTGGCAC GGCTAGCTACAACGA ATGAAGCG	CGCTTCAT G GTGCCACC
2496	GTGGTGGC GGCTACTACGACGA ACATGAAG	CTTCATGT G GCCACCAC
2499	GGCGTGGT GGCTAGCTACAACGA GGCACATG	CATGTCC A ACCACGCC
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2511	CCTGATGC GGCTAGCTACAACGA GCACGGCG	CGCCGTGC G GCATCAGG
2513	CCCCTGAT GGCTAGCTACAACGA GCGCACGG	CCGTGCGC A ATCAGGGG
2520	GGACTIGC GGCTAGCTACAACGA CCCTGAIG	CATCAGGG G GCAAGTCC

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2531 2536 2538 2546 2546	CIGGACGI	CIRGRACGI GCCIAGCIACAACGA AGGACIIG	ACT 16	CAMBILLI A ACCITOCO
2536 2538 2546 2551	CACTGGAC	CACTGGAC GGCTAGCTACAACGA GTAGGACT	GGACT	AGECCEAC G GECCAGEG
2538 2546 2551	CCTGGCAC	CCTGGCAC GGCTAGCTACAACGA TGGACGTA	ACGTA	TACGTCCA G GIGCCAGG
2546	CCCCTGGC	CCCTGGC GGCTAGCTACAACGA ACTGGACG	GGACG	CGTCCAGT G GCCAGGGG
2551	TGCGGGAT	TGCGGGAT GGCTAGCTACAACGA CCCCTGGC	creec	GCCAGGGG A ATCCCGCA
	AGCCCTGC	AGCCCTGC GGCTAGCTACAACGA GGGATCCC	ATCCC	GGGATCCC G GCAGGGCT
2556	GATGGAGC	GATGGAGC GGCTAGCTACAACGA CCTGCGGG	90000	CCCGCAGG G GCTCCATC
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2572	AGAGCAGC	AGAGCAGC GGCTAGCTACAACGA GTGGAGAG	GAGAG	CICICCAC G GCTGCTCT
2575	TGCAGAGC	TGCAGAGC GGCTAGCTACAACGA AGCGTGGA	GTGGA	TCCACGCT G GCTCTGCA
2580	CAGGCTGC	CAGGCTGC GGCTAGCTACAACGA AGAGCAGC	AGCAGC	GCTGCTCT G GCAGCCTG
2583	GCACAGGC	GCACAGGC GGCTAGCTACAACGA TGCAGAGC	CAGAGC	GCTCTGCA G GCCTGTGC
2587	CGTAGCAC	CGTAGCAC GGCTAGCTACAACGA AGGCTGCA	SCTGCA	TGCAGCCT G GTGCTACG
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2592	GTCGCCGT	GTCGCCGT GGCTAGCTACAACGA AGCACAGG	CACAGG	CCTGTGCT A ACGGCGAC
2595	CATGTCGC	CATGICGC GGCTAGCTACAACGA CGTAGCAC	TAGCAC	GTGCTACG G GCGACATG
2598	CTCCATGT	CTCCATGT GGCTAGCTACAACGA CGCCGTAG	CCGTAG	CTACGGCG A ACATGGAG
2600	TTCTCCAT	TTCTCCAT GGCTAGCTACAACGA GTCGCCGT	CGCCGT	ACGCCGAC A ATGCAGAA
2607	CAGCTTGT	CAGCTIGI GGCTAGCTACAACGA TCTCCAIG	TCCATG	CATGGAGA A ACAAGCTG
2611	CAAACAGC	CAAACAGC GGCTAGCTACAACGA TIGITCIC	GTTCTC	GAGAACAA G GCTG1T1G
2614	CCGCAAAC	CCGCAAAC GGCTAGCTACAACGA AGCTTGTT	CTTGTT	AACAAGCT G GTTTGCGG
2618	ATCCCCGC	ATCCCCGC GGCTAGCTACAACGA AAACAGCT	ACAGCT	AGCTGTTT G GCGGGGAT
2624	CGCCGAAT	CGCCGAAT GGCTAGCTACAACGA CCCCGCAA	CCGCAA	TIGGGGG A AITCGGCG
2629	CGTCCCGC	CGTCCCGC GGCTAGCTACAACGA CGAATCCC	AATCCC	GGGATTCG G GCGGGACG
2634	CAGCCCGT	CAGCCCGT GGCTAGCTACGA CCCGCCGA	CGCCGA	TCGGCGGG A ACGGGCTG
2638	GGAGCAGC	GGAGCAGC GGCTAGCTACAACGA CCGTCCCG	GTCCCG	CGGGACGG G GCTGCTCC
2641	GCAGGAGC	GCAGGAGC GGCTAGCTACAACGA AGCCCGTC	CCCGTC	GACGGGCT G GCTCCTGC
2647	CCANACGC	CCAAACGC GGCTAGCTACAACGA AGGAGCAG	IGAGCAG	CIGCICCI G GCGIIIGG
2649	CACCAAAC	CACCAAAC GGCTAGCTACAACGA GCAGGAGC	AGGAGC	GCTCCTGC G GTTTGGTG

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TCATCCAC GGCIACCTACTACCA CCACCAAA	TITGGIGG A AIGAITIC
CAAGAAAT GGCTAGCTACAACGA CATCCACC	GGTGGATG A ATTTCTTG
TCACCAAC GGCTAGCTACAACGA AAGAAATC	GATTICIT G GITGGIGA
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TCTTCTAC GGCTAGCTACAACGA AGGGAAGT	ACTICCCT G GIAGAGA
GECCTOST GCCTAGCTACAACGA CTTCTACA	TGTAGAAG A ACGAGGCC
CCCAGGC GGCTAGCTACAACGA CTCGTCTT	AAGACGAG G GCCCTGGG

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2802	AGCCGTGC GGCTAGCTACAACGA CACCCAGG	CCTGGGTG G GCACGGCT
2804	AAAGCCGT GGCTAGCTACAACGA GCCACCCA	TGGGTGGC A ACGCCTTT
2807	ACAMANGE GGETAGETACAACGA CGTGCCAC	GIGGCACG G GCITITGT
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2847	CAGGCCGC GGCTAGCTACAACGA ACCAGGGG	CCCTGGT G GCGCCTG
2850	CAGCAGGC GGCTAGCTACAACGA CGCACCAG	creerece e eccreere
2854	CCAGCAGC GGCTAGCTACAACGA AGGCCGCA	TGCGGCCT G GCTGCTGG
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3006	AAACAGGC GGCTAGCTACGACGA TGTGACAC	GIGICACA G GCCTGTTF
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CAACATCT A ACAAGATC	TCTACAAG A ATCCTCCT	ATCCTCCT G GCTGCAGG	CTCCTGCT G GCAGGCGT	TGCTGCAG G GCGTACAG	CTGCAGGC G GTACAGGI	GCAGGCGT A ACAGGTTT	GCGTACAG G GTTTCACG	CAGGITTC A ACCCATGI	GGTTTCAC G GCATGTGT	TTTCACGC A ATGIGIGG	TCACGCAT G GIGIGCIG	ACGCATGT G GTGCTGCA	GCATGTGT G GCTGCAGC	TGTGTGCT G GCAGCTCC	GIGCIGCA G GCICCCAI	CAGCTCCC A ATTICATO	CCCATITC A ATCAGGAA	TITCATCA G GCAAGITI	ATCAGCAA G GITTGGAA	TIGGAAGA A ACCCCACA	AGAACCCC A ACATTIT	AACCCCAC A ATTITICC	TITITICI G GCGCGICA	TITCCIGC G GCGICAIC	TCCTGCGC G GTCATCTC	TGCGCGTC A ATCTCTGA	CATCTCTG A ACACGGCC	TCTCTGAC A ACGGCCTC	CTGACACG G GCCTCCCT	CTCCCTCT G GCTACTCC
TIG	AGA	GAT	GAG	GCA	cag	T0C	292	CTG	AACC	SAAA	STGA	CCT	ATGC	PACA	SCAC	scre	rece	SAAA	PGAT	CCAA	ITCI	CCTT	AAAA	GAAA	AGGA	cccA	GATC	GAGA	TCAG	GGAG
GATCTIGT GGCTAGCTACAACGA AGATGTTG	AGGAGGAT GGCTAGCTACAACGA CTTGTAGA	CCTGCAGC GGCTAGCTACAACGA AGGAGGAT	ACCCCTGC GGCTAGCTACAACGA AGCAGGAG	CTGTACGC GGCTAGCTACAACGA CTGCAGCA	ACCTGTAC GGCTAGCTACAACGA GCCTGCAG	AAACCTGT GGCTAGCTACAACGA ACGCCTGC	CGTGAAAC GGCTAGCTACAACGA CTGTACGC	ACATGCGT GGCTAGCTACAACGA GAAACCTG	ACACATGC GGCTAGCTACAACGA GTGAAACC	GCACACAT GGCTAGCTACAACGA GCGTGAAA	CAGCACAC GGCTAGCTACAACGA ATGCGTGA	TGCAGCAC GGCTAGCTACAACGA ACATGCGT	GCTGCAGC GGCTAGCTACAACGA ACACATGC	GGAGCTGC GGCTAGCTACAACGA AGCACACA	ATGGGAGC GGCTAGCTACAACGA TGCAGCAC	GATGAAAT GGCTAGCTACAACGA GGGAGCTG	TTGCTGAT GGCTAGCTACAACGA GAAATGGG	AAACTIGC GGCTAGCTACAACGA TGATGAAA	TTCCAAAC GGCTAGCTACAACGA TTGCTGAT	TGTGGGGT GGCTAGCTACAACGA TCTTCCAA	AAAAATGT GGCTAGCTACAACGA GGGGTTCT	GGAAAAT GGCTAGCTACAACGA GTGGGGTT	TGACGCGC GGCTAGCTACAACGA AGGAAAAA	GATGACGC GGCTAGCTACAACGA GCAGGAAA	GAGATGAC GGCTAGCTACAACGA GCGCAGGA	TCAGAGAT GGCTAGCTACAACGA GACGCGCA	GGCCGTGT GGCTAGCTACAACGA CAGAGATG	GAGGCCGT GCCTACCTACGACGA GTCAGAGA	AGGGAGGC GCCTAGCTACAACGA CGTGTCAG	GGAGTAGC GGCTAGCTACAACGA AGAGGGAG
GATCTIGE	AGGAGGAT	CCTGCAGC	ACGCCTGC	CTGTACGC	ACCTGTAC	AAACCTGT	CGTGAAAC	ACATGCGT	ACACATGC	GCACACAT	CAGCACAC	TGCAGCAC	GCTGCAGC	GGAGCTGC	ATGGGAGC	GATGAAAT	TTGCTGAT	AAACTTGC	TTCCAAAC	TGTGGGGT	AAAAATGT	GGRAAAAT	TGACGCGC	GATGACGC	GAGATGAC	TCAGAGAT	GGCCGTGT	GAGGCCGT	AGGGAGGC	GGAGTAGC

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CCTCTGCT A ACTCCATC	GCTACTCC A ATCCTGAA	TCCTGAAA G GCCAAGAA	AGCCAAGA A ACGCAGGG	CCAAGAAC G GCAGGGAT	ACGCAGGG A ATGTCGCT	GCAGGGAT G GTCGCTGG	GGGATGIC G GCTGGGGG	. CGCTGGGG G GCCAAGGG	GGCCAAGG G GCGCCGCC	CCAAGGGC G GCCGCCGG	AGGGCGCC G GCCGGCCC	CGCCGCCG G GCCCTCTG	GGCCCTCT G GCCCTCCG	CCTCCGAG G GCCGTGCA	CCGAGGCC G GTGCAGTG	GAGGCCGT G GCAGTGGC	GCCGIGCA G GTGGCTGT	GTGCAGTG G GCTGTGCC	CAGIGGCI G GIGCCACC	GIGGCTGI G GCCACCAA	GCTGTGCC A ACCAAGCA	GCCACCAA G GCATTCCT	CACCAAGC A ATTCCTGC	GCATTCCT G GCTCAAGC	CTGCTCAA G GCTGACTC	TCAAGCTG A ACTCGACA	CTGACTCG A ACACCGTG	GACTICGAC A ACCGIGIC	TCGACACC G GIGICACC	GACACCGT G GTCACCTA
GATGGAGT GGCTAGCTACAACGA AGCAGAGG	TICAGGAI GGCTAGCIACAACGA GGAGIAGC	TICTIGGC GGCTAGCTACGA TITCAGGA	CCCTGCGT GGCTAGCTACAACGA TCTTGGCT	ATCCCTGC GGCTAGCTACAACGA GTTCTTGG	AGCGACAT GGCTAGCTACAACGA CCCTGCGT	CCAGCGAC GGCTAGCTACGA ATCCCTGC	CCCCCAGC GGCTAGCTACAACGA GACATCCC	CCCTTGGC GGCTAGCTACAACGA CCCCAGCG	GGCGGCGC GGCTAGCTACGA CCTTGGCC	CCGCCGGC GGCTAGCTACAACGA GCCCTTGG	GGGCCGGC GGCTAGCTACAACGA GGCGCCCT	CAGAGGGC GGCTAGCTACAACGA CGGCGGCG	CGGAGGGC GGCTAGCTACAACGA AGAGGGCC	TGCACGGC GGCTAGCTACAACGA CTCGGAGG	CACTGCAC GGCTAGCTACAACGA GGCCTCGG	GCCACTGC GGCTAGCTACAACGA ACGGCCTC	ACAGCCAC GGCTAGCTACAACGA TGCACGGC	GGCACAGC GGCTAGCTACAACGA CACTGCAC	GGTGGCAC GGCTAGCTACAACGA AGCCACTG	TTGGTGGC GGCTAGCTACAACGA ACAGCCAC	TGCTTGGT GGCTAGCTACAACGA GGCACAGC	AGGAATGC GGCTAGCTACAACGA TTGGTGGC	GCAGGAAT GGCTAGCTACAACGA GCTTGGTG	GCTTGAGC GGCTAGCTACAACGA AGGAATGC	GAGTCAGC GGCTAGCTACAACGA TTGAGCAG	TGTCGAGT GGCTAGCTACAACGA CAGCTTGA	CACGGTGT GGCTAGCTACAACGA CGAGTCAG	GACACGGT GGCTAGCTACAACGA GTCGAGTC	GGTGACAC GGCTACTACAACGA GGTGTCGA	TAGGIGAC GGCTACTACAACGA ACGGIGIC
3186	3191	3200	3207	3209	3215	3217	3220	3227	3234	3236	3239	3243	3250	3260	3263	3265	3268	3271	3274	3276	3279	3284	3286	3292	3298	3302	3307	3309	3312	3314

3317	ACGTAGGT GGCTAGCTACAACGA GACACGGT	ACCGTGTC A ACCTACGT
3321	TGGCACGT GGCTAGCTACAACGA AGGTGACA	TGTCACCT A ACGTGCCA
3323	AGTGGCAC GGCTAGCTACAACGA GTAGGTGA	TCACCTAC G GTGCCACT
3325	GGAGTGGC GGCTAGCTACAACGA ACGTAGGT	ACCTACGT G GCCACTCC
3328	CCAGGAGT GGCTAGCTACAACGA GGCACGTA	TACGIGCC A ACTCCIGG
3337	TGAGTGAC GGCTAGCTACAACGA CCCAGGAG	CTCCTGGG G GTCACTCA
3340	TCCTGAGT GGCTAGCTACAACGA GACCCCAG	CTGGGGTC A ACTCAGGA
3347	TGGGCTGT GGCTAGCTACGA CCTGAGTG	CACTCAGG A ACAGCCCA
3350	GTCTGGGC GGCTAGCTACAACGA TGTCCTGA	TCAGGACA G GCCCAGAC
3356	AGCTGCGT GGCTAGCTACAACGA CTGGGCTG	CAGCCCAG A ACGCAGCT
3358	TCAGCTGC GGCTAGCTACAACGA GTCTGGGC	GCCCAGAC G GCAGCTGA
3361	GACTCAGC GGCTAGCTACAACGA TGCGTCTG	CAGACGCA G GCTGAGTC
3366	CTTCCGAC GGCTAGCTACAACGA TCAGCTGC	GCAGCTGA G GTCGGAAG
3373	CCGGGAGC GGCTAGCTACAACGA TTCCGACT	AGTOGGAA G GCTCCCGG
3383	AGCGTCGT GGCTAGCTACAACGA CCCCGGGA	TCCCGGGG A ACGACGCT
3386	GTCAGCGT GGCTAGCTACAACGA CGTCCCCG	CGGGGACG A ACGCTGAC
3388	CAGTCAGC GGCTAGCTACAACGA GTCGTCCC	GGGACGAC G GCTGACTG
3392	AGGGCAGT GGCTAGCTACAACGA CAGCGTCG	CGACGCTG A ACTGCCCT
3395	TCCAGGGC GGCTAGCTACAACGA AGTCAGCG	CGCTGACT G GCCCTGGA
3404	GCTGCGGC GGCTAGCTACAACGA CTCCAGGG	CCCTGGAG G GCCGCAGC
3407	TIGGCIGC GGCIAGCTACAAGGA GGCCTCCA	TGGAGGCC G GCAGCCAA
3410	GGGTTGGC GGCTACTACAACGA TGCGGCCT	AGGCCGCA G GCCAACCC
3414	TGCCGGGT GGCTAGCTACAACGA TGGCTGCG	CGCAGCCA A ACCCGGCA
3419	GGCAGTGC GGCTAGTACAACGA CGGGTTGG	CCAACCCG G GCACTGCC
3421	AGGCAGT GGCTAGCTACAACGA GCCGGGTT	AACCCGGC A ACTGCCCT
3424	CTGAGGGC GGCTAGCTACGA AGTGCCGG	CCGGCACT G GCCCTCAG
3432	CITGAAGT GGCTAGCTACAACGA CTGAGGGC	GCCCTCAG A ACTICAAG
3440	AGGATGGT GGCTAGCTACAACGA CTTGAAGT	ACTICAAG A ACCATCCT
3443	TCCAGGAT GGCTAGCTACAACGA GGTCTTGA	TCAAGACC A ATCCTGGA
3450	CCATCAGT GGCTAGCTACAACGA CCAGGATG	CATCCTGG A ACTGATGG
3454	GIGGCCAT GGCTAGCTACAACGA CAGTCCAG	CTGGACTG A ATGGCCAC

3467	CERCTICE GOCTAGCTACAACGA CATCAGTC	GACTGATG G GCCACCCG
1000	KULLECOUC KOCKECKECO TOO TOO TOO	TRATIGACE A ACCEGECE
3460	GGGCGGGT GGCTAGATCARCGA GGCCATCA	0.0000000000000000000000000000000000000
3464	CTGTGGGC GGCTAGCTACAACGA GGGTGGCC	GGCCACCC G GCCCACAG
3468	CTGGCTGT GGCTAGCTACAACGA GGGCGGGT	ACCCGCCC A ACAGCCAG
3471	GGCCTGGC GGCTAGCTACAACGA TGTGGGCG	CGCCCACA G GCCAGGCC
3476	CTCTCGGC GGCTAGCTACAACGA CTGGCTGT	ACAGCCAG G GCCGAGAG
3483	GTGTCTGC GGCTAGCTACAACGA TCTCGGCC	GGCCGAGA G GCAGACAC
3487	GCTGGTGT GGCTAGCTACAACGA CTGCTCTC	GAGAGCAG A ACACCAGC
3489	CTGCTGGT GGCTAGCTACAACGA GTCTGCTC	GAGCAGAC A ACCAGCAG
3493	AGGGCTGC GGCTAGCTACAACGA TGGTGTCT	AGACACCA G GCAGCCCT
3496	GACAGGGC GGCTAGCTACAACGA TGCTGGTG	CACCAGCA G GCCCTGTC
3501	GGCGTGAC GGCTAGCTACAACGA AGGGCTGC	GCAGCCCT G GTCACGCC
3504	CCCGGCGT GGCTAGCTACAACGA GACAGGGC	GCCCTGTC A ACGCCGGG
3506	AGCCCGGC GGCTAGCTACAACGA GTGACAGG	CCTGTCAC G GCCGGGCT
3511	CGTAGAGC GGCTAGCTACAACGA CCGGCGTG	CACGCCGG G GCTCTACG
3516	TGGGACGT GGCTAGCTACAACGA AGAGCCCG	CGGGCTCT A ACGTCCCA
3518	CCTGGGAC GGCTAGCTACAACGA GTAGAGCC	GGCTCTAC G GTCCCAGG
3535	TGGGCCGC GGCTAGCTACAACGA CCCTCCCT	AGGGAGGG G GCGGCCCA
3538	GTGTGGGC GGCTAGCTACAACGA CGCCCCTC	GAGGGCG G GCCCACAC
3542	CTGGGTGT GGCTAGCTACGA GGGCCGCC	GGCGGCCC A ACACCCAG
3544	GCCTGGGT GGCTACTACGA GTGGGCCG	CGGCCCAC A ACCCAGGC
3550	GIGCGGGC GGCTAGCTACAACGA CIGGGIGT	ACACCCAG G GCCCGCAC
3554	AGCGGTGC GGCTAGCTACGA GGGCCTGG	CCAGGCCC G GCACCGCT
3556	CCAGCGGT GGCTAGCTACAACGA GCGGGCCT	AGGCCCGC A ACCGCTGG
3559	CTCCCAGC GGCTAGCTACGA GGTGCGGG	CCCGCACC G GCTGGGAG
3566	CCTCAGAC GGCTACCTACAACGA TCCCAGCG	CGCTGGGA G GTCTGAGG
3573	ACTCAGGC GGCTAGCTACAACGA CTCAGACT	AGTCTGAG G GCCTGAGT
3579	ACACTCAC GGCTAGCTACAACGA TCAGGCCT	AGGCCTGA G GTGAGTGT
3583	CCAAACAC GGCTAGCTACAACGA TCACTCAG	CTGAGTGA G GTGTTTGG
3585	GGCCAAAC GGCTAGCTACAACGA ACTCACTC	GAGTGAGT G GTTTGGCC
3590	GCCTCGGC GGCTAGCTACAACGA CAAACACT	AGIGITIG G GCCGAGGC

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TOGCCGAG G GCCTGCAT	CGAGGCCT G GCATGTCC	AGGCCTGC A ATGTCCGG	SCCTSCAT G STCCGGCT	CATGUCCS G GCTSAAGG	GGCTGAAG G GCTGAGTG	AAGGCTGA G GTGTCCGG	SGCIGAGT S GTCCSGCT	AGTGTCCG G GCTGAGGC	CGGCTGAG G GCCTGAGC	AGGCCTGA G GCGAGTGT	CTGAGCGA G GTGTCCAG	GAGCGAGT G GTCCAGCC	AGTGTCCA G GCCAAGGG	AGCCAAGG G GCTGAGTG	AGGGCTGA G GTGTCCAG	GGCTGAGT G GTCCAGCA	AGTGTCCA G GCACACCT	TGTCCAGC A ACACCTGC	TCCAGCAC A ACCTGCCG	GCACACCT G GCCGTCTT	CACCTGCC G GTCTTCAC	CCGICITIC A ACTICCCC	ACTICCCC A ACAGGCIG	CCCCACAG G GCTGGCGC	ACAGGCTG G GCGCTCGG	AGGCTGGC G GCTCGGCT	SGCGCTCG G GCTCCACC	TURGUTCE A ACCCCAGG	ACCCARGE G GCCAGCTT	Thinks o constant	CAGGGCCA & GCIIIICC
CCA	TCG	ICCI	2990	ATG	2250	CTT	AGCC.	CACT	3008	SCCT	rcag	SCTC	CACT	3GCT	CCCT	AGCC	CACT	GACA	TGGA	GTGC	GGTG	ACGG	AAGT	3636	CTGT	GCCT	COCC	2000	accom.	19999	ccre
ATIGCAGGC GGCTAGCTACAACGA CTCGGCCA	GGACATGC GGCTAGCTACAACGA AGGCCTCG	CCGGACAT SGCTAGCTACAACGA GCAGGCCT	AGCCGGAC GGCTAGCTACAACGA ATGCAGGC	CCTTCAGC GGCTAGCTACAACGA CGGACATG	CACTCAGC GGCTAGCTACAACGA CTTCAGCC	CCGGACAC GGCTAGCTACAACGA TCAGCCTT	AGCCGGAC GGCTAGCTACAACGA ACTCAGCC	GCCTCAGC GGCTAGCTACAACGA CGGACACT	GCTCAGGC GGCTAGCTACAACGA CTCAGCCG	ACACTOGO GGCTAGCTACAACGA TCAGGCCT	CTGGACAC GGCTAGCTACAACGA TCGCTCAG	GGCTGGAC GGCTAGCTACAACGA ACTCGCTC	CCCTTGGC GGCTAGCTACAACGA TGGACACT	CACTCAGE GGCTAGCTACAACGA CCTTGGCT	CTRGACAC GGCTAGCTACAACGA TCAGCCCT	TOCTOGE GGCTAGCTACAACGA ACTCAGCC	AGGEGGG GGCTAGGAGGA TGGACACT	CONTOUR COURSE TA CARACTA GCTGGACA	COCCAGE COCTAGETACTACGA GIGCTGGA	ANGAGES COCTAGETACTACGA AGGTGTGC	GTGBAGAC GGCTAGCTACAACGA GGCAGGTG	GGGGAAGT GGCTAGCTACAACGA GAAGACGG	TOWNER GEOTTACTACTACGA GGGGAAGT	GCGCCAGC GGCTAGGTACAACGA CTGTGGGG	CCGAGCTIC GGCTAGCTACAACGA CAGCCTGT	NOCCEASE GGCTAGCTACAACGA GCCAGCCT	CONCORD COMMON ACTION OF THE COMMON C	GGCIAGCIACAACGA GGAG	CCTGGGGT GGCTAGCTACAACGA GGAGCCGA	AAGCTGGC GGCTAGCTACAACGA CCTGGGGI	GSAAAAGC GGCTAGCTACAACGA TGGCCCTG
ATGCAGGC	GGACATGC	CCGGACAT	AGCCGGAC (CCTTCAGC	CACTCAGC	CCGGACAC	AGCCGGAC	GCCTCAGC	GCTCAGGC	ACACTOGO	CTGGACAC	GGCTGGAC	CCCTTGGC	CACTCAGC	CTGGACAC	JASOUTOUT.	Concrete	20101000	COCCAGG	Jagarday	GEGRAGAC	GGGGAAGT	TEMOUSTRO	GCGCCAGC	COGAGOGO	COCCORGO	20000000	GGTGGAGC	CCTGGGGT	AAGCTGGC	GGAAAAGC
3596	3600	3602	3604	3609	3616	3621	3623	3628	3634	3640	1644	3646	3651	3658	3663	200	2000	0/05	3672	2000	26.00	7687	9000	0090	3703	2000	00/0	3710	3715	3723	3727

2727	CTCCTGGT GGCTAGCTACAACGA GAGGAAAA	TTTTCTC A ACCAGGAG	
3744	AGCCGGGC GGCTAGCTACAACGA TCCTGGTG	CACCAGGA G GCCCGGCT	
3749	GUGGAAGC GGCTAGCTACAACGA CGGGCTCC	GGAGCCCG G GCTTCCAC	
3755	TOGGGAGT GGCTAGCTACAACGA GGAAGCCG	CGGCTTCC A ACTCCCCA	
3762	TCCTATGT GGCTAGCTACAACGA GGGGAGTG	CACTCCCC A ACATAGGA	
3764	ATTCCTAT GGCTAGCTACAACGA GTGGGGAG	CTCCCCAC A ATAGGAAT	
3770	TGGACTAT GGCTAGCTACAACGA TCCTATGT	ACATAGGA A ATAGTCCA	
3773	GGATGGAC GGCTAGCTACAACGA TATTCCTA	TAGGAATA G GTCCATCC	
3777	CTGGGGAT GGCTAGCTACAACGA GGACTATT	AATAGTCC A ATCCCCAG	
3785	TGGCGAAT GGCTAGCTACAACGA CTGGGGGAT	ATCCCCAG A ATTCGCCA	
3789	ACAATGGC GGCTAGCTACAACGA GAATCTGG	CCAGATTC G GCCATTGT	
3792	TGAACAAT GGCTAGCTACAACGA GGCGAATC	GATTCGCC A AITGITCA	
3795	GGGTGAAC GGCTAGCTACAACGA AATGGCGA	TCGCCATT G GITCACCC	
3799	CGAGGGGT GGCTAGCTACAACGA GAACAATG	CATTGITC A ACCCCTCG	
3806	GGCAGGGC GGCTAGCTACAACGA GAGGGGTG	CACCCCTC G GCCCTGCC	
1811	AGGAGGG GGCTAGCTACAACGA AGGGCGAG	CICGCCCI G GCCCICCI	
3821	TEGRAGEC GECTACTACAACGA AAAGGAGG	CCTCCTTT G GCCTTCCA	
3828	GTGGGGGT GGCTAGCTACAACGA GGAAGGCA	TGCCTTCC A ACCCCAC	
3834	TGGATGGT GGCTAGCTACAACGA GG3GGTGG	CCACCCC A ACCATCCA	
2837	ACCTGGAT GGCTAGCTACAACGA GGTGGGGG	CCCCCACC A ATCCAGGT	
3843	GTCTCCAC GGCTAGCTACAACGA CTGGATGG	CCATCCAG G GTGGAGAC	
3849	CTCAGGGT GGCTAGCTACAACGA CTCCACCT	AGGTGGAG A ACCCTGAG	
3861	CCCAGGGT GGCTAGCTACAACGA CCTTCTCA	TGAGAAGG A ACCCTGGG	
3870	CCCAGAGC GGCTAGCTACAACGA TCCCAGGG	CCCTGGGA G GCTCTGGG	
2070	CTCCAAAT GGCTAGCTACAACGA TCCCAGAG	CTCTGGGA A ATTTGGAG	
2006	TIGGICE GGCTAGCTACAACGA TCCAAATT	AATTIGGA G GIGACCAA	
2000	CCTTTTGGT GGCTAGCTACAACGA CACTCCAA	TTGGAGTG A ACCAAAGG	
2896	GGGCACAC GGCTAGCTACAACGA CITTGGTC	GACCAAAG G GTGTGCCC	
3898	CAGGGCAC GGCTAGCTACAACGA ACCTTTGG	CCAAAGGT G GTGCCCTG	
3900	TACAGGG GGCTAGCTACAACGA ACACCTTT	AAAGGTGT G GCCCTGTA	
3005	CTGTGTAC GGCTAGCTACAACGA AGGGCACA	TGTGCCCT G GTACACAG	
2000	CICION CONTRACTOR		

Table 16

3907	GCCTGTGT GGCTAGCTACAACGA ACAGGGCA	TGCCCTGT A ACACAGGC
3909	TCGCCTGT GGCTAGCTACAACGA GTACAGGG	CCCTGTAC A ACAGGCGA
3913	GTCCTCGC GGCTAGCTACAACGA CTGTGTAC	GTACACAG G GOGAGGAC
3919	TGCAGGGT GGCTAGCTACAACGA CCTCGCCT	AGGCGAGG A ACCCTGCA
3924	CCAGGTGC GGCTAGAACGA AGGGTCCT	AGGACCCT G GCACCTGG
3926	ATCCAGGT GGCTAGCACGA GCAGGGTC	GACCCTGC A ACCTGGAT
3932	ACCCCAT GGCTAGCTACAACGA CCAGGTGC	GCACCTGG A ATGGGGGT
3938	ACAGGGAC GGCTAGCTACAACGA CCCCATCC	GGATGGGG G GTCCCTGT
3944	TGACCCAC GGCTAGCTACAACGA AGGGACCC	GOGTCCCT G GTGGGTCA
3948	AATTTGAC GGCTAGCTACAACGA CCACAGGG	CCCTGTGG G GTCAAATT
3953	CCCCCAAT GGCTAGCTACAACGA TTGACCCA	TGGGTCAA ATTGGGGG
3964	CACAGCAC GGCTAGCTACAACGA CTCCCCCC	GGGGGGAG G GTGCTGTG
3966	CCCACAGC GGCTAGCTACAACGA ACCTCCCC	GGGGAGGT G GCTGTGGG
3969	ACTCCCAC GGCTAGCTACGA AGCACCTC	GAGGTGCT G GTGGGAGT
3975	TATTITAC GGCIAGCIACAACGA TCCCACAG	CTGTGGGA G GTAAAATA
3980	TTCAGTAT GGCTAGCTACAACGA TTTACTCC	GGAGTAAA A ATACTGAA
3982	TATTCAGT GGCTAGCTACAACGA ATTTTACT	AGTAAAAT A ACTGAATA
3987	TCATATAT GGCTAGCTACAACGA TCAGTATT	AATACTGA A ATATATGA
3989	ACTCATAT GGCTAGCTACAACGA ATTCAGTA	TACTGAAT A ATATGAGT
3991	AAACTCAT GGCTAGCTACAACGA ATATTCAG	CTGAATAT A ATGAGTIT
3995	TGAAAAAC GGCTAGCTACAACGA TCATATAT	ATATATGA G GITITICA
4003	TTCAAAAC GGCTAGCTACAACGA TGAAAAAC	GITITICA G GITITICAA

Seq! = ITERT (Homo superns reformerase reverse transcriptuse (TERT) mRNA, 4015 bp); Nakamura et al., Science 277 (5328), 955-959 (1997) Cut Site = R/Y (Parine/Pyrimicine) Stem Length = 8 Core Sequence = GGCTAGCTACAACGA

343 Table 17

Table 17: Anti-TERT HH and G-Cleaver Ribozymes

Alias	Ribozyme Sequence	Length (nt)
нн		
TERT-1051	AGGAGUA CUGAUGAGGCCGUUAGGCCGAA AGGAAGU	36
TERT-1053	UGAGGAG CUGAUGAGGCCGUUAGGCCGAA AGAGGAA	36
TERT-1918	UGAAGCG CUGAUGAGGCCGUUAGGCCGAA AGUCUGG	36
TERT-2383	GAGCCAC CUGAUGAGGCCGUUAGGCCGAA AACUGUC	36
TERT-2485	UGAAGCG CUGAUGAGGCCGUUAGGCCGAA AGGAAGA	36
TERT-2566	GCGUGGA CUGAUGAGGCCGUUAGGCCGAA AGGAUGG	36
TERT-3181	AGUAGCA CUGAUGAGGCCGUUAGGCCGAA AGGGAGG	36
TERT-3691	CUGUGGG CUGAUGAGGCCGUUAGGCCGAA AAGUGAA	36
TERT-3758	AUGUGGG CUGAUGAGGCCGUUAGGCCGAA AGUGGAA	36
TERT-3794	GGUGAAC CUGAUGAGGCCGUUAGGCCGAA AUGGCGA	36
G-Cleaver		
TERT-757	UUGGG UGAUGGCAUGCACUAUGCGCG AACGGCAGAC	36
TERT-2353	UCUGU UGAUGGCAUGCACUAUGCGCG AAGGUAGAGA	36
TERT-3795	GUGAA UGAUGGCAUGCACUAUGCGCG AAUGGCGAAU	36

Table 18

Table 18: Human BACE Hammerhead Ribozyme and Target Sequence

Pos	Substrate	Seq ID	Ribozyme	Rz Seq ID
9	CCACGCGU C CGCAGCCC	1	GGGCUGCG CUGAUGAG X CGAA ACGCGUGG	1776
47	AGCUGGAU U AUGGUGGC	2	GCCACCAU CUGAUGAG X CGAA AUCCAGCU	1777
48	GCUGGAUU A UGGUGGCC	3	GGCCACCA CUGAUGAG X CGAA AAUCCAGC	1778
93	GGAGCCCU U GCCCCUGC	4	GCAGGGGC CUGAUGAG X CGAA AGGGCUCC	1779
163	COGCCCCU C CCAGCCCC	5	GGGGCUGG CUGAUGAG X CGAA AGGGGCGG	1780
221	GCCGAUGU A GCGGGCUC	6	GAGCCCGC CUGAUGAG X CGAA ACAUCGGC	1781
229	AGCGGGCU C CGGAUCCC	7	GGGAUCCG CUGAUGAG X CGAA AGCCCGCU	1782
235	CUCCGGAU C CCAGCCUC	8	GAGGCUGG CUGAUGAG X CGAA AUCCGGAG	1783
243	CCCAGCCU C UCCCCUGC	9	GCAGGGGA CUGAUGAG X CGAA AGGCUGGG	1784
245	CAGCCUCU C CCCUGCUC	10	GAGCAGGG CUGAUGAG X CGAA AGAGGCUG	1785
253	CCCCUGCU C CCGUGCUC	11	GAGCACGG CUGAUGAG X CGAA AGCAGGGG	1786
261	CCCGUGCU C UGCGGAUC	12	GAUCCGCA CUGAUGAG X CGAA AGCACGGG	1787
269	CUGCGGAU C UCCCCUGA	13	UCAGGGGA CUGAUGAG X CGAA AUCCGCAG	1788
271	GCGGAUCU C CCCUGACC	14	GGUCAGGG CUGAUGAG X CGAA AGAUCCGC	1789
283	UGACCGCU C UCCACAGC	15	GCUGUGGA CUGAUGAG X CGAA AGCGGUCA	1790
285	ACCGCUCU C CACAGCCC	16	GGGCUGUG CUGAUGAG X CGAA AGAGCGGU	1791
334	CCUGGCGU C CUGAUGCC	17	GGCAUCAG CUGAUGAG X CGAA ACGCCAGG	1792
351	CCCAAGCU C CCUCUCCU	18	AGGAGAGG CUGAUGAG X CGAA AGCUUGGG	1793
355	AGCUCCCU C UCCUGAGA	19	UCUCAGGA CUGAUGAG X CGAA AGGGAGCU	1794
357	CUCCCUCU C CUGAGAAG	20	CUUCUCAG CUGAUGAG X CGAA AGAGGGAG	1795
386	CCCAGACU U GGGGGCAG	21	CUGCCCC CUGAUGAG X CGAA AGUCUGGG	. 1796
477	CCCUGGCU C CUGCUGUG	22	CACAGCAG CUGAUGAG X CGAA AGCCAGGG	1797
531	CACGGCAU C CGGCUGCC	23	GGCAGCCG CUGAUGAG X CGAA AUGCCGUG	1798
632	GGGCAGCU U UGUGGAGA	24	UCUCCACA CUGAUGAG X CGAA AGCUGCCC	1799
633	GGCAGCUU U GUGGAGAU	25	AUCUCCAC CUGAUGAG X CGAA AAGCUGCC	1800
665	GGGCAAGU C GGGGCAGG	26	CCUGCCCC CUGAUGAG X CGAA ACUUGCCC	1801
677	GCAGGGCU A CUACGUGG	27	CCACGUAG CUGAUGAG X CGAA AGCCCUGC	1802
680	GGGCUACU A CGUGGAGA	28	UCUCCACG CUGAUGAG X CGAA AGUAGCCC	1803
717	CAGACGCU C AACAUCCU	29	AGGAUGUU CUGAUGAG X CGAA AGCGUCUG	1804
723	CUCAACAU C CUGGUGGA	30	UCCACCAG CUGAUGAG X CGAA AUGUUGAG	1805
733	UGGUGGAU A CAGGCAGC	31	GCUGCCUG CUGAUGAG X CGAA AUCCACCA	1806
745	GCAGCAGU A ACUUUGCA	32	UGCAAAGU CUGAUGAG X CGAA ACUGCUGC	1807
749	CAGUAACU U UGCAGUGG	33	CCACUGCA CUGAUGAG X CGAA AGUUACUG	1808
750	AGUAACUU U GCAGUGGG	34	CCCACUGC CUGAUGAG X CGAA AAGUUACU	1809
776	CCACCCCU U CCUGCAUC	35	GAUGCAGG CUGAUGAG X CGAA AGGGGUGG	1810
777	CACCCCUU C CUGCAUCG	36	CGAUGCAG CUGAUGAG X CGAA AAGGGGUG	1811
784	UCCUGCAU C GCUACUAC	37	GUAGUAGC CUGAUGAG X CGAA AUGCAGGA	1812
788	GCAUCGCU A CUACCAGA	38	UCUGGUAG CUGAUGAG X CGAA AGCGAUGC	1813
791	UCGCUACU A CCAGAGGC	39	GCCUCUGG CUGAUGAG X CGAA AGUAGCGA	1814
806	GCAGCUGU C CAGCACAU	40	AUGUGCUG CUGAUGAG X CGAA ACAGCUGC	1815
815	CAGCACAU A CCGGGACC	41	GGUCCCGG CUGAUGAG X CGAA AUGUGCUG	1816
	CGGGACCU C CGGAAGGG	42	CCCUUCCG CUGAUGAG X CGAA AGGUCCCG	1817
		43	AGGGCACA CUGAUGAG X CGAA ACACACCC	1818
		44	CCUGGGUG CUGAUGAG X CGAA AGGGCACA	1819
		45		1820
		46	CCAUGGG CUGAUGAG X CGAA AUGCUUAC	1821
		47		1822
825 839 848 891 897 915	CGGGACCU C CGGAAGGG GGGUGUG A UGUGCCCU UGUGCCCU A CACCCAGG GACCUGGU A AGCAUCCC GUAAGCAU C CCCCAUGG CCCAACGU C ACUGUGCG	43 44 45 46	AGGGCACA CUGAUGAG X CGAA ACACACCC CCUGGGUG CUGAUGAG X CGAA AGGGCACA GGGAUGCU CUGAUGAG X CGAA ACCAGGUC	_

Table 18

			able 10	
933	GCCAACAU U GCUGCCAU	48	AUGGCAGC CUGAUGAG X CGAA AUGUUGGC	1823
942	GCUGCCAU C ACUGAAUC	49	GAUUCAGU CUGAUGAG X CGAA AUGGCAGC	1824
950	CACUGAAU C AGACAAGU	50	ACUUGUCU CUGAUGAG X CGAA AUUCAGUG	1825
959	AGACAAGU U CUUCAUCA	51	UGAUGAAG CUGAUGAG X CGAA ACUUGUCU	1826
960	GACAAGUU C UUCAUCAA	52	UUGAUGAA CUGAUGAG X CGAA AACUUGUC	1827
962	CAAGUUCU U CAUCAACG	53	CGUUGAUG CUGAUGAG X CGAA AGAACUUG	1828
963	AAGUUCUU C AUCAACGG	54	CCGUUGAU CUGAUGAG X CGAA AAGAACUU	1829
966	UUCUUCAU C AACGGCUC	55	GAGCCGUU CUGAUGAG X CGAA AUGAAGAA	1830
974	CAACGGCU C CAACUGGG	56	CCCAGUUG CUGAUGAG X CGAA AGCCGUUG	1831
990	GAAGGCAU C CUGGGGCU	57	AGCCCCAG CUGAUGAG X CGAA AUGCCUUC	1832
1004	GCUGGCCU A UGCUGAGA	58	UCUCAGCA CUGAUGAG X CGAA AGGCCAGC	1833
1014	GCUGAGAU U GCCAGGCC	59	GGCCUGGC CUGAUGAG X CGAA AUCUCAGC	1834
1031	UGACGACU C CCUGGAGC	60	GCUCCAGG CUGAUGAG X CGAA AGUCGUCA	1835
1042	UGGAGCCU U UCUUUGAC	61	GUCAAAGA CUGAUGAG X CGAA AGGCUCCA	1836
1043	GGAGCCUU U CUUUGACU	62	AGUCAAAG CUGAUGAG X CGAA AAGGCUCC	1837
1044	GAGCCUUU C UUUGACUC	63	GAGUCAAA CUGAUGAG X CGAA AAAGGCUC	1838
1046	GCCUUUCU U UGACUCUC	64	GAGAGUCA CUGAUGAG X CGAA AGAAAGGC	1839
1047	CCUUUCUU U GACUCUCU	65	AGAGAGUC CUGAUGAG X CGAA AAGAAAGG	1840
1052	CUUUGACU C UCUGGUAA	66	UUACCAGA CUGAUGAG X CGAA AGUCAAAG	1841
1054	UUGACUCU C UGGUAAAG	67	CUUUACCA CUGAUGAG X CGAA AGAGUCAA	. 1842
1059	UCUCUGGU A AAGCAGAC	68	GUCUGCUU CUGAUGAG X CGAA ACCAGAGA	1843
1074	ACCCACGU U CCCAACCU	69	AGGUUGGG CUGAUGAG X CGAA ACGUGGGU	1844
1075	CCCACGUU C CCAACCUC	70	GAGGUUGG CUGAUGAG X CGAA AACGUGGG	1845
1083	CCCAACCU C UUCUCCCU	71	AGGGAGAA CUGAUGAG X CGAA AGGUUGGG	1846
1085	CAACCUCU U CUCCCUGC	72	GCAGGGAG CUGAUGAG X CGAA AGAGGUUG	1847
1086	AACCUCUU C UCCCUGCA	73	UGCAGGGA CUGAUGAG X CGAA AAGAGGUU	1848
1088	CCUCUUCU C CCUGCAGC	74	GCUGCAGG CUGAUGAG X CGAA AGAAGAGG	1849
1098	CUGCAGCU U UGUGGUGC	75	GCACCACA CUGAUGAG X CGAA AGCUGCAG	1850
1099	UGCAGCUU U GUGGUGCU	76	AGCACCAC CUGAUGAG X CGAA AAGCUGCA	1851
1112	IIGCUGGCU U CCCCCUCA	77	UGAGGGG CUGAUGAG X CGAA AGCCAGCA	1852
1113	GCUGGCUU C CCCCUCAA	78	UUGAGGGG CUGAUGAG X CGAA AAGCCAGC	1853
1119	UUCCCCCU C AACCAGUC	79	GACUGGUU CUGAUGAG X CGAA AGGGGGAA	1854
1127	CAACCAGU C UGAAGUGC	80	GCACUUCA CUGAUGAG X CGAA ACUGGUUG	1855
1142	GCUGGCCU C UGUCGGAG	81	CUCCGACA CUGAUGAG X CGAA AGGCCAGC	1856
1146	GCCUCUGU C GGAGGGAG	82	CUCCCUCC CUGAUGAG X CGAA ACAGAGGC	1857
1161	AGCAUGAU C AUUGGAGG	83	CCUCCAAU CUGAUGAG X CGAA AUCAUGCU	1858
1164	AUGAUCAU U GGAGGUAU	84	AUACCUCC CUGAUGAG X CGAA AUGAUCAU	1859
1171	UUGGAGGU A UCGACCAC	85	GUGGUCGA CUGAUGAG X CGAA ACCUCCAA	1860
1173	GGAGGUAU C GACCACUC	86	GAGUGGUC CUGAUGAG X CGAA AUACCUCC	1861
1181	CGACCACU C GCUGUACA	87	UGUAÇAGC CUGAUGAG X CGAA AGUGGUCG	1862
1187	CUCGCUGU A CACAGGCA	88	UGCCUGUG CUGAUGAG X CGAA ACAGCGAG	1863
1198	CAGGCAGU C UCUGGUAU	89	AUACCAGA CUGAUGAG X CGAA ACUGCCUG	1864
1200	GGCAGUCU C UGGUAUAC	90	GUAUACCA CUGAUGAG X CGAA AGACUGCC	1865
1205	UCUCUGGU A UACACCCA	91	UGGGUGUA CUGAUGAG X CGAA ACCAGAGA	1866
1207	UCUGGUAU A CACCCAUC	92	GAUGGGUG CUGAUGAG X CGAA AUACCAGA	1367
1215	ACACCCAU C CGGCGGGA	93	UCCCGCCG CUGAUGAG X CGAA AUGGGUGU	1868
1229	GGAGUGGU A UUAUGAGG	94	CCUCAUAA CUGAUGAG X CGAA ACCACUCC	1869
	AGUGGUAU U AUGAGGUG	95	CACCUCAU CUGAUGAG X CGAA AUACCACU	1870
1231	GUGGUAUU A UGAGGUGA	96	UCACCUCA CUGAUGAG X CGAA AAUACCAC	1871
1232	GAGGUGAU C AUUGUGCG	97	CGCACAAU CUGAUGAG X CGAA AUCACCUC	1872
1242	GUGAUCAU U GUGCGGGU	98	ACCCGCAC CUGAUGAG X CGAA AUGAUCAC	1873
1245	GUGAUCAU U GUGCGGGU		ACCCOUNT COGNOGNO A CONN MODROCNE	

Table 18

			UGUCCAUU CUGAUGAG X CGAA AUCUCCAC	1874
1260	GUGGAGAU C AAUGGACA	99	CAULILIUCA CUGAUGAG X CGAA AUCUCCAC	1874
1273	GACAGGAU C UGAAAAUG CAAGGAGU A CAACUAUG	100	CAUGUUCA CUGAUGAG X CGAA AUCCUGUC CAUAGUUG CUGAUGAG X CGAA ACUCCUUG	1876
1295		101	UCUTIGUCA CUGAUGAG X CGAA ACUCGUAC	1877
1301	GUACAACU A UGACAAGA		CUGUCCAC CUGAUGAG X CGAA AUGCUCUU	1878
1314	AAGAGCAU U GUGGACAG	103	GGCAAACG CUGAUGAG X CGAA AGGUUGGU	1879
1338	ACCAACCU U CGUUUGCC	104		
1339	CCAACCUU C GUUUGCCC	105	GGGCAAAC CUGAUGAG X CGAA AAGGUUGG	1880
1342	ACCUUCGU U UGCCCAAG	106	CUUGGGCA CUGAUGAG X CGAA ACGAAGGU	1881
1343	CCUUCGUU U GCCCAAGA	107	UCUUGGGC CUGAUGAG X CGAA AACGAAGG	1882
1358	GAAAGUGU U UGAAGCUG	108	CAGCUUCA CUGAUGAG X CGAA ACACUUUC	1883
1359	AAAGUGUU U GAAGCUGC	109	GCAGCUUC CUGAUGAG X CGAA AACACUUU	1884
1371	GCUGCAGU C AAAUCCAU	110	AUGGAUUU CUGAUGAG X CGAA ACUGCAGC	1885
1376	AGUCAAAU C CAUCAAGG	111	CCUUGAUG CUGAUGAG X CGAA AUUUGACU	1886
1380	AAAUCCAU C AAGGCAGC	112	GCUGCCUU CUGAUGAG X CGAA AUGGAUUU	1887
1391	GGCAGCCU C CUCCACGG	113	CCGUGGAG CUGAUGAG X CGAA AGGCUGCC	1888
1394	AGCCUCCU C CACGGAGA	114	UCUCCGUG CUGAUGAG X CGAA AGGAGGCU	1889
1406	GGAGAAGU U CCCUGAUG	115	CAUCAGGG CUGAUGAG X CGAA ACUUCUCC	1890
1407	GAGAAGUU C CCUGAUGG	116	CCAUCAGG CUGAUGAG X CGAA AACUUCUC	1891
1417	CUGAUGGU U UCUGGCUA	117	UAGCCAGA CUGAUGAG X CGAA ACCAUCAG	1892
1418	UGAUGGUU U CUGGCUAG	118	CUAGCCAG CUGAUGAG X CGAA AACCAUCA	1893
1419	GAUGGUUU C UGGCUAGG	119	CCUAGCCA CUGAUGAG X CGAA AAACCAUC	1894
1425	UUCUGGCU A GGAGAGCA	120	UGCUCUCC CUGAUGAG X CGAA AGCCAGAA	1895
1465	CCACCCCU U GGAACAUU	121	AAUGUUCC CUGAUGAG X CGAA AGGGGUGG	1896
1473	UGGAACAU U UUCCCAGU	122	ACUGGGAA CUGAUGAG X CGAA AUGUUCCA	1897
1474	GGAACAUU U UCCCAGUC	123	GACUGGGA CUGAUGAG X CGAA AAUGUUCC	1898
1475	GAACAUUU U CCCAGUCA	124	UGACUGGG CUGAUGAG X CGAA AAAUGUUC	1899
1476	AACAUUUU C CCAGUCAU	125	AUGACUGG CUGAUGAG X CGAA AAAAUGUU	1900
1482	UUCCCAGU C AUCUCACU	126	AGUGAGAU CUGAUGAG X CGAA ACUGGGAA	1901
1485	CCAGUCAU C UCACUCUA	127	UAGAGUGA CUGAUGAG X CGAA AUGACUGG	1902
1487	AGUCAUCU C ACUCUACC	128	GGUAGAGU CUGAUGAG X CGAA AGAUGACU	1903
1491	AUCUCACU C UACCUAAU	129	AUUAGGUA CUGAUGAG X CGAA AGUGAGAU	1904
1493	CUCACUCU A CCUAAUGG	130	CCAUUACG CUGAUGAG X CGAA AGAGUGAG	1905
1497	CUCUACCU A AUGGGUGA	131	UCACCCAU CUGAUGAG X CGAA AGGUAGAG	1906
1509	GGUGAGGU U ACCAACCA	132	UGGUUGGU CUGAUGAG X CGAA ACCUCACC	1907
1510	GUGAGGUU A CCAACCAG	133	CUGGUUGG CUGAUGAG X CGAA AACCUCAC	1908
1520	CAACCAGU C CUUCOGCA	134	UGCGGAAG CUGAUGAG X CGAA ACUGGUUG	1909
1523	CCAGUCCU U CCGCAUCA	135	UGAUGCGG CUGAUGAG X CGAA AGGACUGG	1910
1524	CAGUCCUU C CGCAUCAC	136	GUGAUGCG CUGAUGAG X CGAA AAGGACUG	1911
1530	UUCCGCAU C ACCAUCCU	137	AGGAUGGU CUGAUGAG X CGAA AUGCGGAA	1912
1536	AUCACCAU C CUUCCGCA	138	UGCGGAAG CUGAUGAG X CGAA AUGGUGAU	1913
1539	ACCAUCCU U CCGCAGCA	139	UGCUGCGG CUGAUGAG X CGAA AGGAUGGU	1914
1540	CCAUCCUU C CGCAGCAA	140	UUGCUGCG CUGAUGAG X CGAA AAGGAUGG	1915
1550	GCAGCAAU A CCUGCGGC	141	GCCGCAGG CUGAUGAG X CGAA AUUGCUGC	1916
1580	GGCCACGU C CCAAGACG	142	CGUCUUGG CUGAUGAG X CGAA ACGUGGCC	1917
1594	ACGACUGU U ACAAGUUU	143	AAACUUGU CUGAUGAG X CGAA ACAGUCGU	1918
1595	CGACUGUU A CAAGUUUG	144	CAAACUUG CUGAUGAG X CGAA AACAGUCG	1919
1601	UUACAAGU U UGCCAUCU	145	AGAUGGCA CUGAUGAG X CGAA ACUUGUAA	1920
1602	UACAAGUU U GCCAUCUC	146	GAGAUGGC CUGAUGAG X CGAA AACUUGUA	1921
1608	UUUGCCAU C UCACAGUC	147	GACUGUGA CUGAUGAG X CGAA AUGGCAAA	1922
1610	UGCCAUCU C ACAGUCAU	148	AUGACUGU CUGAUGAG X CGAA AGAUGGCA	1923
1616	CUCACAGU C AUCCACGG	149	CCGUGGAU CUGAUGAG X CGAA ACUGUGAG	1924

Table 18

		150	UGCCCGUG CUGAUGAG X CGAA AUGACUGU	1925
1619	ACAGUCAU C CACGGGCA	151	GCUCCCAU CUGAUGAG X CGAA ACAGUGCC	1926
1632	GGCACUGU U AUGGGAGC	152	AGCUCCCA CUGAUGAG X CGAA AACAGUGC	1927
1633	GCACUGUU A UGGGAGCU GGAGCUGU U AUCAUGGA	153	UCCAUGAU CUGAUGAG X CGAA ACAGCUCC	1928
1644	GGAGCUGU U AUCAUGGA GAGCUGUU A UCAUGGAG	154	CUCCAUGA CUGAUGAG X CGAA AACAGCUC	1929
1645	GAGCUGUU A UCAUGGAG GCUGUUAU C AUGGAGGG	155	CCCUCCAU CUGAUGAG X CGAA AUAACAGC	1930
1647		156	CAACGUAG CUGAUGAG X CGAA AGCCCUCC	1931
1658	GGAGGGCU U CUACGUUG	157	ACAACGUA CUGAUGAG X CGAA AAGCCCUC	1932
1659	GAGGGCUU C UACGUUGU	157	AGACAACG CUGAUGAG X CGAA AGAAGCCC	1933
1661	GGGCUUCU A CGUUGUCU	159	UCAAAGAC CUGAUGAG X CGAA ACGUAGAA	1934
1665	UUCUACGU U GUCUUUGA	160	CGAUCAAA CUGAUGAG X CGAA ACAACGUA	1935
1668	UACGUUGU C UUUGAUCG CGUUGUCU U UGAUCGGG	161	CCCGAUCA CUGAUGAG X CGAA AGACAACG	1936
1670		162	GCCCGAUCA CUGAUGAG X CGAA AAGACAAC	1937
1671	GUUGUCUU U GAUCGGGC	163	UCGGGCCC CUGAUGAG X CGAA AUCAAAGA	1938
1675	UCUUUGAU C GGGCCCGA	164	GCAAAGCC CUGAUGAG X CGAA AUUCGUUU	1939
1692	AAACGAAU U GGCUUUGC	165	UGACAGCA CUGAUGAG X CGAA AGCCAAUU	1940
1697	AAUUGGCU U UGCUGUCA	166	CUGACAGC CUGAUGAG X CGAA AAGCCAAU	1941
1698	AUUGGCUU U GCUGUCAG UUUGCUGU C AGCGCUUG	167	CAAGCGCU CUGAUGAG X CGAA ACAGCAAA	1942
1704	UUUGCUGU C AGCGCUUG UCAGCGCU U GCCAUGUG	168	CACAUGGC CUGAUGAG X CGAA AGCGCUGA	1943
1711		169	CCGUCCUG CUGAUGAG X CGAA ACUCAUCG	1944
1730	CGAUGAGU U CAGGACGG GAUGAGUU C AGGACGGC	170	GCCGUCCU CUGAUGAG X CGAA AACUCAUC	1945
1731	GAUGAGUU C AGGACGGC AAGGCCCU U UUGUCACC	171	GGUGACAA CUGAUGAG X CGAA AGGGCCUU	1946
1756	AGGCCCUU U UGUCACCU	172	AGGUGACA CUGAUGAG X CGAA AAGGGCCU	1947
1757	GGCCCUUU U GUCACCUU	173	AAGGUGAC CUGAUGAG X CGAA AAAGGGCC	1948
1758	CCUUUUGU C ACCUUGGA	174	UCCAAGGU CUGAUGAG X CGAA ACAAAAGG	1949
1761	UGUCACCU U GGACAUGG	175	CCAUGUCC CUGAUGAG X CGAA AGGUGACA	1950
1766	CUGUGGCU A CAACAUUC	176	GAAUGUUG CUGAUGAG X CGAA AGCCACAG	1951
1794	UACAACAU U CCACAGAC	177	GUCUGUGG CUGAUGAG X CGAA AUGUUGUA	1952
1794	ACAACAUU C CACAGACA	178	UGUCUGUG CUGAUGAG X CGAA AAUGUUGU	1953
1811	AGAUGAGU C AACCCUCA	179	UGAGGGUU CUGAUGAG X CGAA ACUCAUCU	1954
1818	HCAACCCU C AUGACCAU	180	AUGGUCAU CUGAUGAG X CGAA AGGGUUGA	1955
1827	AUGACCAU A GCCUAUGU	181	ACAUAGGC CUGAUGAG X CGAA AUGGUCAU	1956
1832	CAUAGCCU A UGUCAUGG	182	CCAUGACA CUGAUGAG X CGAA AGGCUAUG	1957
1836	GCCUAUGU C AUGGCUGC	183	GCAGCCAU CUGAUGAG X CGAA ACAUAGGC	1958
1848	GCUGCCAU C UGCGCCCU	184	AGGGCGCA CUGAUGAG X CGAA AUGGCAGC	1959
1857	UGCGCCCU C UUCAUGCU	185	AGCAUGAA CUGAUGAG X CGAA AGGGCGCA	1960
1859	CGCCCUCU U CAUGCUGC	186	GCAGCAUG CUGAUGAG X CGAA AGAGGGCG	1961
1860	GCCCUCUU C AUGCUGCC	187	GGCAGCAU CUGAUGAG X CGAA AAGAGGGC	1962
1872	CUGCCACU C UGCCUCAU	188	AUGAGGCA CUGAUGAG X CGAA AGUGGCAG	1963
1878	CUCUGCCU C AUGGUGUG	189	CACACCAU CUGAUGAG X CGAA AGGCAGAG	1964
1888	UGGUGUGU C AGUGGCGC	190	GCGCCACU CUGAUGAG X CGAA ACACACCA	1965
1902	CGCUGCCU C CGCUGCCU	191	AGGCAGCG CUGAUGAG X CGAA AGGCAGCG	1966
1931	UGAUGACU U UGCUGAUG	192	CAUCAGCA CUGAUGAG X CGAA AGUCAUCA	1967
1932	GAUGACUU U GCUGAUGA	193	UCAUCAGC CUGAUGAG X CGAA AAGUCAUC	1968
1944	GAUGACAU C UCCCUGCU	194	AGCAGGGA CUGAUGAG X CGAA AUGUCAUC	1969
1946	UGACAUCU C CCUGCUGA	195	UCAGCAGG CUGAUGAG X CGAA AGAUGUCA	1970
1981	CAGAAGAU A GAGAUUCC	196	GGAAUCUC CUGAUGAG X CGAA AUCUUCUG	1971
1987	AUAGAGAU U CCCCUGGA	197	UCCAGGGG CUGAUGAG X CGAA AUCUCUAU	1972
1988	UAGAGAUU C CCCUGGAC	198	GUCCAGGG CUGAUGAG X CGAA AAUCUCUA	1973
2004	CCACACCU C CGUGGUUC	199	GAACCACG CUGAUGAG X CGAA AGGUGUGG	1974
2011	UCCGUGGU U CACUUUGG	200	CCAAAGUG CUGAUGAG X CGAA ACCACGGA	1975

Table 18

	TOWNS OF THE PROPERTY OF	201	ACCAAAGU CUGAUGAG X CGAA AACCACGG	1976
2012	GGUUCACU U UGGUCACA	202	UGUGACCA CUGAUGAG X CGAA AGUGAACC	1977
2016	GUUCACUU U GGUCACAA	203	UUGUGACC CUGAUGAG X CGAA AAGUGAAC	1978
2017	ACUUUGGU C ACAAGUAG	204	CUACIDIGU CUGAUGAG X CGAA ACCAAAGU	1979
2021	UCACAAGU A GGAGACAC	205	GUGUCUCC CUGAUGAG X CGAA ACUUGUGA	1980
2028	GAGCACCU C AGGACCCU	206	AGGGUCCU CUGAUGAG X CGAA AGGUGCUC	1981
2063	AGGACCCU C AGGACCCO	207	UGGGUGGG CUGAUGAG X CGAA AGGGUCCU	1982
2072	AAAUGCCU C UGCCUUGA	208	UCAAGGCA CUGAUGAG X CGAA AGGCAUUU	1983
2091	CUCUGCCU U GAUGGAGA	209	UCUCCAUC CUGAUGAG X CGAA AGGCAGAG	1984
2097	AGGUGGGU U CCAGGGAC	210	GUCCCUGG CUGAUGAG X CGAA ACCCACCU	1985
2129	GGUGGGUU C CAGGGACU	211	AGUCCCUG CUGAUGAG X CGAA AACCCACC	1986
2130	GGGACUGU A CCUGUAGG	212	CCUACAGG CUGAUGAG X CGAA ACAGUCCC	1987
2141		213	CUGUUUCC CUGAUGAG X CGAA ACAGGUAC	1988
2147	GUACCUGU A GGAAACAG GAAGCACU C UGCUGGCG	213	CGCCAGCA CUGAUGAG X CGAA AGUGCUUC	1989
2177	GCGGGAAU A CUCUUGGU	215	ACCAAGAG CUGAUGAG X CGAA AUUCCCGC	1990
2191		216	GUGACCAA CUGAUGAG X CGAA AGUAUUCC	1991
2194		217	AGGUGACC CUGAUGAG X CGAA AGAGUAUU	1992
2196	AAUACUCU U GGUCACCU CUCUUGGU C ACCUCAAA	217	UUUGAGGU CUGAUGAG X CGAA ACCAAGAG	1993
2200		219	UUAAAUUU CUGAUGAG X CGAA AGGUGACC	1994
2205	GGUCACCU C AAAUUUAA	219	CCGACUUA CUGAUGAG X CGAA AUUUGAGG	1995
2210	CCUCAAAU U UAAGUCGG	220	CCCGACUU CUGAUGAG X CGAA AAUUUGAG	1996
2211	CUCAAAUU U AAGUCGGG	221	UCCCGACU CUGAUGAG X CGAA AAAUUUGA	1997
2212	UCAAAUUU A AGUCGGGA	222	AAUUUCCC CUGAUGAG X CGAA ACUUAAAU	1998
2216	AUUUAAGU C GGGAAAUU CGGGAAAU U CUGCUGCU	224	AGCAGCAG CUGAUGAG X CGAA AUUUCCCG	1999
2224	GGGAAAUU C UGCUGCUU	225	AAGCAGCA CUGAUGAG X CGAA AAUUUCCC	2000
2225	CUGCUGCU U GAAACUUC	225	GAAGUUUC CUGAUGAG X CGAA AGCAGCAG	2001
2233	UUGAAACU U CAGCCCUG	227	CAGGGCUG CUGAUGAG X CGAA AGUUUCAA	2002
2240	UGAAACUU C AGCCCUGA	228	UCAGGGCU CUGAUGAG X CGAA AAGUUUCA	2003
	CUGAACCU U UGUCCACC	229	GGUGGACA CUGAUGAG X CGAA AGGUUCAG	2004
2254	UGAACCUU U GUCCACCA	230	UGGUGGAC CUGAUGAG X CGAA AAGGUUCA	2005
2258	ACCUUUGU C CACCAUUC	231	GAAUGGUG CUGAUGAG X CGAA ACAAAGGU	2006
2258	UCCACCAU U CCUUUAAA	232	UUUAAAGG CUGAUGAG X CGAA AUGGUGGA	2007
2265	CCACCAUU C CUUUAAAU	233	AUUUAAAG CUGAUGAG X CGAA AAUGGUGG	2008
2269	CCAUUCCU U UAAAUUCU	234	AGAAUUUA CUGAUGAG X CGAA AGGAAUGG	2009
2270	CAUUCCUU U AAAUUCUC	235	GAGAAUUU CUGAUGAG X CGAA AAGGAAUG	2010
2270	AUUCCUUU A AAUUCUCC	236	GGAGAAUU CUGAUGAG X CGAA AAAGGAAU	2011
2275	CUUUAAAU U CUCCAACC	237	GGUUGGAG CUGAUGAG X CGAA AUUUAAAG	2012
2275	UUUAAAUU C UCCAACCC	238	GGGUUGGA CUGAUGAG X CGAA AAUUUAAA	2013
2278	UAAAUUCU C CAACCCAA	239	UUGGGUUG CUGAUGAG X CGAA AGAAUUUA	2014
2270	CCCAAAGU A UUCUUCUU	240	AAGAAGAA CUGAUGAG X CGAA ACUUUGGG	2015
2292	CAAAGUAU U CUUCUUUU	241	AAAAGAAG CUGAUGAG X CGAA AUACUUUG	2016
2293	AAAGUAUU C UUCUUUUC	242	GAAAAGAA CUGAUGAG X CGAA AAUACUUU	2017
2295	AGUAUUCU U CUUUUCUU	243	AAGAAAAG CUGAUGAG X CGAA AGAAUACU	2018
2296	GUAUUCUU C UUUUCUUA	244	UAAGAAAA CUGAUGAG X CGAA AAGAAUAC	2019
2298	AUUCUUCU U UUCUUAGU	245	ACUAAGAA CUGAUGAG X CGAA AGAAGAAU	2020
2299	DUCUUCUU U UCUUAGUU	246	AACUAAGA CUGAUGAG X CGAA AAGAAGAA	2021
2300	UCUUCUUU U CUUAGUUU	247	AAACUAAG CUGAUGAG X CGAA AAAGAAGA	2022
2301	CUUCUUUU C UUAGUUUC	248	GAAACUAA CUGAUGAG X CGAA AAAAGAAG	2023
2303	UCUUUUCU U AGUUUCAG	249	CUGAAACU CUGAUGAG X CGAA AGAAAAGA	2024
2303	CULIUUCUU A GUUUCAGA	250	UCUGAAAC CUGAUGAG X CGAA AAGAAAAG	2025
2307	UUCUUAGU U UCAGAAGU	251	ACUUCUGA CUGAUGAG X CGAA ACUAAGAA	2026
2307			L	

Table 18

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2308	UCUUAGUU U CAGAAGUA	252	UACUUCUG CUGAUGAG X CGAA AACUAAGA	2027
2309	CUUAGUUU C AGAAGUAC	253	GUACUUCU CUGAUGAG X CGAA AAACUAAG	2028
2316	UCAGAAGU A CUGGCAUC	254	GAUGCCAG CUGAUGAG X CGAA ACUUCUGA	2029
2324	ACUGGCAU C ACACGCAG	255	CUGCGUGU CUGAUGAG X CGAA AUGCCAGU	2030
2335	ACGCAGGU U ACCUUGGC	256	GCCAAGGU CUGAUGAG X CGAA ACCUGCGU	2031
2336	CGCAGGUU A CCUUGGCG	257	CGCCAAGG CUGAUGAG X CGAA AACCUGCG	2032
2340	GGUUACCU U GGCGUGUG	258	CACACGCC CUGAUGAG X CGAA AGGUAACC	2033
2350	GCGUGUGU C CCUGUGGU	259	ACCACAGG CUGAUGAG X CGAA ACACACGC	2034
2359	CCUGUGGU A CCCUGGCA	260	UGCCAGGG CUGAUGAG X CGAA ACCACAGG	2035
2384	ACCAAGCU U GUUUCCCU	261	AGGGAAAC CUGAUGAG X CGAA AGCUUGGU	2036
2387	AAGCUUGU U UCCCUGCU	262	AGCAGGGA CUGAUGAG X CGAA ACAAGCUU	2037
2388	AGCUUGUU U CCCUGCUG	263	CAGCAGGG CUGAUGAG X CGAA AACAAGCU	2038
2389	GCUUGUUU C CCUGCUGG	264	CCAGCAGG CUGAUGAG X CGAA AAACAAGC	2039
2405	GCCAAAGU C AGUAGGAG	265	CUCCUACU CUGAUGAG X CGAA ACUUUGGC	2040
2409	AAGUCAGU A GGAGAGGA	266	UCCUCUCC CUGAUGAG X CGAA ACUGACUU	2041
2426	UGCACAGU U UGCUAUUU	267	AAAUAGCA CUGAUGAG X CGAA ACUGUGCA	2042
2427	GCACAGUU U GCUAUUUG	268	CAAAUAGC CUGAUGAG X CGAA AACUGUGC	2043
2431	AGUUUGCU A UUUGCUUU	269	AAAGCAAA CUGAUGAG X CGAA AGCAAACU	2044
2433	UUUGCUAU U UGCUUUAG	270	CUAAAGCA CUGAUGAG X CGAA AUAGCAAA	2045
2434	UUGCUAUU U GCUUUAGA	271	UCUAAAGC CUGAUGAG X CGAA AAUAGCAA	2046
2438	UAUUUGCU U UAGAGACA	272	UGUCUCUA CUGAUGAG X CGAA AGCAAAUA	2047
2439	AUUUGCUU U AGAGACAG	273	CUGUCUCU CUGAUGAG X CGAA AAGCAAAU	2048
2440	UUUGCUUU A GAGACAGG	274	CCUGUCUC CUGAUGAG X CGAA AAAGCAAA	2049
2455	GGGACUGU A UAAACAAG	275	CUUGUUUA CUGAUGAG X CGAA ACAGUCCC	2050
2457	GACUGUAU A AACAAGCC	276	GGCUUGUU CUGAUGAG X CGAA AUACAGUC	2051
2467	ACAAGCCU A ACAUUGGU	277	ACCAAUGU CUGAUGAG X CGAA AGGCUUGU	2052
2472	CCUAACAU U GGUGCAAA	278	UUUGCACC CUGAUGAG X CGAA AUGUUAGG	2053
2484	GCAAAGAU U GCCUCUUG	279	CAAGAGGC CUGAUGAG X CGAA AUCUUUGC	2054
2489	GAUUGCCU C UUGAAUUA	280	UAAUUCAA CUGAUGAG X CGAA AGGCAAUC	2055
2491	UUGCCUCU U GAAUUAAA	281	UUUAAUUC CUGAUGAG X CGAA AGAGGCAA	2056
2496	UCUUGAAU U AAAAAAAA	282	UUUUUUUU CUGAUGAG X CGAA AUUCAAGA	2057
2497	CUUGAAUU A AAAAAAAA	283	UUUUUUUU CUGAUGAG X CGAA AAUUCAAG	2058
2510	AAAAAACU A GAAAAAAA	284	UUUUUUUC CUGAUGAG X CGAA AGUUUUUU	2059

Input Sequence = AF190725. Cut Site = G/.
Stem Length = 8 - Core Sequence = CUGAUJAG X CGAA (X = GCCGUUAGGC or other stem II)
AF190725 (Komo sapiens beta-site APP cleaving enzyme (BACE) mRNA: 2526 bp)

Table 19

Table 19: Human BACE NCH Ribozyme and Target Sequence

Pos	Substrate	Seq ID	Ribozyme	Rz Seq ID
10	CACGCGUC C GCAGCCCG	285	CGGGCUGC CUGAUGAG X CGAA IACGCGUG	2060
13	GCGUCCGC A GCCCGCCC	286	GGGCGGGC CUGAUGAG X CGAA ICGGACGC	2061
16	UCCGCAGC C CGCCCGGG	287	CCCGGGCG CUGAUGAG X CGAA ICUGCGGA	2062
17	CCGCAGCC C GCCCGGGA	288	UCCCGGGC CUGAUGAG X CGAA IGCUGCGG	2063
20	CAGCCCGC C CGGGAGCU	289	AGCUCCCG CUGAUGAG X CGAA ICGGGCUG	2064
21	AGCCCGCC C GGGAGCUG	290	CAGCUCCC CUGAUGAG X CGAA IGCGGGCU	2065
28	CCGGGAGC U GCGAGCCG	291	CGGCUCGC CUGAUGAG X CGAA ICUCCCGG	2056
35	CUGCGAGC C GCGAGCUG	292	CAGCUCGC CUGAUGAG X CGAA ICUCGCAG	2067
42	CCGCGAGC U GGAUUAUG	293	CAUAAUCC CUGAUGAG X CGAA ICUCGCGG	2068
56	AUGGUGGC C UGAGCAGC	294	GCUGCUCA CUGAUGAG X CGAA ICCACCAU	2069
57	UGGUGGCC U GAGCAGCC	295	GGCUGCUC CUGAUGAG X CGAA IGCCACCA	2070
62	GCCUGAGC A GCCAACGC	296	GCGUUGGC CUGAUGAG X CGAA ICUCAGGC	2071
65	UGAGCAGC C AACGCAGC	297	GCUGCGUU CUGAUGAG X CGAA ICUGCUCA	2072
66	GAGCAGCC A ACGCAGCC	298	GGCUGCGU CUGAUGAG X CGAA IGCUGCUC	2073
71	GCCAACGC A GCCGCAGG	299	CCUGCGGC CUGAUGAG X CGAA ICGUUGGC	2074
74	AACGCAGC C GCAGGAGC	300	GCUCCUGC CUGAUGAG X CGAA ICUGCGUU	2075
77	GCAGCCGC A GGAGCCCG	301	CGGGCUCC CUGAUGAG X CGAA ICGGCUGC	2076
83	GCAGGAGC C CGGAGCCC	302	GGGCUCCG CUGAUGAG X CGAA ICUCCUGC	2077
84	CAGGAGCC C GGAGCCCU	303	AGGGCUCC CUGAUGAG X CGAA IGCUCCUG	2078
90	CCCGGAGC C CUUGCCCC	304	GGGGCAAG CUGAUGAG X CGAA ICUCCGGG	2079
91	CCGGAGCC C UUGCCCCU	305	AGGGGCAA CUGAUGAG X CGAA IGCUCCGG	2080
92	CGGAGCCC U UGCCCCUG	306	CAGGGGCA CUGAUGAG X CGAA IGGCUCCG	2081
96	GCCCUUGC C CCUGCCCG	307	CGGGCAGG CUGAUGAG X CGAA ICAAGGGC	2082
97	CCCUUGCC C CUGCCCGC	308	GCGGGCAG CUGAUGAG X CGAA IGCAAGGG	2083
98	CCUUGCCC C UGCCCGCG	309	CGCGGGCA CUGAUGAG X CGAA IGGCAAGG	2084
99	CUUGCCCC U GCCCGCGC	310	GCGCGGGC CUGAUGAG X CGAA IGGGCAAG	2085
102	GCCCCUGC C CGCGCCGC	311	GCGGCGCG CUGAUGAG X CGAA ICAGGGGC	2086
103	CCCCUGCC C GCGCCGCC	312	GGCGGCGC CUGAUGAG X CGAA IGCAGGGG	2087
108	GCCGCGC C GCCGCCCG	313	CGGGCGGC CUGAUGAG X CGAA ICGCGGGC	2088
111	CGCGCCGC C GCCCGCCG	314	CGGCGGGC CUGAUGAG X CGAA ICGGCGCG	2089
114	GCCGCCGC C CGCCGGGG	315	CCCCGGCG CUGAUGAG X CGAA ICGGCGGC	2090
115	CCGCCGCC C GCCGGGGG	316	CCCCCGGC CUGAUGAG X CGAA IGCGGCGG	2091
118	CCGCCCGC C GGGGGGAC	317	GUCCCCCC CUGAUGAG X CGAA ICGGGCGG	2092
127	GGGGGAC C AGGGAAGC	318	GCUUCCCU CUGAUGAG X CGAA IUCCCCCC	2093
128	GGGGGACC A GGGAAGCC	319	GGCUUCCC CUGAUGAG X CGAA IGUCCCCC	2094
136	AGGGAAGC C GCCACCGG	320	CCGGUGGC CUGAUGAG X CGAA ICUUCCCU	2095
139	GAAGCCGC C ACCGGCCC	321	GGGCCGGU CUGAUGAG X CGAA ICGGCUUC	2096
140	AAGCCGCC A CCGGCCCG	322	CGGGCCGG CUGAUGAG X CGAA IGCGGCUU	2097
142	GCCGCCAC C GGCCCGCC	323	GGCGGGCC CUGAUGAG X CGAA IUGGCGGC	2098
146	CCACCGGC C CGCCAUGC	324	GCAUGGCG CUGAUGAG X CGAA ICCGGUGG	2099
147	CACCGGCC C GCCAUGCC	325	GGCAUGGC CUGAUGAG X CGAA IGCCGGUG	2100
150	CGGCCCGC C AUGCCCGC	326	GCGGGCAU CUGAUGAG X CGAA ICGGGCCG	2101
151	GGCCCGCC A UGCCCGCC	327	GGCGGGCA CUGAUGAG X CGAA IGCGGGCC	2102
155	CGCCAUGC C CGCCCCUC	328	GAGGGGCG CUGAUGAG X CGAA ICAUGGCG	2103
156	GCCAUGCC C GCCCCUCC	329	GGAGGGC CUGAUGAG X CGAA IGCAUGGC	2104
159	AUGCCCGC C CCUCCCAG	330	CUGGGAGG CUGAUGAG X CGAA ICGGGCAU	2105
160	UGCCCGCC C CUCCCAGC	331	GCUGGGAG CUGAUGAG X CGAA IGCGGGCA	2106

. Table 19

			The second of th	2102
161	GCCCGCCC C UCCCAGCC	332	GGCUGGGA CUGAUGAG X CGAA IGGCGGGC	2107
162	CCCGCCCC U CCCAGCCC	333	GGGCUGGG CUGAUGAG X CGAA IGGGCGGG	2109
164	CGCCCCUC C CAGCCCCG	334	CGGGGCUG CUGAUGAG X CGAA IAGGGGCG	2110
165	GCCCCUCC C AGCCCCGC	335	GCGGGGCU CUGAUGAG X CGAA IGAGGGGC	2111
166	CCCCUCCC A GCCCCGCC	336	GGCGGGGC CUGAUGAG X CGAA IGGAGGGG	2111
169	CUCCCAGC C CCGCCGGG	337	CCCGGCGG CUGAUGAG X CGAA ICUGGGAG	2112
170	UCCCAGCC C CGCCGGGA	338	UCCCGGCG CUGAUGAG X CGAA IGCUGGGA	
171	CCCAGCCC C GCCGGGAG	339	CUCCCGGC CUGAUGAG X CGAA IGGCUGGG	2114
174	AGCCCCGC C GGGAGCCC	340	GGGCUCCC CUGAUGAG X CGAA ICGGGGCU	2115
181	CCGGGAGC C CGCGCCCG	341	CGGGCGCG CUGAUGAG X CGAA ICUCCCGG	2116
182	CGGGAGCC C GCGCCCGC	342	GCGGGCGC CUGAUGAG X CGAA IGCUCCCG	
187	GCCCGCGC C CGCUGCCC	343	GGGCAGCG CUGAUGAG X CGAA ICGCGGGC	2118
188	CCCGCGCC C GCUGCCCA	344	UGGGCAGC CUGAUGAG X CGAA IGCGCGGG	2119
191	GCGCCCGC U GCCCAGGC	345	GCCUGGGC CUGAUGAG X CGAA ICGGGCGC	
194	CCCGCUGC C CAGGCUGG	346	CCAGCCUG CUGAUGAG X CGAA ICAGCGGG	2121
195	CCGCUGCC C AGGCUGGC	347	GCCAGCCU CUGAUGAG X CGAA IGCAGCGG	2122
196	CGCUGCCC A GGCUGGCC	348	GGCCAGCC CUGAUGAG X CGAA IGGCAGCG	2123
200	GCCCAGGC U GGCCGCCG	349	CGGCGGCC CUGAUGAG X CGAA ICCUGGGC	2124
204	AGGCUGGC C GCCGCCGU	350	ACGGCGGC CUGAUGAG X CGAA ICCAGCCU	2125
207	CUGGCCGC C GCCGUGCC	351	GGCACGGC CUGAUGAG X CGAA ICGGCCAG	2126
210	GCCGCCGC C GUGCCGAU	352	AUCGGCAC CUGAUGAG X CGAA ICGGCGGC	2127
215	CGCCGUGC C GAUGUAGC	353	GCUACAUC CUGAUGAG X CGAA ICACGGCG	2128
228	UAGCGGGC U CCGGAUCC	354	GGAUCCGG CUGAUGAG X CGAA ICCCGCUA	2129
230	GCGGGCUC C GGAUCCCA	355	UGGGAUCC CUGAUGAG X CGAA IAGCCCGC	2130
236	UCCGGAUC C CAGCCUCU	356	AGAGGCUG CUGAUGAG X CGAA IAUCCGGA	2131
237	CCGGAUCC C AGCCUCUC	357	GAGAGGCU CUGAUGAG X CGAA IGAUCCGG	2132
238	CGGAUCCC A GCCUCUCC	358	GGAGAGGC CUGAUGAG X CGAA IGGAUCCG	2133
241	AUCCCAGC C UCUCCCCU	359	AGGGGAGA CUGAUGAG X CGAA ICUGGGAU	2134
242	UCCCAGCC U CUCCCCUG	360	CAGGGGAG CUGAUGAG X CGAA IGCUGGGA	2135
244	CCAGCCUC U CCCCUGCU	361	AGCAGGGG CUGAUGAG X CGAA IAGGCUGG	2136
246	AGCCUCUC C CCUGCUCC	362	GGAGCAGG CUGAUGAG X CGAA IAGAGGCU	2137
247	GCCUCUCC C CUGCUCCC	363	GGGAGCAG CUGAUGAG X CGAA IGAGAGGC	2138
248	CCUCUCCC C UGCUCCCG	364	CGGGAGCA CUGAUGAG X CGAA IGGAGAGG	2139
249	CUCUCCCC U GCUCCCGU	365	ACGGGAGC CUGAUGAG X CGAA IGGGAGAG	2140
252	UCCCCUGC U CCCGUGCU	366	AGCACGGG CUGAUGAG X CGAA ICAGGGGA	2141
254	CCCUGCUC C CGUGCUCU	367	AGAGCACG CUGAUGAG X CGAA IAGCAGGG	2142
255	CCUGCUCC C GUGCUCUG	368	CAGAGCAC CUGAUGAG X CGAA IGAGCAGG	2143
260	UCCCGUGC U CUGCGGAU	369	AUCCGCAG CUGAUGAG X-CGAA ICACGGGA	2144
262	CCGUGCUC U GCGGAUCU	370	AGAUCCGC CUGAUGAG X CGAA IAGCACGG	2145
270	UGCGGAUC U CCCCUGAC	371	GUCAGGGG CUGAUGAG X CGAA IAUCCGCA	2146
272	CGGAUCUC C CCUGACCG	372	CGGUCAGG CUGAUGAG X CGAA TAGAUCCG	2147
273	GGAUCUCC C CUGACCGC	373	GCGGUCAG CUGAUGAG X CGAA IGAGAUCC	2148
274	GAUCUCCC C UGACCGCU	374	AGCGGUCA CUGAUGAG X CGAA IGGAGAUC	2149
275	AUCUCCCC U GACCGCUC	375	GAGCGGUC CUGAUGAG X CGAA IGGGAGAU	2150
279	CCCCUGAC C GCUCUCCA	376	UGGAGAGC CUGAUGAG X CGAA IUCAGGGG	2151
282	CUGACCGC U CUCCACAG	377	CUGUGGAG CUGAUGAG X CGAA ICGGUCAG	2152
284	GACCGCUC U CCACAGCC	378	GGCUGUGG CUGAUGAG X CGAA IAGCGGUC	2153
286	CCGCUCUC C ACAGCCCG	379	CGGGCUGU CUGAUGAG X CGAA IAGAGCGG	2154
287	CGCUCUCC A CAGCCCGG	380	CCGGGCUG CUGAUGAG X CGAA IGAGAGCG	2155
289	CUCUCCAC A GCCCGGAC	381	GUCCGGGC CUGAUGAG X CGAA IUGGAGAG	2156
292	UCCACAGC C CGGACCCG	382	CGGGUCCG CUGAUGAG X CGAA ICUGUGGA	2157

Table 19

293	CCACAGCC C GGACCCGG	383	CCGGGUCC CUGAUGAG X CGAA IGCUGUGG	2158
298	GCCCGGAC C CGGGGGCU	384	AGCCCCCG CUGAUGAG X CGAA IUCCGGGC	2159
299	CCCGGACC C GGGGGCUG	385	CAGCCCCC CUGAUGAG X CGAA IGUCCGGG	2160
306	CCGGGGGC U GGCCCAGG	386	CCUGGGCC CUGAUGAG X CGAA ICCCCCGG	2161
310	GGGCUGGC C CAGGGCCC	387	GGGCCCUG CUGAUGAG X CGAA ICCAGCCC	2162
311	GGCUGGCC C AGGGCCCU	388	AGGGCCCU CUGAUGAG X CGAA IGCCAGCC	2163
312	GCUGGCCC A GGGCCCUG	389	CAGGGCCC CUGAUGAG X CGAA IGGCCAGC	2164
317	CCCAGGGC C CUGCAGGC	390	GCCUGCAG CUGAUGAG X CGAA ICCCUGGG	2165
318	CCAGGGCC C UGCAGGCC	391	GGCCUGCA CUGAUGAG X CGAA IGCCCUGG	2166
319	CAGGGCCC U GCAGGCCC	392	GGGCCUGC CUGAUGAG X CGAA IGGCCCUG	2167
322	GGCCCUGC A GGCCCUGG	393	CCAGGGCC CUGAUGAG X CGAA ICAGGGCC	2168
326	CUGCAGGC C CUGGCGUC	394	GACGCCAG CUGAUGAG X CGAA ICCUGCAG	2169
327	UGCAGGCC C UGGCGUCC	395	GGACGCCA CUGAUGAG X CGAA IGCCUGCA	2170
328	GCAGGCCC U GGCGUCCU	396	AGGACGCC CUGAUGAG X CGAA IGGCCUGC	2171
335	CUGGCGUC C UGAUGCCC	397	GGGCAUCA CUGAUGAG X CGAA IACGCCAG	2172
336	UGGCGUCC U GAUGCCCC	398	GGGGCAUC CUGAUGAG X CGAA IGACGCCA	2173
342	CCUGAUGC C CCCAAGCU	399	AGCUUGGG CUGAUGAG X CGAA ICAUCAGG	2174
	CUGAUGCC C CCAAGCUC	400	GAGCUUGG CUGAUGAG X CGAA IGCAUCAG	2175
343	UGAUGCCC C CAAGCUCC	401	GGAGCUUG CUGAUGAG X CGAA IGGCAUCA	2176
	GAUGCCCC C AAGCUCCC	402	GGGAGCUU CUGAUGAG X CGAA IGGGCAUC	2177
345	AUGCCCCC A AGCUCCCU	403	AGGGAGCU CUGAUGAG X CGAA IGGGGCAU	2178
346	CCCCAAGC U CCCUCUCC	404	GGAGAGGG CUGAUGAG X CGAA ICUUGGGG	2179
350	CCAAGCUC C CUCUCCUG	405	CAGGAGAG CUGAUGAG X CGAA IAGCUUGG	2180
352	CAAGCUCC C UCUCCUGA	406	UCAGGAGA CUGAUGAG X CGAA IGAGCUUG	2181
353	AAGCUCCC U CUCCUGAG	407	CUCAGGAG CUGAUGAG X CGAA IGGAGCUU	2182
354	GCUCCCUC U CCUGAGAA	408	UUCUCAGG CUGAUGAG X CGAA IAGGGAGC	2183
356	UCCCUCUC C UGAGAAGC	409	GCUUCUCA CUGAUGAG X CGAA IAGAGGGA	2184
358	CCCUCUCC U GAGAAGCC	410	GGCUUCUC CUGAUGAG X CGAA IGAGAGGG	2185
359	UGAGAAGC C ACCAGCAC	411	GUGCUGGU CUGAUGAG X CGAA ICUUCUCA	2186
367	GAGAAGCC A CCAGCACC	412	GGUGCUGG CUGAUGAG X CGAA IGCUUCUC	2187
368	GAGGCCAC C AGCACCAC	413	GUGGUGCU CUGAUGAG X CGAA IUGGCUUC	2188
370	AAGCCACC A GCACCACC	414	GGUGGUGC CUGAUGAG X CGAA IGUGGCUU	2189
371	CCACCAGC A CCACCCAG	415	CUGGGUGG CUGAUGAG X CGAA ICUGGUGG	2190
	ACCAGCAC C ACCCAGAC	416	GUCUGGGU CUGAUGAG X CGAA IUGCUGGU	2191
376	CCAGCACC A CCCAGACU	417	AGUCUGGG CUGAUGAG X CGAA IGUGCUGG	2192
377	AGCACCAC C CAGACUUG	418	CAAGUCUG CUGAUGAG X CGAA IUGGUGCU	2193
379	GCACCACC C AGACUUGG	419	CCAAGUCU CUGAUGAG X CGAA IGUGGUGC	2194
380	CACCACCC A GACUUGGG	420	CCCAAGUC CUGAUGAG X CGAA IGGUGGUG	2195
	ACCCAGAC U UGGGGGCA	421	UGCCCCCA CUGAUGAG X CGAA IUCUGGGU	2196
385	UUGGGGGC A GGCGCCAG	422	CUGGCGCC CUGAUGAG X CGAA ICCCCCAA	2197
393	GCAGGCGC C AGGGACGG	423	CCGUCCCU CUGAUGAG X CGAA ICGCCUGC	2198
399	CAGGCGCC A GGGACGGA	424	UCCGUCCC CUGAUGAG X CGAA IGCGCCUG	2199
416	ACGUGGGC C AGUGCGAG	425	CUCGCACU CUGAUGAG X CGAA ICCCACGU	2200
	CGUGGGCC A GUGCGAGC	426	GCUCGCAC CUGAUGAG X CGAA IGCCCACG	2201
417	GUGCGAGC C CAGAGGGC	427	GCCCUCUG CUGAUGAG X CGAA ICUCGCAC	2202
426	UGCGAGCC C AGAGGGCC	428	GGCCCUCU CUGAUGAG X CGAA IGCUCGCA	2203
427	GCGAGCC A GAGGGCCC	429	GGGCCCUC CUGAUGAG X CGAA IGGCUCGC	2204
428	CAGAGGGC C CGAAGGCC	430	GGCCUUCG CUGAUGAG X CGAA ICCCUCUG	2205
435	AGAGGGCC C GAAGGCCG	431	CGGCCUUC CUGAUGAG X CGAA IGCCCUCU	2206
436	CCGAAGGC C GGGGCCCA	432	UGGGCCCC CUGAUGAG X CGAA ICCUUCGG	2207
443	GCCGGGGC C CACCAUGG	433	CCAUGGUG CUGAUGAG X CGAA ICCCCGGC	2208
449	GCCGGGGC C CACCAUGG	4,33		

Table 19

			TOCOCCOC	2209
450	CCGGGGCC C ACCAUGGC	434	GCCAUGGU CUGAUGAG X CGAA IGCCCCGG	2210
451	CGGGGCCC A CCAUGGCC	435	GGCCAUGG CUGAUGAG X CGAA IGGCCCCG	2211
453	GGGCCCAC C AUGGCCCA	436	UGGGCCAU CUGAUGAG X CGAA IUGGGCCC	2212
454	GGCCCACC A UGGCCCAA	437	UUGGGCCA CUGAUGAG X CGAA IGUGGGCC	2212
459	ACCAUGGC C CAAGCCCU	438	AGGGCUUG CUGAUGAG X CGAA ICCAUGGU	2213
460	CCAUGGCC C AAGCCCUG	439	CAGGGCUU CUGAUGAG X CGAA IGCCAUGG	2214
461	CAUGGCCC A AGCCCUGC	440	GCAGGGCU CUGAUGAG X CGAA IGGCCAUG	
465	GCCCAAGC C CUGCCCUG	441	CAGGGCAG CUGAUGAG X CGAA ICUUGGGC	2216
466	CCCAAGCC C UGCCCUGG	442	CCAGGGCA CUGAUGAG X CGAA IGCUUGGG	2217
467	CCAAGCCC U GCCCUGGC	443	GCCAGGGC CUGAUGAG X CGAA IGGCUUGG	2218
470	AGCCCUGC C CUGGCUCC	444	GGAGCCAG CUGAUGAG X CGAA ICAGGGCU	2219
471	GCCCUGCC C UGGCUCCU	445	AGGAGCCA CUGAUGAG X CGAA IGCAGGGC	2220
472	CCCUGCCC U GGCUCCUG	446	CAGGAGCC CUGAUGAG X CGAA IGGCAGGG	2221
476	GCCCUGGC U CCUGCUGU	447	ACAGCAGG CUGAUGAG X CGAA ICCAGGGC	2222
478	CCUGGCUC C UGCUGUGG	448	CCACAGCA CUGAUGAG X CGAA IAGCCAGG	2223
479	CUGGCUCC U GCUGUGGA	449	UCCACAGC CUGAUGAG X CGAA IGAGCCAG	2224
482	GCUCCUGC U GUGGAUGG	450	CCAUCCAC CUGAUGAG X CGAA ICAGGAGC	2225
503	GGGAGUGC U GCCUGCCC	451	GGGCAGGC CUGAUGAG X CGAA ICACUCCC	2226
506	AGUGCUGC C UGCCCACG	452	CGUGGGCA CUGAUGAG X CGAA ICAGCACU	2227
507	GUGCUGCC U GCCCACGG	453	CCGUGGGC CUGAUGAG X CGAA IGCAGCAC	2228
510	CUGCCUGC C CACGGCAC	454	GUGCCGUG CUGAUGAG X CGAA ICAGGCAG	2229
511	UGCCUGCC C ACGGCACC	455	GGUGCCGU CUGAUGAG X CGAA IGCAGGCA	2230
512	GCCUGCCC A CGGCACCC	456	GGGUGCCG CUGAUGAG X CGAA IGGCAGGC	2231
517	CCCACGGC A CCCAGCAC	457	GUGCUGGG CUGAUGAG X CGAA ICCGUGGG	2232
519	CACGGCAC C CAGCACGG	458	CCGUGCUG CUGAUGAG X CGAA IUGCCGUG	2233
520	ACGGCACC C AGCACGGC	459	GCCGUGCU CUGAUGAG X CGAA IGUGCCGU	2234
521	CGGCACCC A GCACGGCA	460	UGCCGUGC CUGAUGAG X CGAA IGGUGCCG	2235
524	CACCCAGC A CGGCAUCC	461	GGAUGCCG CUGAUGAG X CGAA ICUGGGUG	2236
529	AGCACGGC A UCCGGCUG	462	CAGCCGGA CUGAUGAG X CGAA ICCGUGCU	2237
532	ACGCAUC C GGCUGCCC	463	GGGCAGCC CUGAUGAG X CGAA IAUGCCGU	2238
536	CAUCOGGC U GCCCCUGC	464	GCAGGGGC CUGAUGAG X CGAA ICCGGAUG	2239
539	CCGGCUGC C CCUGCGCA	465	UGCGCAGG CUGAUGAG X CGAA 1CAGCCGG	2240
540	CGGCUGCC C CUGCGCAG	466	CUGCGCAG CUGAUGAG X CGAA IGCAGCCG	2241
541	GGCUGCCC C UGCGCAGC	467	GCUGCGCA CUGAUGAG X CGAA IGGCAGCC	2242
542	GCUGCCCC U GCGCAGCG	468	CGCUGCGC CUGAUGAG X CGAA IGGGCAGC	2243
547	CCCUGCGC A GCGGCCUG	469	CAGGCCGC CUGAUGAG X CGAA ICGCAGGG	2244
553	GCAGCGGC C UGGGGGGC	470	GCCCCCCA CUGAUGAG X CGAA ICCGCUGC	2245
553	CAGCGGCC U GGGGGGCG	471	CGCCCCC CUGAUGAG X CGAA IGCCGCUG	2246
564	GGGGGCGC C CCCCUGGG	472	CCCAGGGG CUGAUGAG X CGAA ICGCCCCC	2247
565	GGGGCGCC C CCCUGGGG	473	CCCCAGGG CUGAUGAG X CGAA IGCGCCCC	2248
566	GGGCGCCC C CCUGGGGC	474	GCCCCAGG CUGAUGAG X CGAA IGGCGCCC	2249
567	GGCGCCC C CUGGGGCU	475	AGCCCCAG CUGAUGAG X CGAA IGGGCGCC	2250
568	GCGCCCCC C UGGGGCUG	476	CAGCCCCA CUGAUGAG X CGAA IGGGGCGC	2251
569	CGCCCCC U GGGGCUGC	477	GCAGCCCC CUGAUGAG X CGAA IGGGGGCG	2252
	CCUGGGGC U GCGGCUGC	478	GCAGCCGC CUGAUGAG X CGAA ICCCCAGG	2253
575	GCUGGGGC U GCCCCGGG	479	CCCGGGGC CUGAUGAG X CGAA ICCGCAGC	2254
581	GCGGCUGC C CCGGGAGA	480	UCUCCCGG CUGAUGAG X CGAA ICAGCCGC	2255
584	CGGCUGC C CCGGGAGAC	481	GUCUCCCG CUGAUGAG X CGAA IGCAGCCG	2256
585	GGCUGCC C CGGGAGACC	482	GGUCUCCC CUGAUGAG X CGAA IGGCAGCC	2257
586	CGGGAGAC C GACGAAGA	483	UCUUCGUC CUGAUGAG X CGAA IUCUCCCG	2258
594		483	GCUCCUCG CUGAUGAG X CGAA ICUCUUCG	2259
605	CGAAGAGC C CGAGGAGC	484	GCCCCCC CTGLICAN II CGILL	

Table 19

		.05	GGCUCCUC CUGAUGAG X CGAA IGCUCUUC	2260
606	GAAGAGCC C GAGGAGCC	485	UCCGGCCG CUGAUGAG X CGAA ICUCCUCG	2251
614	CGAGGAGC C CGGCCGGA	486	CUCCGGCC CUGAUGAG X CGAA IGCUCCUC	2262
615	GAGGAGCC C GGCCGGAG		GCCCUCC CUGAUGAG X CGAA ICCGGGCU	2263
619	AGCCCGGC C GGAGGGGC	488	CACAAAGC CUGAUGAG X CGAA ICCCCUCC	2264
628	GGAGGGGC A GCUUUGUG	489	CUCCACAA CUGAUGAG X CGAA ICUGCCCC	2265
631	GGGGCAGC U UUGUGGAG	490	CCUCAGGU CUGAUGAG X CGAA IUCCACCA	2266
649	UGGUGGAC A ACCUGAGG	491	GCCCUCA CUGAUGAG X CGAA IUUGUCCA	2267
652	UGGACAAC C UGAGGGGC	492		2268
653	GGACAACC U GAGGGGCA	493	UGCCCCUC CUGAUGAG X CGAA IGUUGUCC	2269
661	UGAGGGC A AGUCGGGG	494	CCCCGACU CUGAUGAG X CGAA ICCCCUCA	2270
671	GUCGGGGC A GGGCUACU	495	AGUAGCCC CUGAUGAG X CGAA ICCCCGAC	2271
676	GGCAGGGC U ACUACGUG	496	CACGUAGU CUGAUGAG X CGAA ICCCUGCC	
679	AGGGCUAC U ACGUGGAG	497	CUCCACGU CUGAUGAG X CGAA IUAGCCCU	2272
693	GAGAUGAC C GUGGGCAG	498	CUGCCCAC CUGAUGAG X CGAA IUCAUCUC	
700	CCGUGGGC A GCCCCCCG	499	CGGGGGGC CUGAUGAG X CGAA ICCCACGG	2274
703	UGGGCAGC C CCCCGCAG	500	CUGCGGGG CUGAUGAG X CGAA ICUGCCCA	2275
704	GGGCAGCC C CCCGCAGA	501	UCUGCGGG CUGAUGAG X CGAA IGCUGCCC	2276
705	GGCAGCCC C CCGCAGAC	502	GUCUGCGG CUGAUGAG X CGAA IGGCUGCC	2277
706	GCAGCCCC C CGCAGACG	503	CGUCUGCG CUGAUGAG X CGAA IGGGCUGC	2278
707	CAGCCCCC C GCAGACGC	504	GCGUCUGC CUGAUGAG X CGAA IGGGGCUG	2279
710	CCCCCCGC A GACGCUCA	505	UGAGCGUC CUGAUGAG X CGAA ICGGGGGG	2280
716	GCAGACGC U CAACAUCC	506	GGAUGUUG CUGAUGAG X CGAA ICGUCUGC	2281
718	AGACGCUC A ACAUCCUG	507	CAGGAUGU CUGAUGAG X CGAA IAGCGUCU	2282
721	CGCUCAAC A UCCUGGUG	508	CACCAGGA CUGAUGAG X CGAA IUUGAGCG	2283
724	UCAACAUC C UGGUGGAU	509	AUCCACCA CUGAUGAG X CGAA IAUGUUGA	2284
725	CAACAUCC U GGUGGAUA	510	UAUCCACC CUGAUGAG X CGAA IGAUGUUG	2285
735	GUGGAUAC A GGCAGCAG	511	CUGCUGCC CUGAUGAG X CGAA IUAUCCAC	2286
739	AUACAGGC A GCAGUAAC	512	GUUACUGC CUGAUGAG X CGAA ICCUGUAU	2287
742	CAGGCAGC A GUAACUUU	513	AAAGUUAC CUGAUGAG X CGAA ICUGCCUG	2288
748	GCAGUAAC U UUGCAGUG	514	CACUGCAA CUGAUGAG X CGAA IUUACUGC	2289
753	AACUUUGC A GUGGGUGC	515	GCACCCAC CUGAUGAG X CGAA ICAAAGUU	2290
762	GUGGGUGC U GCCCCCCA	516	UGGGGGC CUGAUGAG X CGAA ICACCCAC	2291
765	GGUGCUGC C CCCCACCC	517	GGGUGGGG CUGAUGAG X CGAA ICAGCACC	2292
766	GUGCUGCC C CCCACCCC	518	GGGGUGGG CUGAUGAG X CGAA IGCAGCAC	2293
767	UGCUGCCC C CCACCCCU	519	AGGGGUGG CUGAUGAG X CGAA IGGCAGCA	2294
768	GCUGCCCC C CACCCCUU	520	AAGGGGUG CUGAUGAG X CGAA IGGGCAGC	2295
769	CUGCCCCC C ACCCCUUC	521	GAAGGGGU CUGAUGAG X CGAA IGGGGCAG	2296
770	UGCCCCCC A CCCCUUCC	522	GGAAGGG CUGAUGAG X CGAA IGGGGGCA	2297
772	CCCCCCAC C CCUUCCUG	523	CAGGAAGG CUGAUGAG X CGAA IUGGGGGG	2298
773	CCCCCACC C CUUCCUGC	524	GCAGGAAG CUGAUGAG X CGAA IGUGGGGG	2299
774	CCCCACCC C UUCCUGCA	525	UGCAGGAA CUGAUGAG X CGAA IGGUGGGG	2300
775	CCCACCCC U UCCUGCAU	526	AUGCAGGA CUGAUGAG X CGAA IGGGUGGG	2301
778	ACCCCUUC C UGCAUCGC	527	GCGAUGCA CUGAUGAG X CGAA IAAGGGGU	2302
779	CCCCUUCC U GCAUCGCU	528	AGCGAUGC CUGAUGAG X CGAA IGAAGGGG	2303
782	CUUCCUGC A UCGCUACU	529	AGUAGCGA CUGAUGAG X CGAA ICAGGAAG	2304
787	UGCAUCGC U ACUACCAG	530	CUGGUAGU CUGAUGAG X CGAA ICGAUGCA	2305
790	AUCGCUAC U ACCAGAGG	531	CCUCUGGU CUGAUGAG X CGAA IUAGCGAU	2306
	GCUACUAC C AGAGGCAG	532	CUGCCUCU CUGAUGAG X CGAA IUAGUAGC	2307
793	CUACUACC A GAGGCAGC	533	GCUGCCUC CUGAUGAG X CGAA IGUAGUAG	2308
794	CCAGAGGC A GCUGUCCA	534	UGGACAGC CUGAUGAG X CGAA ICCUCUGG	2309
800	GAGGCAGC U GUCCAGCA	535	UGCUGGAC CUGAUGAG X CGAA ICUGCCUC	2310
803	GAGGCAGC U GUCCAGCA	1 333	00000011	

Table 19

				2211
807	CAGCUGUC C AGCACAUA	536	UAUGUGCU CUGAUGAG X CGAA IACAGCUG	2311
808	AGCUGUCC A GCACAUAC	537	GUAUGUGC CUGAUGAG X CGAA IGACAGCU	2312
811	UGUCCAGC A CAUACCGG	538	CCGGUAUG CUGAUGAG X CGAA ICUGGACA	
813	UCCAGCAC A UACCGGGA	539	UCCCGGUA CUGAUGAG X CGAA IUGCUGGA	2314
817	GCACAUAC C GGGACCUC	540	GAGGUCCC CUGAUGAG X CGAA IUAUGUGC	
823	ACCGGGAC C UCCGGAAG	541	CUUCCGGA CUGAUGAG X CGAA IUCCCGGU	2316
824	CCGGGACC U CCGGAAGG	542	CCUUCCGG CUGAUGAG X CGAA IGUCCCGG	2317
826	GGGACCUC C GGAAGGGU	543	ACCCUUCC CUGAUGAG X CGAA IAGGUCCC	2318
845	GUAUGUGC C CUACACCC	544	GGGUGUAG CUGAUGAG X CGAA ICACAUAC	2319
846	UAUGUGCC C UACACCCA	545	UGGGUGUA CUGAUGAG X CGAA IGCACAUA	2320
847	AUGUGCCC U ACACCCAG	546	CUGGGUGU CUGAUGAG X CGAA IGGCACAU	2321
850	UGCCCUAC A CCCAGGGC	547	GCCCUGGG CUGAUGAG X CGAA IUAGGGCA	2322
852	CCCUACAC C CAGGGCAA	548	UUGCCCUG CUGAUGAG X CGAA 1UGUAGGG	2323
853	CCUACACC C AGGGCAAG	549	CUUGCCCU CUGAUGAG X CGAA IGUGUAGG	2324
854	CUACACCC A GGGCAAGU	550	ACUUGCCC CUGAUGAG X CGAA IGGUGUAG	2325
859	CCCAGGGC A AGUGGGAA	551	UUCCCACU CUGAUGAG X CGAA ICCCUGGG	2326
875	AGGGGAGC U GGGCACCG	552	CGGUGCCC CUGAUGAG X CGAA ICUCCCCU	2327
880	AGCUGGGC A CCGACCUG	553	CAGGUCGG CUGAUGAG X CGAA ICCCAGCU	2328
882	CUGGGCAC C GACCUGGU	554	ACCAGGUC CUGAUGAG X CGAA IUGCCCAG	2329
886	GCACCGAC C UGGUAAGC	555	GCUUACCA CUGAUGAG X CGAA IUCGGUGC	2330
887	CACCGACC U GGUAAGCA	556	UGCUUACC CUGAUGAG X CGAA IGUCGGUG	2331
895	UGGUAAGC A UCCCCCAU	557	AUGGGGGA CUGAUGAG X CGAA ICUUACCA	2332
898	UAAGCAUC C CCCAUGGC	558	GCCAUGGG CUGAUGAG X CGAA IAUGCUUA	2333
899	AAGCAUCC C CCAUGGCC	559	GGCCAUGG CUGAUGAG X CGAA IGAUGCUU	2334
900	AGCAUCCC C CAUGGCCC	560	GGGCCAUG CUGAUGAG X CGAA IGGAUGCU	2335
901	GCAUCCCC C AUGGCCCC	561	GGGGCCAU CUGAUGAG X CGAA IGGGAUGC	2336
902	CAUCCCCC A UGGCCCCA	562	UGGGGCCA CUGAUGAG X CGAA IGGGGAUG	2337
907	CCCAUGGC C CCAACGUC	563	GACGUUGG CUGAUGAG X CGAA ICCAUGGG	2338
908	CCAUGGCC C CAACGUCA	564	UGACGUUG CUGAUGAG X CGAA IGCCAUGG	2339
909	CAUGGCCC C AACGUCAC	565	GUGACGUU CUGAUGAG X CGAA IGGCCAUG	2340
910	AUGGCCCC A ACGUCACU	566	AGUGACGU CUGAUGAG X CGAA IGGGCCAU	2341
916	CCAACGUC A CUGUGCGU	567	ACGCACAG CUGAUGAG X CGAA IACGUUGG	2342
918	AACGUCAC U GUGCGUGC	568	GCACGCAC CUGAUGAG X CGAA IUGACGUU	2343
927	GUGCGUGC C AACAUUGC	569	GCAAUGUU CUGAUGAG X CGAA ICACGCAC	2344
927	UGCGUGCC A ACAUUGCU	570	AGCAAUGU CUGAUGAG X CGAA IGCACGCA	2345
931	GUGCCAAC A UUGCUGCC	571	GGCAGCAA CUGAUGAG X CGAA IUUGGCAC	2346
931	AACAUUGC U GCCAUCAC	572	GUGAUGGC CUGAUGAG X CGAA ICAAUGUU	2347
939	AIRIGCUGC C AUCACUGA	573	UCAGUGAU CUGAUGAG X CGAA ICAGCAAU	2348
939	UUGCUGCC A UCACUGAA	574	UUCAGUGA CUGAUGAG X CGAA IGCAGCAA	2349
940	CUGCCAUC A CUGAAUCA	575	UGAUUCAG CUGAUGAG X CGAA IAUGGCAG	2350
943	GCCAUCAC U GAAUCAGA	576	UCUGAUUC CUGAUGAG X CGAA IUGAUGGC	2351
951	ACUGAAUC A GACAAGUU	577	AACUUGUC CUGAUGAG X CGAA IAUUCAGU	2352
951	AAUCAGAC A AGUUCUUC	578	GAAGAACU CUGAUGAG X CGAA IUCUGAUU	2353
961	ACAAGUUC U UCAUCAAC	579	GUUGAUGA CUGAUGAG X CGAA IAACUUGU	2354
	AGUUCUUC A UCAACGGC	580	GCCGUUGA CUGAUGAG X CGAA IAAGAACU	2355
964	UCUUCAUC A ACGGCUCC	581	GGAGCCGU CUGAUGAG X CGAA IAUGAAGA	2356
	UCAACGGC U CCAACUGG	582	CCAGUUGG CUGAUGAG X CGAA ICCGUUGA	2357
973	AACGGCUC C AACUGGGA	583	UCCCAGUU CUGAUGAG X CGAA IAGCCGUU	2358
975	ACGGCUCC A ACUGGGAA	584	UUCCCAGU CUGAUGAG X CGAA IGAGCCGU	2359
976		585	GCCUUCCC CUGAUGAG X CGAA IUUGGAGC	2360
979		586	CCCCAGGA CUGAUGAG X CGAA ICCUUCCC	2361
988	GGGAAGGC A UCCUGGCG			

Table 19

		587	CAGCCCCA CUGAUGAG X CGAA IAUGCCUU	2362
991	AAGGCAUC C UGGGGCUG	588	CCAGCCCC CUGAUGAG X CGAA IGAUGCCU	2363
992	AGGCAUCC U GGGGCUGG	589	CAUAGGCC CUGAUGAG X CGAA ICCCCAGG	2364
998	CCUGGGC U GGCCUAUG	590	UCAGCAUA CUGAUGAG X CGAA ICCAGCCC	2365
1002	GGGCUGGC C UAUGCUGA	591	CUCAGCAU CUGAUGAG X CGAA IGCCAGCC	2366
1003	GGCUGGCC U AUGCUGAG		GCAAUCUC CUGAUGAG X CGAA ICAUAGGC	2367
1008	GCCUAUGC U GAGALIUGC	592	UCAGGCCU CUGAUGAG X CGAA ICAAUCUC	2368
1017	GAGAUUGC C AGGCCUGA	593	GUCAGGCC CUGAUGAG X CGAA IGCAAUCU	2369
1018	AGAUUGCC A GGCCUGAC	594	AGUCGUCA CUGAUGAG X CGAA ICCUGGCA	2370
1022	UGCCAGGC C UGACGACU	595	GAGUCGUC CUGAUGAG X CGAA IGCCUGGC	2371
1023	GCCAGGCC U GACGACUC	596	CUCCAGGG CUGAUGAG X CGAA IUCGUCAG	2372
1030	CUGACGAC U CCCUGGAG	597	GGCUCCAG CUGAUGAG X CGAA IAGUCGUC	2373
1032	GACGACUC C CUGGAGCC	598	AGGCUCCA CUGAUGAG X CGAA IAGUCGU	2374
1033	ACGACUCC C UGGAGCCU	599	AAGGCUCCA CUGAUGAG X CGAA IGAGUCG	2375
1034	CGACUCCC U GGAGCCUU	600	CAAAGAAA CUGAUGAG X CGAA ICUCCAGG	2376
1040	CCUGGAGC C UUUCUUUG	601	UCAAAGAA CUGAUGAG X CGAA ICUCCAG	2377
1041	CUGGAGCC U UUCUUUGA	602		2378
1045	AGCCUUUC U UUGACUCU	603	AGAGUCAA CUGAUGAG X CGAA IAAAGGCU	2379
1051	UCUUUGAC U CUCUGGUA	604	UACCAGAG CUGAUGAG X CGAA IUCAAAGA	2380
1053	UUUGACUC U CUGGUAAA	605	UUUACCAG CUGAUGAG X CGAA IAGUCAAA	2381
1055	UGACUCUC U GGUAAAGC	606	GCUUUACC CUGAUGAG X CGAA IAGAGUCA	2382
1064	GGUAAAGC A GACCCACG	607	CGUGGGUC CUGAUGAG X CGAA ICUUUACC	2383
1068	AAGCAGAC C CACGUUCC	608	GGAACGUG CUGAUGAG X CGAA IUCUGCUU	2384
1069	AGCAGACC C ACGUUCCC	609	GGGAACGU CUGAUGAG X CGAA IGUCUGCU	2385
1070	GCAGACCC A CGUUCCCA	610	UGGGAACG CUGAUGAG X CGAA IGGUCUGC	2386
1076	CCACGUUC C CAACCUCU	611	AGAGGUUG CUGAUGAG X CGAA IAACGUGG	2387
1077	CACGUUCC C AACCUCUU	612	AAGAGGUU CUGAUGAG X CGAA IGAACGUG	2388
1078	ACGUUCCC A ACCUCUUC	613	GAAGAGGU CUGAUGAG X CGAA IGGAACGU	2389
1081	UUCCCAAC C UCUUCUCC	614	GGAGAAGA CUGAUGAG X CGAA IUUGGGAA	2390
1082	UCCCAACC U CUUCUCCC	615	GGGAGAAG CUGAUGAG X CGAA IGUUGGGA	2391
1084	CCAACCUC U UCUCCCUG	616	CAGGGAGA CUGAUGAG X CGAA IAGGUUGG	2391
1087	ACCUCUUC U CCCUGCAG	617	CUGCAGGG CUGAUGAG X CGAA IAAGAGGU	2392
1089	CUCUUCUC C CUGCAGCU	618	AGCUGCAG CUGAUGAG X CGAA IAGAAGAG	2393
1090	UCUUCUCC C UGCAGCUU	619	AAGCUGCA CUGAUGAG X CGAA IGAGAAGA	2394
1091	CUUCUCCC U GCAGCUUU	620	AAAGCUGC CUGAUGAG X CGAA IGGAGAAG	2396
1094	CUCCCUGC A GCUUUGUG	621	CACAAAGC CUGAUGAG X CGAA ICAGGGAG	2396
1097	CCUGCAGC U UUGUGGUG	622	CACCACAA CUGAUGAG X CGAA ICUGCAGG	2398
1107	UGUGGUGC U GGCUUCCC	623	GGGAAGCC CUGAUGAG X CGAA ICACCACA	2398
1111	GUGCUGGC U UCCCCCUC	624	GAGGGGGA CUGAUGAG X CGAA ICCAGCAC	2400
1114	CUGGCUUC C CCCUCAAC	625	GUUGAGGG CUGAUGAG X CGAA TAAGCCAG	2400
1115	UGGCUUCC C CCUCAACC	626	GGUUGAGG CUGAUGAG X CGAA IGAAGCCA	2401
1116	GGCUUCCC C CUCAACCA	627	UGGUUGAG CUGAUGAG X CGAA IGGAAGCC	2402
1117	GCUUCCCC C UCAACCAG	628	CUGGUUGA CUGAUGAG X CGAA IGGGAAGC	2403
1118	CUUCCCCC U CAACCAGU	629	ACUGGUUG CUGAUGAG X CGAA IGGGGAAG	2404
1120	UCCCCCUC A ACCAGUCU	630	AGACUGGU CUGAUGAG X CGAA IAGGGGGA	
1123	CCCUCAAC C AGUCUGAA	631	UUCAGACU CUGAUGAG X CGAA IUUGAGGG	2406
1124	CCUCAACC A GUCUGAAG	632	CUUCAGAC CUGAUGAG X CGAA IGUUGAGG	2407
1128	AACCAGUC U GAAGUGCU	633	AGCACUUC CUGAUGAG X CGAA IACUGGUU	2408
1136	UGAAGUGC U GGCCUCUG	634	CAGAGGCC CUGAUGAG X CGAA ICACUUCA	2409
1140	GUGCUGGC C UCUGUCGG	635	CCGACAGA CUGAUGAG X CGAA ICCAGCAC	2410
1141	UGCUGGCC U CUGUCGGA	636	UCCGACAG CUGAUGAG X CGAA IGCCAGCA	2411
1143	CUGGCCUC U GUCGGAGG	637	CCUCCGAC CUGAUGAG X CGAA IAGGCCAG	2412

Table 19

			Tarana a sanagara	2413
1156	GAGGGAGC A UGAUCAUU	638	AAUGAUCA CUGAUGAG X CGAA ICUCCCUC	2414
1162	GCAUGAUC A UUGGAGGU	639	ACCUCCAA CUGAUGAG X CGAA IAUCAUGC	2415
1177	GUAUCGAC C ACUCGCUG	640	CAGCGAGU CUGAUGAG X CGAA IUCGAUAC	2416
1178	UAUCGACC A CUCGCUGU	641	ACAGCGAG CUGAUGAG X CGAA IGUCGAUA	2417
1180	UCGACCAC U CGCUGUAC	642	GUACAGCG CUGAUGAG X CGAA IUGGUCGA	2417
1184	CCACUCGC U GUACACAG	643	CUGUGUAC CUGAUGAG X CGAA ICGAGUGG	2418
1189	CGCUGUAC A CAGGCAGU	644	ACUGCCUG CUGAUGAG X CGAA IUACAGCG	
1191	CUGUACAC A GGCAGUCU	645	AGACUGCC CUGAUGAG X CGAA IUGUACAG	2420
1195	ACACAGGC A GUCUCUGG	646	CCAGAGAC CUGAUGAG X CGAA ICCUGUGU	2421
1199	AGGCAGUC U CUGGUAUA	647	UAUACCAG CUGAUGAG X CGAA IACUGCCU	2422
1201	GCAGUCUC U GGUAUACA	648	UGUAUACC CUGAUGAG X CGAA IAGACUGC	2423
1209	UGGUAUAC A CCCAUCCG	649	CGGAUGGG CUGAUGAG X CGAA IUAUACCA	2424
1211	GUAUACAC C CAUCCGGC	650	GCCGGAUG CUGAUGAG X CGAA IUGUAUAC	2425
1211	UAUACACC C AUCCGGCG	651	CGCCGGAU CUGAUGAG X CGAA IGUGUAUA	2426
1213	AUACACCC A UCCGGCGG	652	CCGCCGGA CUGAUGAG X CGAA IGGUGUAU	2427
1215	CACCCAUC C GGCGGGAG	653	CUCCOGCC CUGAUGAG X CGAA IAUGGGUG	2428
1243	AGGUGAUC A UUGUGCGG	654	CCGCACAA CUGAUGAG X CGAA IAUCACCU	2429
1243	UGGAGAUC A AUGGACAG	655	CUGUCCAU CUGAUGAG X CGAA IAUCUCCA	2430
	CAAUGGAC A GGAUCUGA	656	UCAGAUCC CUGAUGAG X CGAA IUCCAUUG	2431
1268	ACAGGAUC U GAAAAUGG	657	CCAUUUUC CUGAUGAG X CGAA IAUCCUGU	2432
1274	AAAUGGAC U GCAAGGAG	658	CUCCUUGC CUGAUGAG X CGAA IUCCAUUU	2433
1285	UGGACUGC A AGGAGUAC	659	GUACUCCU CUGAUGAG X CGAA ICAGUCCA	2434
1288	AGGAGUAC A ACUAUGAC	660	GUCAUAGU CUGAUGAG X CGAA IUACUCCU	2435
1297	AGUACAAC U AUGACAAG	661	CUUGUCAU CUGAUGAG X CGAA IUUGUACU	2436
1300		662	AAUGCUCU CUGAUGAG X CGAA IUCAUAGU	2437
1306	ACUAUGAC A AGAGCAUU	663	GUCCACAA CUGAUGAG X CGAA ICUCUUGU	2438
1312	ACAAGAGC A UUGUGGAC	664	GGUGCCAC CUGAUGAG X CGAA IUCCACAA	2439
1321	UUGUGGAC A GUGGCACC	665	GUUGGUGG CUGAUGAG X CGAA ICCACUGU	2440
1327	ACAGUGGC A CCACCAAC	666	AGGUUGGU CUGAUGAG X CGAA IUGCCACU	2441
1329	AGUGGCAC C ACCAACCU	667	AAGGUUGG CUGAUGAG X CGAA IGUGCCAC	2442
1330	GUGGCACC A CCAACCUU	668	CGAAGGUU CUGAUGAG X CGAA IUGGUGCC	2443
1332	GGCACCAC C AACCUUCG	669	ACGAAGGU CUGAUGAG X CGAA IGUGGUGC	2444
1333	GCACCACC A ACCUUCGU	670	CAAACGAA CUGAUGAG X CGAA IUUGGUGG	2445
1336	CCACCAAC C UUCGUUUG	4	GCAAACGA CUGAUGAG X CGAA IGUUGGUG	2446
1337	CACCAACC U UCGUUUGC	671	CUUUCUUG CUGAUGAG X CGAA ICAAACGA	2447
1346	UCGUUUGC C CAAGAAAG	672	ACUUUCUU CUGAUGAG X CGAA IGCAAACG	2448
1347	CGUUUGCC C AAGAAAGU	673	CACUUCU CUGAUGAG X CGAA IGGCAAAC	2449
1348	GUUUGCCC A AGAAAGUG	674	CACODECS COORDERS II COLL	2450
1365	UUUGAAGC U GCAGUCAA	675	UUGACUGC CUGAUGAG X CGAA ICUUCAAA GAUUUGAC CUGAUGAG X CGAA ICAGCUUC	2451
1368	GAAGCUGC A GUCAAAUC	676	GAUGGAUU CUGAUGAG X CGAA TACUGCAG	2452
1372	CUGCAGUC A AAUCCAUC	677	GAUGGAOO COGADGAC II COILL	2453
1377	GUCAAAUC C AUCAAGGC	678	GCCUUGAU CUGAUGAG X CGAA IAUUUGAC	2454
1378	UCAAAUCC A UCAAGGCA	679	UGCCUUGA CUGAUGAG X CGAA IGAUUUGA	2455
1381	AAUCCAUC A AGGCAGCC	680	GGCUGCCU CUGAUGAG X CGAA IAUGGAUU	2455
1386	AUCAAGGC A GCCUCCUC	681		2457
1389	AAGGCAGC C UCCUCCAC	682	GUGGAGGA CUGAUGAG X CGAA ICUGCCUU	2457
1390	AGGCAGCC U CCUCCACG	683	CGUGGAGG CUGAUGAG X CGAA IGCUGCCU	2458
1392	GCAGCCUC C UCCACGGA	684	UCCGUGGA CUGAUGAG X CGAA IAGGCUGC	
1393	CAGCCUCC U CCACGGAG	685	CUCCGUGG CUGAUGAG X CGAA IGAGGCUG	2460
1395	GCCUCCUC C ACGGAGAA	686	UUCUCCGU CUGAUGAG X CGAA IAGGAGGC	2461
1396	CCUCCUCC A CGGAGAAG	687	CUUCUCCG CUGAUGAG X CGAA IGAGGAGG	2,462
1408		688	ACCAUCAG CUGAUGAG X CGAA IAACUUCU	2463

Table 19

			able 19	
1409	GAAGUUCC C UGAUGGUU	689	AACCAUCA CUGAUGAG X CGAA IGAACUUC	2464
1410	AAGUUCCC U GAUGGUUU	690	AAACCAUC CUGAUGAG X CGAA IGGAACUU	2465
1420	AUGGUUUC U GGCUAGGA	691	UCCUAGCC CUGAUGAG X CGAA IAAACCAU	2466
1424	UUUCUGGC U AGGAGAGC	692	GCUCUCCU CUGAUGAG X CGAA ICCAGAAA	2467
1433	AGGAGAGC A GCUGGUGU	693	ACACCAGC CUGAUGAG X CGAA ICUCUCCU	2468
1436	AGAGCAGC U GGUGUGCU	694	AGCACACC CUGAUGAG X CGAA ICUGCUCU	2469
1444	UGGUGUGC U GGCAAGCA	695	UGCUUGCC CUGAUGAG X CGAA ICACACCA	2470
1448	GUGCUGGC A AGCAGGCA	696	UGCCUGCU CUGAUGAG X CGAA ICCAGCAC	2471
1452	UGGCAAGC A GGCACCAC	697	GUGGUGCC CUGAUGAG X CGAA ICUUGCCA	2472
1456	AAGCAGGC A CCACCCCU	698	AGGGGUGG CUGAUGAG X CGAA ICCUGCUU	2473
1458	GCAGGCAC C ACCCCUUG	699	CAAGGGGU CUGAUGAG X CGAA IUGCCUGC	2474
1459	CAGGCACC A CCCCUUGG	700	CCAAGGGG CUGAUGAG X CGAA IGUGCCUG	2475
1461	GGCACCAC C CCUUGGAA	701	UUCCAAGG CUGAUGAG X CGAA IUGGUGCC	2476
1462	GCACCACC C CUUGGAAC	702	GUUCCAAG CUGAUGAG X CGAA IGUGGUGC	2477
1463	CACCACCC C UUGGAACA	703	UGUUCCAA CUGAUGAG X CGAA IGGUGGUG	2478
1464	ACCACCCC U UGGAACAU	704	AUGUUCCA CUGAUGAG X CGAA IGGGUGGU	2479
1471	CUUGGAAC A UUUUCCCA	705	UGGGAAAA CUGAUGAG X CGAA IUUCCAAG	2480
1477	ACAUUUUC C CAGUCAUC	706	GAUGACUG CUGAUGAG X CGAA IAAAAUGU	2481
_	CAUUUUCC C AGUCAUCU	707	AGAUGACU CUGAUGAG X CGAA IGAAAAUG	2482
1478	AUUUUUCCC A GUCAUCUC	708	GAGAUGAC CUGAUGAG X CGAA IGGAAAAU	2483
	UCCCAGUC A UCUCACUC	709	GAGUGAGA CUGAUGAG X CGAA IACUGGGA	2484
1483	CAGUCAUC U CACUCUAC	710	GUAGAGUG CUGAUGAG X CGAA IAUGACUG	2485
1486	GUCAUCUC A CUCUACCU	711	AGGUAGAG CUGAUGAG X CGAA IAGAUGAC	2486
1488	CAUCUCAC U CUACCUAA	712	UUAGGUAG CUGAUGAG X CGAA IUGAGAUG	2487
1490	UCUCACUC U ACCUAAUG	713	CAUTIAGGU CUGAUGAG X CGAA IAGUGAGA	2488
1492	CACUCUAC C UAAUGGGU	714	ACCCAUUA CUGAUGAG X CGAA IUAGAGUG	2489
1495	ACUCUACO U AAUGGGUG	715	CACCCAUU CUGAUGAG X CGAA IGUAGAGU	2490
1496	GAGGUUAC C AACCAGUC	716	GACUGGUU CUGAUGAG X CGAA IUAACCUC	2491
1512	AGGUUACC A ACCAGUCC	71.7	GGACUGGU CUGAUGAG X CGAA IGUAACCU	2492
	UUACCAAC C AGUCCUUC	718	GAAGGACU CUGAUGAG X CGAA IUUGGUAA	2493
1516	UACCAACC A GUCCUUCC	719	GGAAGGAC CUGAUGAG X CGAA IGUUGGUA	2494
1517	AACCAGUC C UUCCGCAU	720	AUGCGGAA CUGAUGAG X CGAA IACUGGUU	2495
1521	ACCAGUCC U UCCGCAUC	721	GAUGOGGA CUGAUGAG X CGAA IGACUGGU	2496
	AGUCCUUC C GCAUCACC	722	GGUGAUGC CUGAUGAG X CGAA IAAGGACU	2497
1525	CCUUCCGC A UCACCAUC	723	GAUGGUGA CUGAUGAG X CGAA ICGGAAGG	2498
1528	UCOGCAUC A CCAUCCUU	724	AAGGAUGG CUGAUGAG X CGAA IAUGCGGA	2499
1531	CGCAUCAC C AUCCUUCC	725	GGAAGGAU CUGAUGAG X CGAA IUGAUGCG	2500
1533	GCAUCACC A UCCUUCCG	726	CGGAAGGA CUGAUGAG X CGAA IGUGAUGC	2501
1534	UCACCAUC C UUCCGCAG	727	CUGCGGAA CUGAUGAG X CGAA IAUGGUGA	2502
1537	CACCAUCC U UCCGCAGC	728	GCUGCGGA CUGAUGAG X CGAA IGAUGGUG	2503
	CAUCAUCE O UECGCAGE CAUCCUUC C GCAGCAAU	729	AUUGCUGC CUGAUGAG X CGAA IAAGGAUG	2504
1541	CCUUCCGC A GCAAUACC	730	GGUAUUGC CUGAUGAG X CGAA ICGGAAGG	2505
1544		731	GCAGGUAU CUGAUGAG X CGAA ICUGCGGA	2506
1547	UCCGCAGC A AUACCUGC	732	UGGCCGCA CUGAUGAG X CGAA IUAUUGCU	2507
1552	AGCAAUAC C UGCGGCCA	733	CUGGCCGC CUGAUGAG X CGAA IGUAUUGC	2508
1553	GCAAUACC U GCGGCCAG	733	CUUCCACU CUGAUGAG X CGAA ICCGCAGG	2509
1559	CCUGCGGC C AGUGGAAG	734	UCUUCCAC CUGAUGAG X CGAA IGCCGCAG	2510
1560	CUGCGGCC A GUGGAAGA		HIGGGACGU CUGAUGAG X CGAA ICCACAUC	2511
1575	GAUGUGGC C ACGUCCCA	736	UUGGGACGU CUGAUGAG X CGAA ICCACAUC	2512
1576	AUGUGGCC A CGUCCCAA	737	UCGUCUUG CUGAUGAG X CGAA IACGUGGC	2512
1581	GCCACGUC C CAAGACGA	738	GUCGUCUU CUGAUGAG X CGAA TACGUGGC	2514
1582	CCACGUCC C AAGACGAC	/39	GUCGUCUU CUGADGAG X CGAA IGACGOGG	1 232.

Table 19

1583	CACGUCCC A AGACGACU	740	AGUCGUCU CUGAUGAG X CGAA IGGACGUG	2515
1591	AAGACGAC U GUUACAAG	741	CUUGUAAC CUGAUGAG X CGAA IUCGUCUU	2516
1597	ACUGUUAC A AGUUUGCC	742	GGCAAACU CUGAUGAG X CGAA IUAACAGU	2517
1605	AAGUUUGC C AUCUCACA	743	UGUGAGAU CUGAUGAG X CGAA ICAAACUU	2518
1606	AGUUUGCC A UCUCACAG	744	CUGUGAGA CUGAUGAG X CGAA IGCAAACU	2519
1609	UUGCCAUC U CACAGUCA	745	UGACUGUG CUGAUGAG X CGAA IAUGGCAA	2520
1611	GCCAUCUC A CAGUCAUC	746	GAUGACUG CUGAUGAG X CGAA IAGAUGGC	2521
1613	CAUCUCAC A GUCAUCCA	747	UGGAUGAC CUGAUGAG X CGAA IUGAGAUG	2522
1617	UCACAGUC A UCCACGGG	748	CCCGUGGA CUGAUGAG X CGAA IACUGUGA	2523
1620	CAGUCAUC C ACGGGCAC	749	GUGCCCGU CUGAUGAG X CGAA IAUGACUG	2524
1621	AGUCAUCC A CGGGCACU	750	AGUGCCCG CUGAUGAG X CGAA IGAUGACU	2525
1627	CCACGGC A CUGUUAUG	751	CAUAACAG CUGAUGAG X CGAA ICCCGUGG	2526
1629	ACGGGCAC U GUUAUGGG	752	CCCAUAAC CUGAUGAG X CGAA IUGCCCGU	2527
1641	AUGGGAGC U GUUAUCAU	753	AUGAUAAC CUGAUGAG X CGAA ICUCCCAU	2528
1648	CUGUUAUC A UGGAGGGC	754	GCCCUCCA CUGAUGAG X CGAA TAUAACAG	2529
1657	UGGAGGGC U UCUACGUU	755	AACGUAGA CUGAUGAG X CGAA ICCCUCCA	2530
1660	AGGGCUUC U ACGUUGUC	756	GACAACGU CUGAUGAG X CGAA IAAGCCCU	2531
1669	ACGUUGUC U UUGAUCGG	757	CCGAUCAA CUGAUGAG X CGAA IACAACGU	2532
1680	GAUCGGGC C CGAAAACG	758	CGUUUUCG CUGAUGAG X CGAA ICCCGAUC	2533
1681	AUCGGGCC C GAAAACGA	759	UCGUUUUC CUGAUGAG X CGAA IGCCCGAU	2534
1696	GAAUUGGC U UUGCUGUC	760	GACAGCAA CUGAUGAG X CGAA ICCAAUUC	2535
1701	GGCUUUGC U GUCAGCGC	761	GCGCUGAC CUGAUGAG X CGAA ICAAAGCC	2536
1705	UUGCUGUC A GCGCUUGC	762	GCAAGCGC CUGAUGAG X CGAA IACAGCAA	2537
1710	GUCAGOGC U UGCCAUGU	763	ACAUGGCA CUGAUGAG X CGAA ICGCUGAC	2538
1714	GCGCUUGC C AUGUGCAC	764	GUGCACAU CUGAUGAG X CGAA ICAAGCGC	2539
1715	CGCUUGCC A UGUGCACG	765	CGUGCACA CUGAUGAG X CGAA IGCAAGCG	2540
1721	CCAUGUGC A CGAUGAGU	766	ACUCAUCG CUGAUGAG X CGAA ICACAUGG	2541
1732	AUGAGUUC A GGACGGCA	767	UGCCGUCC CUGAUGAG X CGAA IAACUCAU	2542
1740	AGGACGGC A GCGGUGGA	768	UCCACCGC CUGAUGAG X CGAA ICCGUCCU	2543
1753	UGGAAGGC C CUUUUGUC	769	GACAAAAG CUGAUGAG X CGAA ICCUUCCA	2544
1754	GGAAGGCC C UUUUGUCA	770	UGACAAAA CUGAUGAG X CGAA IGCCUUCC	2545
1755	GAAGGCCC U UUUGUCAC	771	GUGACAAA CUGAUGAG X CGAA IGGCCUUC	2546
1762	CUUUUGUC A CCUUGGAC	772	GUCCAAGG CUGAUGAG X CGAA IACAAAAG	2547
1764	UUUGUCAC C UUGGACAU	773	AUGUCCAA CUGAUGAG X CGAA IUGACAAA	2548
1765	UUGUCACC U UGGACAUG	774	CAUGUCCA CUGAUGAG X CGAA IGUGACAA	2549
1771	CCUUGGAC A UGGAAGAC	775	GUCUUCCA CUGAUGAG X CGAA IUCCAAGG	2550
1780	UGGAAGAC U GUGGCUAC	776	GUAGCCAC CUGAUGAG X CGAA IUCUUCCA	2551
1786	ACUGUGGC U ACAACAUU	777	AAUGUUGU CUGAUGAG X CGAA ICCACAGU	2552
1789	GUGGCUAC A ACAUUCCA	778	UGGAAUGU CUGAUGAG X CGAA IUAGCCAC	2553
1792	GCUACAAC A UUCCACAG	779	CUGUGGAA CUGAUGAG X CGAA IUUGUAGC	2554
1796	CAACAUUC C ACAGACAG	780	CUGUCUGU CUGAUGAG X CGAA IAAUGUUG	2555
1797	AACAUUCC A CAGACAGA	781	UCUGUCUG CUGAUGAG X CGAA IGAAUGUU	2556
1799	CAUUCCAC A GACAGAUG	782	CAUCUGUC CUGAUGAG X CGAA IUGGAAUG	2557
1803	CCACAGAC A GAUGAGUC	783	GACUCAUC CUGAUGAG X CGAA IUCUGUGG	2558
1812	GAUGAGUC A ACCCUCAU	784	AUGAGGU CUGAUGAG X CGAA IACUCAUC	2559
1815	GAGUCAAC C CUCAUGAC	785	GUCAUGAG CUGAUGAG X CGAA IUUGACUC	2560
1816	AGUCAACC C UCAUGACC	786	GGUCAUGA CUGAUGAG X CGAA IGUUGACU	2561
1817	GUCAACCC U CAUGACCA	787	UGGUCAUG CUGAUGAG X CGAA IGGUUGAC	2562
1819	CAACCCUC A UGACCAUA	788	UAUGGUCA CUGAUGAG X CGAA IAGGGUUG	2563
1824	CUCAUGAC C AUAGCCUA	789	UAGGCUAU CUGAUGAG X CGAA IUCAUGAG	2564
1825	UCAUGACC A UAGCCUAU	790	AUAGGCUA CUGAUGAG X CGAA IGUCAUGA	2565

Table 19

		,		
1830	ACCAUAGC C UAUGUCAU	791	AUGACAUA CUGAUGAG X CGAA ICUAUGGU	2566
1831	CCAUAGCC U AUGUCAUG	792	CAUGACAU CUGAUGAG X CGAA IGCUAUGG	2567
1837	CCUAUGUC A UGGCUGCC	793	GGCAGCCA CUGAUGAG X CGAA IACAUAGG	2568
1842	GUCAUGGC U GCCAUCUG	794	CAGAUGGC CUGAUGAG X CGAA ICCAUGAC	2569
1845	AUGGCUGC C AUCUGCGC	795	GCGCAGAU CUGAUGAG X CGAA ICAGCCAU	2570
1846	UGGCUGCC A UCUGCGCC	796	GGCGCAGA CUGAUGAG X CGAA IGCAGCCA	2571
1849	CUGCCAUC U GCGCCCUC	797	GAGGGCGC CUGAUGAG X CGAA IAUGGCAG	2572
1854	AUCUGCGC C CUCUUCAU	798	AUGAAGAG CUGAUGAG X CGAA ICGCAGAU	2573
1855	UCUGCGCC C UCUUCAUG	799	CAUGAAGA CUGAUGAG X CGAA IGCGCAGA	2574
1856	CUGCGCCC U CUUCAUGC	800	GCAUGAAG CUGAUGAG X CGAA IGGCGCAG	2575
1858	GCGCCCUC U UCAUGCUG	801	CAGCAUGA CUGAUGAG X CGAA IAGGGCGC	2576
1861	CCCUCUUC A UGCUGCCA	802	UGGCAGCA CUGAUGAG X CGAA IAAGAGGG	2577
1865	CUUCAUGC U GCCACUCU	803	AGAGUGGC CUGAUGAG X CGAA ICAUGAAG	2578
1868	CAUGCUGC C ACUCUGCC	804	GGCAGAGU CUGAUGAG X CGAA ICAGCAUG	2579
1869	AUGCUGCC A CUCUGCCU	805	AGGCAGAG CUGAUGAG X CGAA IGCAGCAU	2580
1871	GCUGCCAC U CUGCCUCA	806	UGAGGCAG CUGAUGAG X CGAA IUGGCAGC	2581
1873	UGCCACUC U GCCUCAUG	807	CAUGAGGC CUGAUGAG X CGAA IAGUGGCA	2582
1876	CACUCUGC C UCAUGGUG	808	CACCAUGA CUGAUGAG X CGAA ICAGAGUG	2583
1877	ACUCUGCC U CAUGGUGU	809	ACACCAUG CUGAUGAG X CGAA IGCAGAGU	2584
1879	UCUGCCUC A UGGUGUGU	810	ACACACCA CUGAUGAG X CGAA IAGGCAGA	2585
1889	GGUGUGUC A GUGGÇGCU	811	AGCGCCAC CUGAUGAG X CGAA IACACACC	2586
1897	AGUGGCGC U GCCUCCGC	812	GCGGAGGC CUGAUGAG X CGAA ICGCCACU	2587
1900	GGCGCUGC C UCCGCUGC	813	GCAGCGGA CUGAUGAG X CGAA ICAGCGCC	2588
1901	GCGCUGCC U CCGCUGCC	814	GGCAGCGG CUGAUGAG X CGAA IGCAGCGC	2589
1903	GCUGCCUC C GCUGCCUG	815	CAGGCAGC CUGAUGAG X CGAA IAGGCAGC	2590
1906	GCCUCCGC U GCCUGCGC	816	GCGCAGGC CUGAUGAG X CGAA ICGGAGGC	2591
1909	UCCGCUGC C UGCGCCAG	817	CUGGCGCA CUGAUGAG X CGAA ICAGCGGA	2592
1910	CCGCUGCC U GCGCCAGC	818	GCUGGCGC CUGAUGAG X CGAA IGCAGCGG	2593
1915	GCCUGCGC C AGCAGCAU	819	AUGCUGCU CUGAUGAG X CGAA ICGCAGGC	2594
1916	CCUGCGCC A GCAGCAUG	820	CAUGCUGC CUGAUGAG X CGAA IGCGCAGG	2595
1919	GCGCCAGC A GCAUGAUG	821	CAUCAUGC CUGAUGAG X CGAA ICUGGCGC	2596
1922	CCAGCAGC A UGAUGACU	822	AGUCAUCA CUGAUGAG X CGAA ICUGCUGG	2597
1930	AUGAUGAC U UUGCUGAU	823	AUCAGCAA CUGAUGAG X CGAA IUCAUCAU	2598
1935	GACUUUGC U GAUGACAU	824	AUGUCAUC CUGAUGAG X CGAA ICAAAGUC	2599
1942	CUGAUGAC A UCUCCCUG	825	CAGGGAGA CUGAUGAG X CGAA IUCAUCAG	2600
1945	AUGACAUC U CCCUGCUG	826	CAGCAGGG CUGAUGAG X CGAA IAUGUCAU	2601
1947	GACAUCUC C CUGCUGAA	827	UUCAGCAG CUGAUGAG X CGAA IAGAUGUC	2602
1948	ACAUCUCC C UGCUGAAG	828	CUUCAGCA CUGAUGAG X CGAA IGAGAUGU	2603
1949	CAUCUCCC U GCUGAAGU	829	ACUUCAGC CUGAUGAG X CGAA IGGAGAUG	2604
1952	CUCCCUGC U GAAGUGAG	830	CUCACUUC CUGAUGAG X CGAA ICAGGGAG	2605
1966	GAGGAGGC C CAUGGGCA	831	UGCCCAUG CUGAUGAG X CGAA ICCUCCUC	2606
1967	AGGAGGCC C AUGGGCAG	832	CUGCCCAU CUGAUGAG X CGAA IGCCUCCU	2607
1968	GGAGGCCC A UGGGCAGA	833	UCUGCCCA CUGAUGAG X CGAA IGGCCUCC	2608
1974	CCAUGGGC A GAAGAUAG	834	CUAUCUUC CUGAUGAG X CGAA ICCCAUGG	2609
1989	AGAGAUUC C CCUGGACC	835	GGUCCAGG CUGAUGAG X CGAA IAAUCUCU	2610
1990	GAGAUUCC C CUGGACCA	836	UGGUCCAG CUGAUGAG X CGAA IGAAUCUC	2611
1991	AGAUUCCC C UGGACCAC	837	GUGGUCCA CUGAUGAG X CGAA IGGAAUCU	2612
1992	GAUUCCCC U GGACCACA	838	UGUGGUCC CUGAUGAG X CGAA IGGGAAUC	2613
1997	CCCUGGAC C ACACCUCC	839	GGAGGUGU CUGAUGAG X CGAA IUCCAGGG	2614
1998	CCUGGACC A CACCUCCG	840	CGGAGGUG CUGAUGAG X CGAA IGUCCAGG	2615
2000	UGGACCAC A CCUCCGUG	841	CACGGAGG CUGAUGAG X CGAA IUGGUCCA	2616

Table 19

2002	GACCACAC C UCCGUGGU	842	ACCACGGA CUGAUGAG X CGAA IUGUGGUC	2617
2003	ACCACACC U CCGUGGUU	843	AACCACGG CUGAUGAG X CGAA IGUGUGGU	2618
2005	CACACCUC C GUGGUUCA	844	UGAACCAC CUGAUGAG X CGAA IAGGUGUG	2619
2013	CGUGGUUC A CUUUGGUC	845	GACCAAAG CUGAUGAG X CGAA IAACCACG	2620
2015	UGGUUCAC U UUGGUCAC	846	GUGACCAA CUGAUGAG X CGAA IUGAACCA	2621
2022	CUUUGGUC A CAAGUAGG	847	CCUACUUG CUGAUGAG X CGAA IACCAAAG	2622
2024	UUGGUCAC A AGUAGGAG	848	CUCCUACU CUGAUGAG X CGAA IUGACCAA	2623
2035	UAGGAGAC A CAGAUGGC	849	GCCAUCUG CUGAUGAG X CGAA IUCUCCUA	2624
2037	GGAGACAC A GAUGGCAC	850	GUGCCAUC CUGAUGAG X CGAA IUGUCUCC	2625
2044	CAGAUGGC A CCUGUGGC	851	GCCACAGG CUGAUGAG X CGAA ICCAUCUG	2626
2046	GAUGGCAC C UGUGGCCA	852	UGGCCACA CUGAUGAG X CGAA IUGCCAUC	2627
2047	AUGGCACC U GUGGCCAG	853	CUGGCCAC CUGAUGAG X CGAA IGUGCCAU	2628
2053	CCUGUGGC C AGAGCACC	854	GGUGCUCU CUGAUGAG X CGAA ICCACAGG	2629
2054	CUGUGGCC A GAGCACCU	855	AGGUGCUC CUGAUGAG X CGAA IGCCACAG	2630
2059	GCCAGAGC A CCUCAGGA	856	UCCUGAGG CUGAUGAG X CGAA ICUCUGGC	2631
2061	CAGAGCAC C UCAGGACC	857	GGUCCUGA CUGAUGAG X CGAA IUGCUCUG	2632
2062	AGAGCACC U CAGGACCC	858	GGGUCCUG CUGAUGAG X CGAA IGUGCUCU	2633
2062	AGCACCUC A GGACCCUC	859	GAGGGUCC CUGAUGAG X CGAA IAGGUGCU	2634
2069	CUCAGGAC C CUCCCCAC	860	GUGGGGAG CUGAUGAG X CGAA IUCCUGAG	2635
2070	UCAGGACC C UCCCCACC	861	GGUGGGGA CUGAUGAG X CGAA IGUCCUGA	2636
2071	CAGGACCC U CCCCACCC	862	GGGUGGGG CUGAUGAG X CGAA IGGUCCUG	2637
2073	GGACCCUC C CCACCCAC	863	GUGGGUGG CUGAUGAG X CGAA IAGGGUCC	2638
2074	GACCCUCC C CACCCACC	864	GGUGGGUG CUGAUGAG X CGAA IGAGGGUC	2639
2075	ACCCUCCC C ACCCACCA	865	UGGUGGGU CUGAUGAG X CGAA IGGAGGGU	2640
2076	CCCUCCCC A CCCACCAA	866	UUGGUGGG CUGAUGAG X CGAA IGGGAGGG	2641
2078	CUCCCCAC C CACCAAAU	867	AUUUGGUG CUGAUGAG X CGAA IUGGGGAG	2642
2079	UCCCCACC C ACCAAAUG	868	CAUUUGGU CUGAUGAG X CGAA IGUGGGGA	2643
2080	CCCCACCC A CCAAAUGC	869	GCAUUUGG CUGAUGAG X CGAA IGGUGGGG	2644
2082	CCACCCAC C AAAUGCCU	870	AGGCAUUU CUGAUGAG X CGAA IUGGGUGG	2645
2083	CACCCACC A AAUGCCUC	871	GAGGCAUU CUGAUGAG X CGAA IGUGGGUG	2646
2089	CCAAAUGC C UCUGCCUU	872	AAGGCAGA CUGAUGAG X CGAA ICAUUUGG	2647
2090	CAAAUGCC U CUGCCUUG	873	CAAGGCAG CUGAUGAG X CGAA IGCAUUUG	2648
2092	AAUGCCUC U GCCUUGAU	874	AUCAAGGC CUGAUGAG X CGAA IAGGCAUU	2649
2095	GCCUCUGC C UUGAUGGA	875	UCCAUCAA CUGAUGAG X CGAA ICAGAGGC	2650
2096	CCUCUGCC U UGAUGGAG	876	CUCCAUCA CUGAUGAG X CGAA IGCAGAGG	2651
2116	GAAAAGGC U GGCAAGGU	877	ACCUUGCC CUGAUGAG X CGAA ICCUUUUC	2652
2120	AGGCUGGC A AGGUGGGU	878	ACCCACCU CUGAUGAG X CGAA ICCAGCCU	2653
2131	GUGGGUUC C AGGGACUG	879	CAGUCCCU CUGAUGAG X CGAA IAACCCAC	2654
2132	UGGGUUCC A GGGACUGU	880	ACAGUCCC CUGAUGAG X CGAA IGAACCCA	2655
2138	CCAGGGAC U GUACCUGU	881	ACAGGUAC CUGAUGAG X CGAA IUCCCUGG	2656
2143	GACUGUAC C UGUAGGAA	882	UUCCUACA CUGAUGAG X CGAA IUACAGUC	2657
2144	ACUGUACC U GUAGGAAA	883	UUUCCUAC CUGAUGAG X CGAA IGUACAGU	2658
2154	UAGGAAAC A GAAAAGAG	884	CUCUUUUC CUGAUGAG X CGAA IUUUCCUA	2659
2174	AAAGAAGC A CUCUGCUG	885	CAGCAGAG CUGAUGAG X CGAA ICUUCUUU	2660
2176	AGAAGCAC U CUGCUGGC	886	GCCAGCAG CUGAUGAG X CGAA IUGCUUCU	2661
2178	AAGCACUC U GCUGGCGG	887	CCGCCAGC CUGAUGAG X CGAA IAGUGCUU	2662
2181	CACUCUGC U GGCGGGAA	888	UUCCCGCC CUGAUGAG X CGAA ICAGAGUG	2663
2193	GGGAAUAC U CUUGGUCA	889	UGACCAAG CUGAUGAG X CGAA IUAUUCCC	2664
2195	GAAUACUC U UGGUCACC	890	GGUGACCA CUGAUGAG X CGAA IAGUAUUC	2665
2201	UCUUGGUC A CCUCAAAU	891	AUUUGAGG CUGAUGAG X CGAA IACCAAGA	2666
2201	UUGGUCAC C UCAAAUUU	892	AAAUUUGA CUGAUGAG X CGAA IUGACCAA	2667
2203	ODGGGCAC C OCAMAGOO	1 332	1	

Table 19

2204	UGGUCACC U CAAAUUUA	893	UAAAUUUG CUGAUGAG X CGAA IGUGACCA	2668
2206	GUCACCUC A AAUUUAAG	894	CUUAAAUU CUGAUGAG X CGAA IAGGUGAC	2669
2226	GGAAAUUC U GCUGCUUG	895	CAAGCAGC CUGAUGAG X CGAA IAAUUUCC	2670
2229	AAUUCUGC U GCUUGAAA	896	UUUCAAGC CUGAUGAG X CGAA ICAGAAUU	2671
2232	UCUGCUGC U UGAAACUU	897	AAGUUUCA CUGAUGAG X CGAA ICAGCAGA	2672
2239	CUUGAAAC U UCAGCCCU	898	AGGGCUGA CUGAUGAG X CGAA IUUUCAAG	2673
2242	GAAACUUC A GCCCUGAA	899	UUCAGGGC CUGAUGAG X CGAA IAAGUUUC	2674
2245	ACUUCAGO C CUGAACOU	900	AGGUUCAG CUGAUGAG X CGAA ICUGAAGU	2675
2246	CUUCAGCC C UGAACCUU	901	AAGGUUCA CUGAUGAG X CGAA IGCUGAAG	2676
2247	UUCAGCCC U GAACCUUU	902	AAAGGUUC CUGAUGAG X CGAA IGGCUGAA	2677
2252	CCCUGAAC C UUUGUCCA	903	UGGACARA CUGAUGAG X CGAR IUUCAGGG	2678
2253	CCUGAACC U UUGUCCAC	904	GUGGACAA CUGAUGAG X CGAA IGUUCAGG	2679
2259	CCUUUGUC C ACCAUUCC	905	GGAAUGGU CUGAUGAG X CGAA IACAAAGG	2680
2260	CUUUGUCC A CCAUUCCU	906	AGGAAUGG CUGAUGAG X CGAA IGACAAAG	2681
2262	UUGUCCAC C AUUCCUUU	907	AAAGGAAU CUGAUGAG X CGAA IUGGACAA	2682
2263	UGUCCACC A UUCCUUUA	908	UAAAGGAA CUGAUGAG X CGAA IGUGGACA	2683
2267	CACCAUUC C UUUAAAUU	909	AAUUUAAA CUGAUGAG X CGAA IAAUGGUG	2684
2268	ACCAUUCC U UUAAAUUC	910	GAAUUUAA CUGAUGAG X CGAA IGAAUGGU	2685
2277	UUAAAUUC U CCAACCCA	911	UGGGUUGG CUGAUGAG X CGAA IAAUUUAA	2686
2279	AAAUUCUC C AACCCAAA	912	UUUGGGUU CUGAUGAG X CGAA IAGAAUUU	2687
2280	AAUUCUCC A ACCCAAAG	913	CUUUGGGU CUGAUGAG X CGAA IGAGAAUU	2688
2283	UCUCCAAC C CAAAGUAU	914	AUACUUUG CUGAUGAG X CGAA IUUGGAGA	2689
2284	CUCCAACC C AAAGUAUU	915	AAUACUUU CUGAUGAG X CGAA IGUUGGAG	2690
2285	UCCAACCC A AAGUAUUC	916	GAAUACUU CUGAUGAG X CGAA IGGUUGGA	2691
2294	AAGUAUUC U UCUUUUCU	917	AGAAAAGA CUGAUGAG X CGAA IAAUACUU	2692
2297	UAUUCUUC U UUUCUUAG	918	CUAAGAAA CUGAUGAG X CGAA IAAGAAUA	2693
2302	UUCUUUUC U UAGUUUCA	919	UGAAACUA CUGAUGAG X CGAA IAAAAGAA	2694
2310	UUAGUUUC A GAAGUACU	920	AGUACUUC CUGAUGAG X CGAA IAAACUAA	2695
2318	AGAAGUAC U GGCAUCAC	921	GUGAUGCC CUGAUGAG X CGAA IUACUUCU	2696
2322	GUACUGGC A UCACACGC	922	GCGUGUGA CUGAUGAG X CGAA ICCAGUAC	2697
2325	CUGGCAUC A CACGCAGG	923	CCUGCGUG CUGAUGAG X CGAA IAUGCCAG	2698
2327	GGCAUCAC A CGCAGGUU	924	AACCUGCG CUGAUGAG X CGAA IUGAUGCC	2699
2331	UCACACGC A GGUUACCU	925	AGGUAACC CUGAUGAG X CGAA ICGUGUGA	2700
2338	CAGGUUAC C UUGGCGUG	926	CACGCCAA CUGAUGAG X CGAA IUAACCUG	2701
2339	AGGUUACC U UGGCGUGU	927	ACACGCCA CUGAUGAG X CGAA IGUAACCU	2702
2351	CGUGUGUC C CUGUGGUA	928	UACCACAG CUGAUGAG X CGAA IACACACG	2703
2352	GUGUGUCC C UGUGGUAC	929	GUACCACA CUGAUGAG X CGAA IGACACAC	2704
2353	UGUGUCCC U GUGGUACC	930	GGUACCAC CUGAUGAG X CGAA IGGACACA	2705
2361	TIGUGGUAC C CUGGCAGA	931	UCUGCCAG CUGAUGAG X CGAA IUACCACA	2706
2362	GUGGUACC C UGGCAGAG	932	CUCUGCCA CUGAUGAG X CGAA IGUACCAC	2707
2363	UGGUACCC U GGCAGAGA	933	UCUCUGCC CUGAUGAG X CGAA IGGUACCA	2708
2367	ACCCUGGC A GAGAAGAG	934	CUCUUCUC CUGAUGAG X CGAA ICCAGGGU	2709
2378	GAAGAGAC C AAGCUUGU	935	ACAAGCUU CUGAUGAG X CGAA IUCUCUUC	2710
2379	AAGAGACC A AGCUUGUU	936	AACAAGCU CUGAUGAG X CGAA IGUCUCUU	2711
2383	GACCAAGC U UGUUUCCC	937	GGGAAACA CUGAUGAG X CGAA ICUUGGUC	2712
2390	CUUGUUUC C CUGCUGGC	938	GCCAGCAG CUGAUGAG X CGAA IAAACAAG	2713
2391	UUGUUUCC C UGCUGGCC	939	GGCCAGCA CUGAUGAG X CGAA IGAAACAA	2714
2392	UGUUUCCC U GCUGGCCA	940	UGGCCAGC CUGAUGAG X CGAA IGGAAACA	2715
2395	UUCCCUGC U GGCCAAAG	941	CUUUGGCC CUGAUGAG X CGAA ICAGGGAA	2716
2399	CUGCUGGC C AAAGUCAG	942	CUGACUUU CUGAUGAG X CGAA ICCAGCAG	2717
2400	UGCUGGCC A AAGUCAGU	943	ACUGACUU CUGAUGAG X CGAA IGCCAGCA	2718
2400	22200000 11 121000100			

UCUCCUAC CUGAUGAG X CGAA IACUUUGG 2719 2406 CCAAAGUC A GUAGGAGA 944 2421 GAGGAUGC A CAGUUUGC 945 GCAAACUG CUGAUGAG X CGAA ICAUCCUC 2720

2423	GGAUGCAC A GUUUGCUA	946	UAGCAAAC CUGAUGAG X CGAA IUGCAUCC	2721
2430	CAGUUUGC U AUUUGCUU	947	AAGCAAAU CUGAUGAG X CGAA ICAAACUG	2722
2437	CUAUUUGC U UUAGAGAC	948	GUCUCUAA CUGAUGAG X CGAA ICAAAUAG	2723
2446	UUAGAGAC A GGGACUGU	949	ACAGUCCC CUGAUGAG X CGAA IUCUCUAA	2724
2452	ACAGGGAC U GUAUAAAC	950	GUUUAUAC CUGAUGAG X CGAA IUCCCUGU	2725
2461	GUAUAAAC A AGCCUAAC	951	GUUAGGCU CUGAUGAG X CGAA IUUUAUAC	2726
2465	AAACAAGC C UAACAUUG	952	CAAUGUUA CUGAUGAG X CGAA ICUUGUUU	2727
2466	AACAAGCC U AACAUUGG	953	CCAAUGUU CUGAUGAG X CGAA IGCUUGUU	2728
2470	AGCCUAAC A UUGGUGCA	954	UGCACCAA CUGAUGAG X CGAA IUUAGGCU	2729
2478	AUUGGUGC A AAGAUUGC	955	GCAAUCUU CUGAUGAG X CGAA ICACCAAU	2730
2487	AAGAUUGC C UCUUGAAU	956	AUUCAAGA CUGAUGAG X CGAA ICANUCUU	2731
2488	AGAUUGCC U CUUGAAUU	957	AAUUCAAG CUGAUGAG X CGAA IGCAAUCU	2732
2490	AUUGCCUC U UGAAUUAA	958	UUAAUUCA CUGAUGAG X CGAA IAGGCAAU	2733
2509	ААААААС U АGААААА	959	UUUUUUCU CUGAUGAG X CGAA IUUUUUUU	2734

Input Sequence = AF190725. Cut Site = G/. Stem Length = 8 . Core Sequence = CUGAUGAG X CGAA (X = GCCGUUAGGC or other stem II) AF190725 (Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA; 2526 bp)

Table 20: Human BACE G-cleaver Ribozyme and Target Sequence

Pos	Substrate	Sed ID	К1Вогуше	KZ Seg
=	ACCOUNT G CAGCCCGC	960	GCGGGCUG UGAUG GCAUGCACUAUGC GCG GGACGCGU	2735
18	CGCAGCCC G CCCGGGAG	961	CUCCCGGG UGAUG GCAUGCACUAUGC GCG GGGCUGCG	2736
29	CGGGAGCU G CGAGCCGC	962	GCGGCUCG UGAUG GCAUGCACUAUGC GCG AGCUCCCG	2737
F	GGAGCUGC G AGCCGCGA	963	UCGCGGCU UGAUG GCAUGCACUAUGC GCG GCAGCUCC	2738
36	UGCGAGCC G CGAGCUGG	964	CCAGCUCG UGAUG GCAUGCACUAUGC GCG GGCUCGCA	2739
8	CGAGCCGC G AGCUGGAU	596	AUCCAGCU UGAUG GCAUGCACUAUGC GCG GCGGCUCG	2740
58	GGUGGCCU G AGCAGCCA	996	UGGCUGCU UGAUG GCAUGCACUAUGC GCG AGGCCACC	2741
69	CAGCCAAC G CAGCCGCA	967	UBCGGCUG UGAUG GCAUGCACUAUGC GCG GUUCGCUG	2742
75	ACGCAGCC G CAGGAGCC	968	GOCUCCUG UGAUG GCAUGCACUAUGC GCG GGCUGCGU	2743
94	GAGCCCUU G CCCCUGCC	696	GGCAGGGG UGAUG GCAUGCACUAUGC GCG AAGGGCUC	2744
100	uneccccu e cccececc	970	GGCGCGGG UGAUG GCAUGCACUAUGC GCG AGGGGCAA	2745
104	condocc e cocceca	971	CBBCGBCG UGAUG GCAUGCACUAUGC GCG GBGCAGGG	2746
106	CUGCCCGC G CCGCCGCC	972	GGCGGCGG UGAUG GCAUGCACUAUGC GCG GCGGGCAG	2747
109	2022222 0 2202222	973	GCGGGCGG UGAUG GCAUGCACUAUGC GCG GGCGCGGG	2748
112	9000000 g 0000000	974	CCGGCGGG UGAUG GCAUGCACUAUGC GCG GGCGGCGC	2749
116	500000000000000000000000000000000000000	975	CCCCCCGG UGAUG GCAUGCACUAUGC GCG GGGCGGCG	2750
137	GGGAAGCC G CCACCGGC	9.46	GCCGGUGG UGAUG GCAUGCACUAUGC GCG GGCUUCCC	2751
148	ACCGGCCC G CCAUGCCC	277	GGGCAUGG UGAUG GCAUGCACUAUGC GCG GGGCCGGU	2752
153	CCCGCCAU G CCCGCCCC	978	GGGGCGGG UGAUG GCAUGCACUAUGC GCG AUGGCGGG	2753
157	ccaugece a eccenece	979	GGGAGGGG UGAUG GCAUGCACUAUGC GCG GGGCAUGG	2754
172	CCAGCCCC G CCGGGAGC	980	GCUCCCGG UGAUG GCAUGCACUAUGC GCG GGGGCUGG	2755
183	GGGAGCCC G CGCCCGCU	186	AGCGGGCG UGAUG GCAUGCACUAUGC GCG GGGCUCCC	2756
185	GAGCCCGC G CCCGCUGC	982	GCAGCGGG UGAUG GCAUGCACUAUGC GCG GCGGGCUC	2757
189	CCGCGCCC G CUGCCCAG	983	CUGGGCAG UGAUG GCAUGCACUAUGC GCG GGGCGCGG	2758
192	свессеей в сесаваей	984	AGCCUAGE UGAUE GCAUGCACUAUGC GCG AGCGGGCG	2759
205	GGCUGGCC G CCGCCGUG	985	CACGGCGG UGAUG GCAUGCACUAUGC GCG GGCCAGCC	2760
208	neeccecc e ccanecce	986	CGGCACGG UGAUG GCAUGCACUAUGC GCG GGCGGCCA	2761
213	GCCGCCGU G CCGAUGUA	987	UACAUCAG UGAUG GCAUGCACUAUGC GCG ACGGCGGC	2762
216	GCCGUGCC G AUGUAGCG	988	CGCUACAU UGAUG GCAUGCACUAUGC GCG GGCACGGC	2763
250	DOUGGEOU G CUCCOGUG	686	CACOGGAG UGAUG GCAUGCACUAUGC GCG AGGGGAGA	2764

258	GCUCCCGU G CUCUGCGG	966	CCGCAGAG UGAUG GCAUGCACUAUGC GCG ACGGGAGC	2765
263	CRURCITOU G COGAUCUC	991	GAGAUCCG UGAUG GCAUGCACUAUGC GCG AGAGCACG	2766
276	ט	992	AGAGCGGU UGAUG GCAUGCACUAUGC GCG AGGGGAGA	2767
280	CCCUGACC G CUCUCCAC	993	GUGGAGAG UGAUG GCAUGCACUAUGC GCG GCUCAGGG	2768
320	U	994	AGGGCCUG UGAUG GCAUGCACUAUGC GCG AGGGCCCU	2769
337	GGCGUCCU G AUGCCCCC	966	939	2770
340	GUCCUGAU G CCCCCAAG	966	CUUGGGGG UGAUG GCAUGCACUAUGC GCG AUCAGGAC	2771
360	CCUCUCCU G AGAAGCCA	766	UGGCUUCU UGAUG GCAUGCACUAUGC GCG AGGAGAGG	2772
397	GGGCAGGC G CCAGGGAC	866	GUCCCUGG UGAUG GCAUGCACUAUGC GCG GCCUGCCC	2773
420	GGCCCAGU G CGAGCCCA	666	UGGGCUCG UGAUG GCAUGCACUAUGC GCG ACUGGCCC	2774
422	U	1000	UCUGGGCU UGAUG GCAUGCACUAUGC GCG GCACUGGC	2775
437	GAGGGCCC G AAGGCCGG	1001	8	2776
468	CAAGCCCU G CCCUGGCU	1002	AGCCAGGG UGAUG GCAUGCACUAUGC GCG AGGGCUUG	2777
480	uggeuceu g cuguggau	1003	AUCCACAG UGAUG GCAUGCACUAUGC GCG AGGAGCCA	2778
493	GGAUGGGC G CGGGAGUG	1004	CACUCCCG UGAUG GCAUGCACUAUGC GCG GCCCAUCC	2779
201	GCGGGAGU G CUGCCUGC	1005	909	2780
504	GGAGUGCU G CCUGCCCA	1006	UGGGCAGG UGAUG GCAUGCACUAUGC GCG AGCACUCC	2781
805	USCUGGE G CCCACGGC	1007	GCCGUGGG UGAUG GCAUGCACUAUGC GCG AGGCAGCA	2782
537	AUCCGGCU G CCCCUGCG	1008	CGCAGGGG UGAUG GCAUGCACUAUGC GCG AGCCGGAU	2783
543	CUGCCCCU G CGCAGCGG	1009	CCGCUGCG UGAUG GCAUGCACUAUGC GCG AGGGGCAG	2784
545	GCCCCUGC G CAGCGGCC	1010	GGCCGCUG UGAUG GCAUGCACUAUGC GCG GCAGGGGC	2785
562	negegge e coccone	1011	ggg	2786
576	CUEGGGCU G CGGCUGCC	1012	GGCAGCCG UGAUG GCAUGCACUAUGC GCG AGCCCCAG	2787
582	CUBCGGCU G CCCCGGGA	1013	SCG	2788
595	GGGAGACC G ACGAAGAG	1014		2789
598	AGACCGAC G AAGAGCCC	1015	GGGCUCUU UGAUG GCAUGCACUAUGC GCG GUCGGUCU	2790
607	AAGAGCCC G AGGAGCCC	1016	GGGCUCCU UGAUG GCAUGCACUAUGC GCG GGGCUCUU	2791
654	GACAACCU G AGGGGCAA	1017	GCAUGCACUAUGC GCG	2792
069	GUGGAGAU G ACCGUGGG	1018	939	2793
708	AGCCCCC G CAGACGCU	1019	99	2794
714	CCGCAGAC G CUCAACAU	1020		2795
751	GUAACUUU G CAGUGGGU	1021	ACCCACUG UGAUG GCAUGCACUAUGC GCG AAAGUUAC	2796
260	CAGUGGGU G CUGCCCCC	1022	GGGGGCAG UGAUG GCAUGCACUAUGC GCG ACCCACUG	2797
763	UGGGUGCU G CCCCCCAC	1023	GUGGGGG UGAUG GCAUGCACUAUGC GCG AGCACCCA	27.98

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780	CCCURCOU G CAUCGCUA	1024	UAGCGAUG UGAUG GCAUGCACUAUGC GCG AGGAAGGG	2799
785	CCUGCAUC G CUACUACO	1025	GGUAGUAG UGAUG GCAUGCACUAUGC GCG GAUGCAGG	2800
843	GUGUAUGU G CCCUACAC	1026	GUGUAGGG UGAUG GCAUGCACUAUGC GCG ACAUACAC	2801
883	U	1027	UACCAGGU UGAUG GCAUGCACUAUGC GCG GGUGCCCA	2802
100	U	1028	UNGGCACG UGAUG GCAUGCACUAUGC GCG ACAGUGAC	2803
926	U	1029	AAUGUUGG UGAUG GCAUGCACUAUGC GCG ACGCACAG	2804
934	CCAACAUU G CUGCCAUC	1030	GAUGGCAG UGAUG GCAUGCACUAUGC GCG AAUGUUGG	2805
937	ACAUUGCU G CCAUCACU	1031	AGUGAUGG UGAUG GCAUGCACUAUGC GCG AGCAAUGU	2806
946	CCAUCACU G AAUCAGAC	1032	GUCUGADU UGAUG GCAUGCACUADGC GCG AGUGAUGG	2807
1006	UGGCCUAU G CUGAGAUU	1033	AAUCUCAG UGAUG GCAUGCACUAUGC GCG AUAGGCCA	2808
1009	CCUAUGCU G AGAUUGCC	1034	900	2809
1015	CUGAGAUU G CCAGGCCU	1035	AGGCCUGG UGAUG GCAUGCACUAUGC GCG AAUCUCAG	2810
1024	CCAGGCCU G ACGACUCC	1036		2811
1027	GGCCUGAC G ACUCCCUG	1037	CAGGGAGU UGAUG GCAUGCACUAUGC GCG GUCAGGCC	2812
1048	CUUUCUUU G ACUCUCUG	1038	CAGAGAGU UGAUG GCAUGCACUAUGC GCG AAAGAAAG	2813
1092	DUCUCCCU G CAGCUUUG	1039	GCAUGCACUAUGC GCG	2814
1105	uniqueeu e cueecuuc	1040	gcg	2815
1129	ACCAGUCU G AAGUGCUG	1041	CAGCACUU UGAUG GCAUGCACUANGC GCG AGACUGGU	2816
1134	UCUGAAGU G CUGGCCUC	1042	GAGGCCAG UGAUG GCAUGCACUAUGC GCG ACUUCAGA	2817
1158	GGGAGCAU G AUCAUUGG	1043	CCAAUGAU UGAUG GCAUGCACUAUGC GCG AUGCUCCC	2818
1174		1044	CGAGUGGU UGAUG GCAUGCACUAUGC GCG GAUACCUC	2819
1182	U	1045	GUGUACAG UGAUG GCAUGCACUAUGC GCG GAGUGGUC	2820
1234	GGUALITAL G AGGUGAUC	1046	GAUCACCU UGAUG GCAUGCACUAUGC GCG AUAAUACC	2821
1239	UAUGAGGU G AUCAUUGU	1047	ACAAUGAU UGAUG GCAUGCACUAUGC GCG ACCUCAUA	2822
1248	AUCAUUGU G CGGGUGGA	1048	UCCACCCG UGAUG GCAUGCACUAUGC GCG ACAAUGAU	2823
1275	CAGGAUCU G NAAAUGGA	1049	UCCAUTUU UGAUG GCAUGCACUAUGC GCG AGAUCCUG	2824
1286	AAUGGACU G CAAGGAGU	1050	900	2825
1303	ACAACUAU G ACAAGAGC	1001	gcg	2826
1344	CUUCGUIU G CCCAAGAA	1052	UNCUUGGG UGAUG GCAUGCACUAUGC GCG AAACGAAG	2827
1360	AAGUGUUU G AAGCUGCA	1053	UGCAGCUU UGAUG GCAUGCACUAUGC GCG ANACACUU	2828
1366	UUGAAGCU G CAGUCAAA	1054	UNUGACUG UGAUG GCAUGCACUAUGC GCG AGCUUCAA	2829
1411	AGUUCCCU G AUGGUUUC	1055	GAAACCAU UGAUG GCAUGCACUAUGC GCG AGGGAACU	2830
1442	GCUGGUGU G CUGGCAAG	1056	CUUGCCAG UGAUG GCAUGCACUAUGC GCG ACACCAGC	2831
1504	UAAUGGGU G AGGUUACC	1057	GGUAACCU UGAUG GCAUGCACUAUGC GCG ACCCAUUA	2832

1526	GINCHING G CAUCACCA	1058	UGGUGAUG UGAUG GCAUGCACUAUGC GCG GGAAGGAC	2833
1543	ALLCCHICC G CAGCAAUA	1059	GCAUGCACUAUGC GCG	2834
1554	Caallacell G EGGCCAGU	1060	ACUGGCCG UGAUG GCAUGCACUAUGC GCG AGGUAUUG	2835
288		1061	GUAACAGU UGAUG GCAUGCACUAUGC GCG GUCUUGGG	2836
1603	e	1062	UGAGAUGG UGAUG GCAUGCACUAUGC GCG AAACUUGU	2837
1672	INTERPORTED G AUCGGGCC	1063	909	2838
1682	IICGGGCC G AAAACGAA	1064	999	2839
1688	CCGABAAC G AAUUGGCU	1065	GCAUGCACUAUGC GCG	2840
1699	UNGGCUUU G CUGUCAGC	1066	GCUGACAG UGAUG GCAUGCACUAUGC GCG AAAGCCAA	2841
1708	lσ	1067	AUGGCAAG UGAUG GCAUGCACUAUGC GCG GCUGACAG	2842
1712	O	1068	GCACAUGG UGAUG GCAUGCACUAUGC GCG AAGCGCUG	2843
1719	UGCCAUGU G CACGAUGA	1069		2844
1723	AUGUGCAC G AUGAGUUC	1070	GAACUCAU UGAUG GCAUGCACUAUGC GCG GUGCACAU	2845
1726	UGCACGAU G AGUUCAGG	1011	CCUGAACU UGAUG GCAUGCACUAUGC GCG AUCGUGCA	2846
1807	AGACAGAU G AGUCAACC	1072	GGUUGACU UGAUG GCAUGCACUAUGC GCG AUCUGUCU	2847
1821	0	1073	GCUAUGGU UGAUG GCAUGCACUAUGC GCG AUGAGGGU	2848
1843	UCAUGGCU G CCAUCUGC	1074	gce	2849
1850	UGCCAUCU G CGCCCUCU	1075	AGAGGGCG UGAUG GCAUGCACUAUGC GCG AGAUGGCA	2850
1852	CCAUCUGC G CCCUCUUC	1076	GAAGAGGG UGAUG GCAUGCACUAUGC GCG GCAGAUGG	2851
1863	CUCUUCAU G CUGCCACU	1077	AGUGGCAG UGAUG GCAUGCACUAUGC GCG AUGAAGAG	2852
1866	UUCAUGCU G	1078	CAGAGUGG UGAUG GCAUGCACUAUGC GCG AGCAUGAA	2853
1874	_	1079	gce	2854
1895	┸	1080	GGAGGCAG UGAUG GCAUGCACUAUGC GCG GCCACUGA	2855
1898	1	1081	AGCGGAGG UGAUG GCAUGCACUAUGC GCG AGCGCCAC	2856
1904	1	1082	GCAGGCAG UGAUG GCAUGCACUAUGC GCG GGAGGCAG	2857
1907	L	1083	GCCCAGG UGAUG GCAUGCACUAUGC GCG AGCGGAGG	2858
1911	CGCUGCCU G CGCCAGCA	1084	UGCUGGCG UGAUG GCAUGCACUAUGC GCG AGGCAGCG	2859
1913	CUGCCUGC G CCAGCAGC	1085	GCUGCUGG UGAUG GCAUGCACUAUGC GCG GCAGGCAG	2860
1924	Τ.	1086	AAAGUCAU UGAUG GCAUGCACUAUGC GCG AUGCUGCU	2861
1927	╀	1087	AGCAAAGU UGAUG GCAUGCACUAUGC GCG AUCAUGCU	2862
1933	1	1088	GUCAUCAG UGAUG GCAUGCACUAUGC GCG AAAGUCAU	2863
1936	╀	1089	GAUGUCAU UGAUG GCAUGCACUAUGC GCG AGCAAAGU	2864
1939	UUGCUGAU G ACAUCUCC	1090	GGAGAUGU UGAUG GCAUGCACUAUGC GCG AUCAGCAA	2865
1950	1	1001	CACUUCAG UGAUG GCAUGCACUAUGC GCG AGGGAGAU	2866

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55450544 5 5550550	AAGOGAGG	1092	CCUCACOO DEADS SCACECACOAGE GEG ASCASSOR	7987
GCUGAAGU G	AGGAGGCC	1093	GGCCUCCU UGAUG GCAUGCACUAUGC GCG ACUUCAGC	2868
CACCADAU G	ccucuacc	1094	GGCAGAGG UGAUG GCAUGCACUAUGC GCG AUUUGGUG	2869
AUGCCUCU G	CCUUGAUG	1095	CAUCAAGG UGAUG GCAUGCACUAUGC GCG AGAGGCAU	2870
DCUGCCUU G	AUGGAGAA	1096	UUCUCCAU UGAUG GCAUGCACUAUGC GCG AAGGCAGA	2871
AGCACUCU G CUGGCGGG	CUGGCGGG	1097	CCCGCCAG UGAUG GCAUGCACUAUGC GCG AGAGUGCU	2872
GAAAUUCU G CUGCUUGA	CUGCUUGA	1098	UCAAGCAG UGAUG GCAUGCACUAUGC GCG AGAAUUUC	2873
AUTCUGCU G CUUGAAAC	CUUGAAAC	1099	GUUUCAAG UGAUG GCAUGCACUAUGC GCG AGCAGAAU	2874
DECUGENT G	AAACUUCA	1100	UGAAGUUU UGAUG GCAUGCACUAUGC GCG AAGCAGCA	2875
UCAGCCCU G	G AACCUUUG	1101	CAAAGGUU UGAUG GCAUGCACUAUGC GCG AGGGCUGA	2876
CAUCACAC G CAGGUUAC	CAGGUUAC	1102	GUAACCUG UGAUG GCAUGCACUAUGC GCG GUGUGAUG	2877
BUNUCCCU 6 CUGGCCAA	CUGGCCAA	1103	UUGGCCAG UGAUG GCAUGCACUAUGC GCG AGGGAAAC	2878
GAGAGGAU G CACAGUUU	CACAGUUU	1104	AAACUGUG UGAUG GCAUGCACUAUGC GCG AUCCUCUC	2879
CACAGUUU G	CUAUUUGC	1105	GCAAAUAG UGAUG GCAUGCACUAUGC GCG AAACUGUG	2880
UGCUAUUU G	CUUUAGAG	1106	CUCUANAG UGAUG GCAUGCACUAUGC GCG AAAUAGCA	2881
ACAUUGGU G CAAAGAUU	CAAAGAUU	1107	AAUCUUUG UGAUG GCAUGCACUAUGC GCG ACCAAUGU	2882
CAAAGAUU G CCUCUUGA	CCUCUUGA	1108	UCAAGAGG UGAUG GCAUGCACUAUGC GCG AAUCUUUG	2883
UGCCUCUU G AAUUNAAA	AAUUAAAA	1109	UUUUAAUU UGAUG GCAUGCACUAUGC GCG AAGAGGCA	2884
GUGCCGAU G UAGCGGGC	UAGCGGGC	1110	GCCCGCUA UGANG GCAUGCACUAUGC GCG AUCGGCAC	2885
cuccuecu e uceauged	UGGAUGGG	1111	CCCAUCCA UGAUG GCAUGCACUAUGC GCG AGCAGGAG	2886
GCAGCUUU G UGGAGAUG	UGGAGAUG	1112	CAUCUCCA UGAUG GCAUGCACUAUGC GCG AAAGCUGC	2887
AGGCAGCU G UCCAGCAC	UCCAGCAC	1113	GUGCUGGA UGAUG GCAUGCACUAUGC GCG AGCUGCCU	2888
GGAAGGGU G UGUAUGUG	UGUAUGUG	1114	CACAUACA UGAUG GCAUGCACUAUGC GCG ACCCUUCC	2889
AAGGGUGU G UAUGUGCC	UAUGUGCC	1115	GGCACAUA UGAUG GCAUGCACUAUGC GCG ACACCCUU	2890
GUGUGUAU G	G UGCCCUAC	1116	GUAGGGCA UGAUG GCAUGCACUAUGC GCG AUACACAC	2891
ACGUCACU G	G UGCGUGCC	1117	GGCACGCA UGAUG GCAUGCACUAUGC GCG AGUGACGU	2892
GCAGCUUU G UGGUGCUG	UGGUGCUG	1118	CAGCACCA UGAUG GCAUGCACUAUGC GCG AAAGCUGC	2893
UGGCCUCU G UCGGAGGG	UCGGAGGG	1119	CCCUCCGA UGAUG GCAUGCACUAUGC GCG AGAGGCCA	2894
CACUCGCU G UACACAGG	UACACAGG	1120	CCUGUGUA UGAUG GCAUGCACUAUGC GCG AGCGAGUG	2895
UGAUCAUU G	g ugcegeue	1121	CACCCGCA UGAUG GCAUGCACUAUGC GCG AAUGAUCA	2896
AGAGCAUU G	G UGGACAGU	1122	ACUGUCCA UGAUG GCAUGCACUAUGC GCG AAUGCUCU	2897
AAGAAAGU G UUUGAAGC	UUUGAAGC	1123	GCUUCAAA UGAUG GCAUGCACUAUGC GCG ACUUUCUU	2898
CAGCUGGU G UGCUGGCA	UGCUGGCA	1124	UGCCAGCA UGAUG GCAUGCACUAUGC GCG ACCAGCUG	2899
GGAAGAII G	DGGAAGAU G UGGCCACG	1125	CGUGGCCA UGAUG GCAUGCACUAUGC GCG AUCUUCCA	2900

Table 20

		AGACGACU G UDACAAGU	1126	ACUUGUAA UGAUG GCAUGCACUAUGC GCG AGUCGUCU	2901
1128 CAUGADA, USADO CAUCACCHUAGO COS ACCUDADA 1130 AUCAAAON USADO CAUCACCHUAGO COS ACCUDADA 1131 AUCCAGACO RESUBBIO CAUCACCHUAGO COS ACCUDADA 1131 AUCCAGACO RESUBBIO CAUCACCHUAGO COS AUGCADA 1131 CACAGACO RESUBBIO CAUCACCHUAGO COS ACCAUGADA 1132 CACAGACO RESUBBIO CAUCACCHUAGO COS ACCAUGADA 1134 CACAGACO RESUBBIO CAUCACCHUAGO COS ACCAUGADA 1134 CACAGACO RESUBBIO CAUCACCHUAGO COS ACCAGACO 1130 GAUCACCHU RESUBBIO CAUCACCHUAGO COS ACCAGACO 1141 CACAGACO RESUBBIO CAUCACCHUAGO COS ACCAGACO 1141 CACAGACOR RESUBBIO CAUCACCHUAGO COS ACGACOCO 1141 CACAGACOR RESUBBIO CAUCACCHUAGO COS ACGACOCO 1141 CACAGACOR RESUBBIO CAUCACCHUAGO COS ACGACOCO 1141 CACAGACOR RESUBBIO CAUCACCHUAGO COS ACGACOCOCO 1141 CACAGACOR RESUBBIO CAUCACCHUAGO COS ACGACOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO	500	SCACU G UNAUGGGA	1127	UCCCAUAA UGAUG GCAUGCACUAUGC GCG AGUGCCCG	2902
1112 AUCOARAN URANG ENUCIOCULUNGO COS ACCUMAN ACCOCION UNIVERSITY OF ACCOCION POPUS CONTROLLOCULUNGO COS MUSICAMOS LITTI CANAGORIA URANG CONTROCCULUNGO COS MUSICAMOS LITTI CANAGORIA URANG CONTROCCULUNGO COS MUSICAMOS LITTI CANAGORIA URANG CONTROCCULUNGO COS MUSICAMOS LITTI ACCOUNTANT UNIVERSITY OF ACCOUNT U	ngg	GAGCU G UDAUCAUG	1128	CAUGAUAA UGAUG GCAUGCACUAUGC GCG AGCUCCCA	2903
1119 AGECTORIO NUMB CROUNCE/CURDE GO RACEAAGC 1111 CAGECTORIO NUMB CROUNCE/CURDE GO RACEAAGC 1112 CAGGGGA NUMB CONTROLLENIMICE GOS MURGCIAN 1113 CAGGGGA REMOTE CANTROLLENIMICE GOS ANDROCIA 1114 CAGGGGA NUMB CONTROLLENIMICE GOS ANDROCIA 1115 CAGGGGA NUMB CONTROLLENIMICE GOS ANDROCIA 1115 CAGGGGA NUMB CONTROLLENIMICE GOS ANDROCIA 1116 CAGGGGA NUMB CONTROLLENIMICE GOS ANDROCIA 1117 CHARLESA NUMB CONTROLLENIMICE GOS ANDROCIA 1118 GUARGOA NUMB CONTROLLENIMICE GOS ANDROCIA 1119 CAGGGGA NUMB CONTROLLENIMICE GOS ANDROCIA 1111 CAGGGGA NUMB CAGGGGGA CON NUMB CONTROLLENIMICE GOS ANDROCIA 1111 CAGGGGA NUMB CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	18	UACGUU G UCUTUGAU	1129	AUCAAAGA UGAUG GCAUGCACUAUGC GCG AACGUAGA	2904
1113 AUCEREACH UBING CONDECUDING COS MORCHOGO COST MORCHOG	le le	nuudeu e ueagegeu	1130	AGCGCUGA UGAUG GCAUGCACUAUGC GCG AGCAAAGC	2905
1113 CANGGORIO NUNIO GAUDICICIUMICE COS PARANSICE III13 CANGGORIO NUNIO GAUDICICALIMICE COS AGUICINE III13 MECCURIO GAUDICICALIMICE COS AGUICINE III13 AGUICINE AGUICINE COS AGUICINE III13 CACCURIS USBATO GAUDICICALIMISE COS AGUICINE III13 CACCURIS USBATO GAUDICICALIMISE COS AGUICINIS III13 UNICAGAIA HONG GAUDICICALIMICE COS AGUICINE III13 GAUDICICALIMICE COS AGUICINE III14 CACCORDE IIII14 CACCORDE IIIII CACCORDE IIIIII CACCORDE IIIII CACCORDE IIIIII CACCORDE IIIII CACCORDE IIIIII CACCORDE IIIII CACCORDE IIII CACCORDE IIIII CACCORDE IIII CACCORDE IIIII CACCORDE IIII CACCORDE	Įΰ	JUGCCAU G UGCACGAU	1131	AUCGUGCA UGAUG GCAUGCACUAUGC GCG AUGGCAAG	2906
1113 UGBINGCO, NUBING CONDOCUMENC COS ABRODOC 1113 ACCOURT IGNIG CONDOCUMENTE COS AUROCUM 1115 CACUGACA UGANIG GONUCCACUMAGE COS AUROCUM 1116 CACUGACA UGANIG GONUCCACUMAGE COS ACCONIGAGE 1118 UCAGACA UGANIG GONUCCACUMAGE COS ACCONIGAGE 1119 UCAGACA UGANIG GONUCCACUMAGE COS AGRICACO 1111 CACAGACA UGANIG GONUCCACUMAGE COS ACAGACACO 1111 CACAGACA UGANIG GONUCCACUMAGE COS AGRICACO 1111 CACAGACA UGANIG CONUCCACUMAGE COS AGRICACO 1111 CACAGACA UGANICA COS COS COS COS CONUCCUMAGE COS COS COS COS COS COS COS COS COS C	Ö	accurate a ucaccura	1132	CAAGGUGA UGAUG GCAUGCACUAUGC, GCG AAAAGGGC	2907
1113 AGCTARUS NUMBO CANDOCAMUNICO COS NUMOCINA 1113 CACTURACA TRUNCO CANDOCAMUNICO COS NUCONOCI 1113 CACTURACA TRUNCO CANDOCAMUNICO COS ACCANDOCA 1113 CACTURACA TRUNCO CANDOCAMUNICO COS ACCANDO 1114 CACCATURA TRUNCO CANDOCAMUNICO COS ACRICCORO 1115 GUARDACA TRUNCO CANDOCAMUNICO COS ACRICCORO 1114 CACCAGARA TRUNCO CACCAGARA 1114 CACCAGARA TRUNCO CANDOCAMUNICO COS ACRICCORO 1114 CACCAGARA TRUNCO CANDOCAMUNICO COS ACRICCORO 1114 CACCAGARA 1114 CACCAGARA TRUNCO CACCAGARA 1114 CACCAGARA 1114 CACCAGARA TRUNCO CACCAGARA 1114 CACCAGA	ō	GAAGACU G UGGCUACA	1133	UGUAGCCA UGAUG GCAUGCACUAUGC GCG AGUCUUCC	2908
1115	Þ	AGCCUAU G UCAUGGCU	1134	AGCCAUGA UGAUG GCAUGCACUAUGC GCG AUAGGCUA	2909
1136 GCCATORIO NUNDO CONDOCADUMOS GOS ADACOMOS 1137 CUCROSCA, IGADO CONDOCADAMICO COS AGRICOCO 1138 UNCAGOTA URBUG CONDOCACHANGO COS AGRICOCO 1140 AUGUSTA URBUG CONDOCACHANGO COS AGRICOCO 1141 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1141 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1142 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1143 GARBARA URBUG CONDOCACHANGO COS AGRICOCO 1144 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1144 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1145 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1146 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1146 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1147 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1148 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1149 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1140 CAGAGARA URBUG CONDOCACHANGO COS AGRICOCO 1141 CAGAGARA URBUGA CONDOCACHANGO COS AGRICOCO	ľ	UCAUGGU G UGUCAGUG	1135	CACUGACA UGAUG GCAUGCACUAUGC GCG ACCAUGAG	2910
1137 UCUGACCA, UBANG GENERACIANNEG GEN AGSUGCOR 1138 ULCAGGAIA, UBANG GENERACIACIUSCO GEN AGGUCORG 1140 AUGENICA, UBANG GENURO-CIANTAGE CAS AGGUCORG 1141 CAGGGARA, UBANG GENURO-CIANTAGE CAS AAGGUCORG 1141 CAGGGARA, UBANG GENURO-CIANTAGE GEN AAGGGAA 1142 CAGGGARA, UBANG GENURO-CIANTAGE GEN AGGGARA 1143 GEBANCER, UBANG GENURO-CIANTAGE GEN AGGGARA 1144 CAGGGARA, UBANG GENURO-CIANTAGE GEN AGGGARA 1145 UBANUA, UBANG GENURO-CIANTAGE GEN AGGGARA 1146 UBANUA, UBANG GENURO-CIANTAGE GEN AGGGARA	0	AUGGUGU G UCAGUGGC	1136	GCCACUGA UGAUG GCAUGCACUAUGC GCG ACACCAUG	2911
1138 UNAGABUR UNDUR GOUDCHAURGE GOA GARICCOUG 1139 UNAGABUR UNDUR GOUDCHAURGE GOA ARGGUNC 1140 AUSSUGAN URANG GOUNCHAURGE GOA ARGGUNC 1141 CARGARAN URANG GOUNCHAURGE GOA ARAGGUNC 1142 CARGARAN URANG GOUNCHAURGE GOA ARGGUNG 1143 GORDACAN URANG GOUNCHAURGE GOA ARGGUNG 1144 GORDACAN URANG GOUNCHAURGE GOA ARGGUNG 1145 URUNURAN URANG GOUNCHAURGE GOA ARGGUNG 1146 URUNURAN URANG GOUNCHAURGE GOA ARGGUNG 1147 URUNURAN URANG GOUNCHAURGE GOA ARGGUNG 1148 URUNURAN URANG GOUNCHAURGE GOA ARGGUNG 1149 URUNURAN URANG GOANCHAURGE GOA ARGCOUGH	P	GGCACCU G UGGCCAGA	1137	UCUGGCCA UGAUG GCAUGCACUAUGC GCG AGGUGCCA	2912
1119 GUIDCOUCH DUBBLE COURDICALINES COST AGROUNDS 1111 CAGGGARA HEADER COUNDCACHINICE COST AAAGGUUC 1111 CAGGGARA HEADER COUNDCACHINICE COST AAAGGUUC 1111 CAGGGARA HEADER COUNDCACHINICE COST AAGGUUC 1111 CAGGGARA HEADER COUNDCACHINICE COST AAGGUUC 1111 CAGGGARA HEADER COUNDCACHINICE COST AAGGUUG 1111 CAGGARA CAGGARA CAGGARA CAGGARA CAGGARA CAGGARA 1111 CAGGARA CAGGARA 1111 CAGGARA CAGGARA 1111 CA	10	AGGGACU G UACCUGUA	1138	UACAGGUA UGAUG GCAUGCACUAUGC GCG AGUCCCUG	2913
1140 AUGUSTIGAN URANG GANDCACHANGC GAS AAAGSUC 1141 CAGGGRAN URANG GANDCACHANGC GAS AAGGSAAG 1142 CAGGGRAN URANG GANDCACHANGC GAS AGGGAAG 1143 GAGGARA URANG GANDCACHANGC GAS AGGGAAC 1144 CAGGGARA URANG GANDCACHANGC GAS AGGGAAC 1145 URANG GANDCACHANGC GAS AGGGAAC	10	UGUACCU G UAGGAAAC	1139	GUUUCCUA UGAUG GCAUGCACUAUGC GCG AGGUACAG	2914
1141 CARGARIA NUMBERO COMPACAMON CON ACCORDA 1143 CARDEGRA TORNI CONTRICTURIO COS ALACOCCA 1144 CARDEGRA TORNI CONTRICTURIO COS ALACOCCA 1145 CARDEGRA TORNI CONTRICTURIO COS ARGENCIC 1146 CARDEGRA TORNI CONTRICTURIO COS ARGENCIC 1147 CARDEGRA TORNI CONTRICTURIO COS ARGENCICO 1148 CARDINIO CONTRICTURIO COS ARGENCICOS	ľ	MACCUUU G UCCACCAU	1140	AUGGUGGA UGAUG GCAUGCACUAUGC GCG AAAGGUUC	2915
1142 CACAGGGA UGANG GCANGCACANIGG COG ACAGGGCA 1143 GAGGBACCH UGANG GCANGCACANAUGG GCG AGGGCACC 1144 CACGGAAA UGANG GCANGCACANGGG GCG AGGCCUGG 1145 UGUUUNIAN UGANG GCANGCACANUGG GCG AGGCCUGG	۲	cunagean a nanceena	1141	CAGGGACA UGAUG GCAUGCACUAUGC GCG ACGCCAAG	2916
1143 GGGIACCA UGANG GCANGCACUANGC GCG AGGGACAC 1141 CAGGGAAA UGANG GCANGCACUANGC GCG AAGCUNGG 1145 UGUUUANA UGANG GCANGCACUANGC GCG AGUCCCUG	12	raccaudu a ucccuand	1142	CACAGGGA UGAUG GCAUGCACUAUGC GCG ACACGCCA	2917
1144 CAGGGAAA UGAUG GCAUGCACUAUGC GCG AAGCUUGG 1145 UGUUUAUA UGAUG GCAUGCACUAUGC GCG AGUCCCUG	10	TUGUCCCU G UGGUACCC	1143	GGGUACCA UGAUG GCAUGCACUAUGC GCG AGGGACAC	2918
1145 UGUUDADA UGADG GCAUGCACUAUGC GCG AGUCCCUG	10	CAAGCUU G UUUCCCUG	1144	CAGGGAAA UGAUG GCAUGCACUAUGC GCG AAGCUUGG	2919
	10	AGGGACU G UAUAAACA	1145	UGUTUANA UGAUG GCAUGCACUAUGC GCG AGUCCCUG	2920

Input Sequence = AF190725. Out Site = 6f, Sequence = AF190725. Out Site = 6f, Sequence Sequence = USANG CANGCACUAUGC GCG State Input Sequence = 190016 GANGCACUAUGC GCG Sequence = 190016 GANGCACUAUGC GCG SIACS) mBSM3, 2526 bp)

Table 21: Human BACE Zinzyme Ribozyme and Target Sequence

Pos	Substrate	Seq ID	Ribozyme	Rz Seq ID
11	ACGCGUCC G CAGCCCGC	960	GCGGGCUG GCCGAAAGGCGAGUCAAGGUCU GGACGCGU	2921
18	CGCAGCCC G CCCGGGAG	961	CUCCCGGG GCCGAAAGGCGAGUCAAGGUCU GGGCUGCG	2922
29	CGGGAGCU G CGAGCCGC	962	GCGGCUCG GCCGAAAGGCGAGUCAAGGUCU AGCUCCCG	2923
36	UGCGAGCC G CGAGCUGG	964	CCAGCUCG GCCGAAAGGCGAGUCAAGGUCU GGCUCGCA	2924
69	CAGCCAAC G CAGCCGCA	967	UGCGGCUG GCCGAAAGGCGAGUCAAGGUCU GUUGGCUG	2925
75	ACGCAGCC G CAGGAGCC	968	GGCUCCUG GCCGAAAGGCGAGUCAAGGUCU GGCUGCGU	2926
94	GAGCCCUU G CCCCUGCC	969	GGCAGGG GCCGAAAGGCGAGUCAAGGUCU AAGGGCUC	2927
100	UUGCCCCU G CCCGCGCC	970	GGCGCGGG GCCGAAAGGCGAGUCAAGGUCU AGGGGCAA	2928
104	CCCUGCCC G CGCCGCCG	971	CGGCGGCG GCCGAAAGGCGAGUCAAGGUCU GGGCAGGG	2929
104	CUGCCCGC G CCGCCGCC	972	GGCGGCGG GCCGAAAGGCGAGUCAAGGUCU GCGGGCAG	2930
109	CCCGCGCC G CCGCCCGC	973	GCGGGCGG GCCGAAAGGCGAGUCAAGGUCU GGCGCGGG	2931
112	GCGCCGCC G CCCGCCGG	974	CCGGCGGG GCCGAAAGGCGAGUCAAGGUCU GGCGGCGC	2932
116	CGCCGCCC G CCGGGGGG	975	CCCCCGG GCCGAAAGGCGAGUCAAGGUCU GGGCGGCG	2933
137	GGGAAGCC G CCACCGGC	976	GCCGGUGG GCCGAAAGGCGAGUCAAGGUCU GGCUUCCC	2934
148	ACCEGCCC G CCAUGCCC	977	GGGCAUGG GCCGAAAGGCGAGUCAAGGUCU GGGCCGGU	2935
153	CCCGCCAU G CCCGCCCC	978	GGGGCGGG GCCGAAAGGCGAGUCAAGGUCU AUGGCGGG	2936
157	CCAUGCCAU G CCCGUCCC	979	GGGAGGG GCCGAAAGGCGAGUCAAGGUCU GGGCAUGG	2937
172	CCAGCCCC G CCGGGAGC	980	GCUCCCGG GCCGAAAGGCGAGUCAAGGUCU GGGGCUGG	2938
183	GGGAGCCC G CGCCCGCU	981	AGCGGGCG GCCGAAAGGCGAGUCAAGGUCU GGGCUCCC	2939
185	GAGCCCGC G CCCGCUGC	982	GCAGCGGG GCCGAAAGGCGAGUCAAGGUCU GCGGGCUC	2940
	CCGCGCCC G CUGCCCAG	983	CUGGGCAG GCCGAAAGGCGAGUCAAGGUCU GGGCGCGG	2941
189	CGCCGCU G CCCAGGCU	984	AGCCUGGG GCCGAAAGGCGAGUCAAGGUCU AGCGGGCG	2942
192	GGCUGGCC G CCGCCGUG	985	CACGGCGG GCCGAAAGGCGAGUCAAGGUCU GGCCAGCC	2943
	UGGCCGCC G CCGUGCCG	986	CGGCACGG GCCGAAAGGCGAGUCAAGGUCU GGCGGCCA	2944
208	GCCGCCGU G CCGAUGUA	987	UACAUCGG GCCGAAAGGCGAGUCAAGGUCU ACGGCGGC	2945
250	UCUCCCCU G CUCCCGUG	989	CACGGGAG GCCGAAAGGCGAGUCAAGGUCU AGGGGAGA	2946
258	GCUCCCGU G CUCUGCGG	990	CCGCAGAG GCCGAAAGGCGAGUCAAGGUCU ACGGGAGC	2947
	CGUGCUCU G CGGAUCUC	991	GAGAUCCG GCCGAAAGGCGAGUCAAGGUCU AGAGCACG	2948
263	CCCUGACC G CUCUCCAC	993	GUGGAGAG GCCGAAAGGCGAGUCAAGGUCU GGUCAGGG	2949
	AGGGCCCU G CAGGCCCU	994	AGGGCCUG GCCGAAAGGCGAGUCAAGGUCU AGGGCCCU	2950
320	GUCCUGAU G CCCCCAAG	996	CUUGGGGG GCCGAAAGGCGAGUCAAGGUCU AUCAGGAC	2951
340	GGGCAGGC G CCAGGGAC	998	GUCCCUGG GCCGAAAGGCGAGUCAAGGUCU GCCUGCCC	2952
420	GGGCCAGU G CGAGCCCA	999	UGGGCUCG GCCGAAAGGCGAGUCAAGGUCU ACUGGCCC	2953
	CAAGCCCU G CCCUGGCU	1002	AGCCAGGG GCCGAAAGGCGAGUCAAGGUCU AGGGCUUG	2954
468	IIGGCUCCU G CUGUGGAU	1002	AUCCACAG GCCGAAAGGCGAGUCAAGGUCU AGGAGCCA	2955
480	GGAUGGGC G CGGGAGUG	1003	CACUCCCG GCCGAAAGGCGAGUCAAGGUCU GCCCAUCC	2956
493	GCGGGAGU G CUGCCUGC	1005	GCAGGCAG GCCGAAAGGCGAGUCAAGGUCU ACUCCCGC	2957
	GGAGUGCU G CCUGCCCA	1005	UGGGCAGG GCCGAAAGGCGAGUCAAGGUCU AGCACUCC	2958
504	UGCUGCCU G CCCACGGC	1007	GCCGUGGG GCCGAAAGGCGAGUCAAGGUCU AGGCAGCA	2959
	AUCCGGCU G CCCCUGCG	1009	CGCAGGGG GCCGAAAGGCGAGUCAAGGUCU AGCCGGAU	2960
537	CUGCCCCU G CGCAGCGG	1009	CCGCUGCG GCCGAAAGGCGAGUCAAGGUCU AGGGGCAG	2961
543	GCCCCUGC G CAGCGGCC	1010	GGCCGCUG GCCGAAAGGCGAGUCAAGGUCU GCAGGGGC	2962
545	UGGGGGGC G CCCCCCUG	1011	CAGGGGG GCCGAAAGGCGAGUCAAGGUCU GCCCCCCA	2963
562		1012	GGCAGCCG GCCGAAAGGCGAGUCAAGGUCU AGCCCCAG	2964
576	CUGGGGCU G CGGCUGCC	1012	UCCCGGGG GCCGAAAGGCGAGUCAAGGUCU AGCCGCAG	2965
582	CUGCGGCU G CCCCGGGA	1013	AGCGUCUG GCCGAAAGGCGAGUCAAGGUCU GGGGGGCU	2966
708	AGCCCCCC G CAGACGCU		AUGUUGAG GCCGAAAGGCGAGUCAAGGUCU GUCUGCGG	2967
714	CCGCAGAC G CUCAACAU	1020	AUGUUGAG GCCGARAGGCGAGGCAAGGCCA	

Table 21

			ACCCACUG GCCGAAAGGCGAGUCAAGGUCU AAAGUUAC	2968
751	GUAACUUU G CAGUGGGU	1021		2969
760	CAGUGGGU G CUGCCCCC	1022	GGGGGCAG GCCGAAAGGCGAGUCAAGGUCU ACCCACUG	2970
763	UGGGUGCU G CCCCCCAC	1023	GUGGGGG GCCGAAAGGCGAGUCAAGGUCU AGCACCCA	2971
780	CCCUUCCU G CAUCGCUA	1024	UAGCGAUG GCCGAAAGGCGAGUCAAGGUCU AGGAAGGG	2971
785	CCUGCAUC G CUACUACC	1025	GGUAGUAG GCCGAAAGGCGAGUCAAGGUCU GAUGCAGG	
843	GUGUAUGU G CCCUACAC	1026	GUGUAGGG GCCGAAAGGCGAGUCAAGGUCU ACAUACAC	2973
921	GUCACUGU G CGUGCCAA	1028	UUGGCACG GCCGAAAGGCGAGUCAAGGUCU ACAGUGAC	2974
925	CUGUGCGU G CCAACAUU	1029	AAUGUUGG GCCGAAAGGCGAGUCAAGGUCU ACGCACAG	2975
934	CCAACAUU G CUGCCAUC	1030	GAUGGCAG GCCGAAAGGCGAGUCAAGGUCU AAUGUUGG	2976
937	ACAUUGCU G CCAUCACU	1031	AGUGAUGG GCCGAAAGGCGAGUCAAGGUCU AGCAAUGU	2977
1006	UGGCCUAU G CUGAGAUU	1033	AAUCUCAG GCCGAAAGGCGAGUCAAGGUCU AUAGGCCA	2978
1015	CUGAGAUU G CCAGGCCU	1035	AGGCCUGG GCCGAAAGGCGAGUCAAGGUCU AAUCUCAG	2979
1092	UUCUCCCU G CAGCUUUG	1039	CAAAGCUG GCCGAAAGGCGAGUCAAGGUCU AGGGAGAA	2980
1105	UUUGUGGU G CUGGCUUC	1040	GAAGCCAG GCCGAAAGGCGAGUCAAGGUCU ACCACAAA	2981
1134	UCUGAAGU G CUGGCCUC	1042	GAGGCCAG GCCGAAAGGCGAGUCAAGGUCU ACUUCAGA	2982
1182	GACCACUC G CUGUACAC	1045	GUGUACAG GCCGAAAGGCGAGUCAAGGUCU GAGUGGUC	2983
1248	AUCAUUGU G CGGGUGGA	1048	UCCACCCG GCCGAAAGGCGAGUCAAGGUCU ACAAUGAU	2984
1286	AAUGGACU G CAAGGAGU	1050	ACUCCUUG GCCGAAAGGCGAGUCAAGGUCU AGUCCAUU	2985
1344	CUUCGUUU G CCCAAGAA	1052	UUCUUGGG GCCGAAAGGCGAGUCAAGGUCU AAACGAAG	2986
1366	UUGAAGCU G CAGUCAAA	1054	UUUGACUG GCCGAAAGGCGAGUCAAGGUCU AGCUUCAA	2987
1442	GCUGGUGU G CUGGCAAG	1056	CUUGCCAG GCCGAAAGGCGAGUCAAGGUCU ACACCAGC	2988
1526	GUCCUUCC G CAUCACCA	1058	UGGUGAUG GCCGAAAGGCGAGUCAAGGUCU GGAAGGAC	2989
1542	AUCCUUCC G CAGCAAUA	1059	UAUUGCUG GCCGAAAGGCGAGUCAAGGUCU GGAAGGAU	2990
1554	CAAUACCU G CGGCCAGU	1060	ACUGGCCG GCCGAAAGGCGAGUCAAGGUCU AGGUAUUG	2991
	ACAAGUUU G CCAUCUCA	1062	UGAGAUGG GCCGAAAGGCGAGUCAAGGUCU AAACUUGU	2992
1603	UUGGCUUU G CUGUCAGC	1066	GCUGACAG GCCGAAAGGCGAGUCAAGGUCU AAAGCCAA	2993
1699	CUGUCAGC G CUUGCCAU	1067	AUGGCAAG GCCGAAAGGCGAGUCAAGGUCU GCUGACAG	2994
1708	CAGCGCUU G CCAUGUGC	1068	GCACAUGG GCCGAAAGGCGAGUCAAGGUCU AAGCGCUG	2995
1712		1069	UCAUCGUG GCCGAAAGGCGAGUCAAGGUCU ACAUGGCA	2996
1719	UGCCAUGU G CACGAUGA	1074	GCAGAUGG GCCGAAAGGCGAGUCAAGGUCU AGCCAUGA	2997
1843	UCAUGGCU G CCAUCUGC	1074	AGAGGGOG GCCGAAAGGCGAGUCAAGGUCU AGAUGGCA	2998
1850	UGCCAUCU G CGCCCUCU	1076	GAAGAGG GCCGAAAGGCGAGUCAAGGUCU GCAGAUGG	2999
1852	CCAUCUGC G CCCUCUUC	1075	AGUGGCAG GCCGAAAGGCGAGUCAAGGUCU AUGAAGAG	3000
1863	CUCUUCAU G CUGCCACU	1077	CAGAGUGG GCCGAAAGGCGAGUCAAGGUCU AGCAUGAA	3001
1866	UUCAUGCU G CCACUCUG		CCAUGAGG GCCGAAAGGCGAGUCAAGGUCU AGAGUGGC	3002
1874	GCCACUCU G CCUCAUGG	1079	GGAGGCAG GCCGAAAGGCGAGUCAAGGUCU GCCACUGA	3003
1895	UCAGUGGC G CUGCCUCC	1080	AGCGGAGG GCCGAAAGGCGAGUCAAGGUCU AGCGCCAC	3004
1898	GUGGCGCU G CCUCCGCU	1081	GCAGGCAG GCCGAAAGGCGAGUCAAGGUCU GGAGGCAG	3005
1904	CUGCCUCC G CUGCCUGC	1082	GCGCAGG GCCGAAAGGCGAGUCAAGGUCU AGCGGAGG	3006
1907	CCUCCGCU G CCUGCGCC	1083	UGCUGGCG GCCGAAAGGCGAGUCAAGGUCU AGGCAGCG	3007
1911	CGCUGCCU G CGCCAGCA	1084	GCUGCUGG GCCGAAAGGCGAGUCAAGGUCU AGGCAGCG GCUGCUGG GCCGAAAGGCGAGUCAAGGUCU GCAGGCAG	3008
1913	CUGCCUGC G CCAGCAGC	1085		3009
1933	AUGACUUU G CUGAUGAC	1088	GUCAUCAG GCCGAAAGGCGAGUCAAGGUCU AAAGUCAU	3010
1950	AUCUCCCU G CUGAAGUG	1091	CACUUCAG GCCGAAAGGCGAGUCAAGGUCU AGGGAGAU	3010
2087	CACCAAAU G CCUCUGCC	1094	GGCAGAGG GCCGAAAGGCGAGUCAAGGUCU AUUUGGUG	3011
2093	AUGCCUCU G CCUUGAUG	1095	CAUCAAGG GCCGAAAGGCGAGUCAAGGUCU AGAGGCAU	
2179	AGCACUCU G CUGGCGGG	1097	CCCGCCAG GCCGAAAGGCGAGUCAAGGUCU AGAGUGCU	3013
2227	GAAAUUCU G CUGCUUGA	1098	UCAAGCAG GCCGAAAGGCGAGUCAAGGUCU AGAAUUUC	3014
2230	AUUCUGCU G CUUGAAAC	1099	GUUUCAAG GCCGAAAGGCGAGUCAAGGUCU AGCAGAAU	3015
2329	CAUCACAC G CAGGUUAC	1102	GUAACCUG GCCGAAAGGCGAGUCAAGGUCU GUGUGAUG	3016
2393	GUUUCCCU G CUGGCCAA	1103	UUGGCCAG GCCGAAAGGCGAGUCAAGGUCU AGGGAAAC	3017
2419		1104	AAACUGUG GCCGAAAGGCGAGUCAAGGUCU AUCCUCUC	3018
2.13			1	

Table 21

2428	CACAGUUU G CUAUUUGC	1105	GCAAAUAG GCCGAAAGGCGAGUCAAGGUCU AAACUGUG	3019
2435	UGCUAUUU G CUUUAGAG	1106	CUCUAAAG GCCGAAAGGCGAGUCAAGGUCU AAAUAGCA	3020
2476	ACAUUGGU G CAAAGAUU	1107	AAUCUUUG GCCGAAAGGCGAGUCAAGGUCU ACCAAUGU	3021
2485	CAAAGAUU G CCUCUUGA	1108	UCAAGAGG GCCGAAAGGCGAGUCAAGGUCU AAUCUUUG	3022
219	GUGCCGAU G UAGCGGGC	1110	GCCCGCUA GCCGAAAGGCGAGUCAAGGUCU AUCGGCAC	3023
483	CUCCUGCU G UGGAUGGG	1111	CCCAUCCA GCCGAAAGGCGAGUCAAGGUCU AGCAGGAG	3024
634	GCAGCUUU G UGGAGAUG	1112	CAUCUCCA GCCGAAAGGCGAGUCAAGGUCU AAAGCUGC	3025
804	AGGCAGCU G UCCAGCAC	1113	GUGCUGGA GCCGAAAGGCGAGUCAAGGUCU AGCUGCCU	3026
835	GGAAGGGU G UGUAUGUG	1114	CACAUACA GCCGAAAGGCGAGUCAAGGUCU ACCCUUCC	3027
837	AAGGGUGU G UAUGUGCC	1115	GGCACAUA GCCGAAAGGCGAGUCAAGGUCU ACACCCUU	3028
841	GUGUGUAU G UGCCCUAC	1116	GUAGGGCA GCCGAAAGGCGAGUCAAGGUCU AUACACAC	3029
919	ACGUCACU G UGCGUGCC	1117	GGCACGCA GCCGAAAGGCGAGUCAAGGUCU, AGUGACGU	3030
1100	GCAGCUUU G UGGUGCUG	1118	CAGCACCA GCCGAAAGGCGAGUCAAGGUCU AAAGCUGC	3031
1144	UGGCCUCU G UCGGAGGG	1119	CCCUCCGA GCCGAAAGGCGAGUCAAGGUCU AGAGGCCA	3032
1185	CACUCGCU G UACACAGG	1120	CCUGUGUA GCCGAAAGGCGAGUCAAGGUCU AGCGAGUG	3033
1246	UGAUCAUU G UGCGGGUG	1121	CACCCGCA GCCGAAAGGCGAGUCAAGGUCU AAUGAUCA	3034
1315	AGAGCAUU G UGGACAGU	1122	ACUGUCCA GCCGAAAGGCGAGUCAAGGUCU AAUGCUCU	3035
1356	AAGAAAGU G UUUGAAGC	1123	GCUUCAAA GCCGAAAGGCGAGUCAAGGUCU ACUUUCUU	3036
1440	CAGCUGGU G UGCUGGCA	1124	UGCCAGCA GCCGAAAGGCGAGUCAAGGUCU ACCAGCUG	3037
1570	UGGAAGAU G UGGCCACG	1125	CGUGGCCA GCCGAAAGGCGAGUCAAGGUCU AUCUUCCA	3038
1592	AGACGACU G UUACAAGU	1126	ACUUGUAA GCCGAAAGGCGAGUCAAGGUCU AGUCGUCU	3039
1630	CGGGCACU G UUAUGGGA	1127	UCCCAUAA GCCGAAAGGCGAGUCAAGGUCU AGUGCCCG	3040
1642	UGGGAGCU G UUAUCAUG	1128	CAUGAUAA GCCGAAAGGCGAGUCAAGGUCU AGCUCCCA	3041
1666	UCUACGUU G UCUUUGAU	1129	AUCAAAGA GCCGAAAGGCGAGUCAAGGUCU AACGUAGA	3042
1702	GCUUUGCU G UCAGCGCU	1130	AGCGCUGA GCCGAAAGGCGAGUCAAGGUCU AGCAAAGC	3043
1717	CUUGCCAU G UGCACGAU	1131	AUCGUGCA GCCGAAAGGCGAGUCAAGGUCU AUGGCAAG	3044
1759	GCCCUUUU G UCACCUUG	1132	CAAGGUGA GCCGAAAGGCGAGUCAAGGUCU AAAAGGGC	3045
1781	GGAAGACU G UGGCUACA	1133	UGUAGCCA GCCGAAAGGCGAGUCAAGGUCU AGUCUUCC	3046
1834	UAGCCUAU G UCAUGGCU	1134	AGCCAUGA GCCGAAAGGCGAGUCAAGGUCU AUAGGCUA	3047
1884	CUCAUGGU G UGUCAGUG	1135	CACUGACA GCCGAAAGGCGAGUCAAGGUCU ACCAUGAG	3048
1886	CAUGGUGU G UCAGUGGC	1136	GCCACUGA GCCGAAAGGCGAGUCAAGGUCU ACACCAUG	3049
2048	UGGCACCU G UGGCCAGA	1137	UCUGGCCA GCCGAAAGGCGAGUCAAGGUCU AGGUGCCA	3050
2139	CAGGGACU G UACCUGUA	1138	UACAGGUA GCCGAAAGGCGAGUCAAGGUCU AGUCCCUG	3051
2145	CUGUACCU G UAGGAAAC	1139	GUUUCCUA GCCGAAAGGCGAGUCAAGGUCU AGGUACAG	3052
2256	GAACCUUU G UCCACCAU	1140	AUGGUGGA GCCGAAAGGCGAGUCAAGGUCU AAAGGUUC	3053
2346	CUUGGCGU G UGUCCCUG	1141	CAGGGACA GCCGAAAGGCGAGUCAAGGUCU ACGCCAAG	3054
2348	UGGCGUGU G UCCCUGUG	1142	CACAGGGA GCCGAAAGGCGAGUCAAGGUCU ACACGCCA	3055
2354	GUGUCCCU G UGGUACCC	1143	GGGUACCA GCCGAAAGGCGAGUCAAGGUCU AGGGACAC	3056
2385	CCAAGCUU G UUUCCCUG	1144	CAGGGAAA GCCGAAAGGCGAGUCAAGGUCU AAGCUUGG	3057
2453	CAGGGACU G UAUAAACA	1145	UGUUUAUA GCCGAAAGGCGAGUCAAGGUCU AGUCCCUG	3058
14	CGUCCGCA G CCCGCCCG	1146	CGGGCGGG GCCGAAAGGCGAGUCAAGGUCU UGCGGACG	3059
26	GCCCGGGA G CUGCGAGC	1147	GCUCGCAG GCCGAAAGGCGAGUCAAGGUCU UCCCGGGC	3060
33	AGCUGCGA G CCGCGAGC	1148	GCUCGCGG GCCGAAAGGCGAGUCAAGGUCU UCGCAGCU	3061
40	AGCCGCGA G CUGGAUUA	1149	UAAUCCAG GCCGAAAGGCGAGUCAAGGUCU UCGCGGCU	3062
51	GGAUUAUG G UGGCCUGA	1150	UCAGGCCA GCCGAAAGGCGAGUCAAGGUCU CAUAAUCC	3063
54	UUAUGGUG G CCUGAGCA	1151	UGCUCAGG GCCGAAAGGCGAGUCAAGGUCU CACCAUAA	3064
	UGGCCUGA G CAGCCAAC	1152	GUUGGCUG GCCGAAAGGCGAGUCAAGGUCU UCAGGCCA	3065
60				3066
	CCUGAGCA G CCAACGCA	1153	UGCGUUGG GCCGAAAGGCGAGUCAAGGUCU UGCUCAGG	
60	CCUGAGCA G CCAACGCA CCAACGCA G CCGCAGGA	1153 1154	UCCUGCGG GCCGAAAGGCGAGUCAAGGUCU UGCGUUGG	3067
60				

Table 21

134	CCAGGGAA G CCGCCACC	1157	GGUGGCGG GCCGAAAGGCGAGUCAAGGUCU UUCCCUGG	3070
144	CGCCACCG G CCCGCCAU	1158	AUGGCGGG GCCGAAAGGCGAGUCAAGGUCU CGGUGGCG	3071
167	CCCUCCCA G CCCCGCCG	1159	CGGCGGGG GCCGAAAGGCGAGUCAAGGUCU UGGGAGGG	3072
179	CGCCGGGA G CCCGCGCC	1160	GGCGCGGG GCCGAAAGGCGAGUCAAGGUCU UCCCGGCG	3073
198	CUGCCCAG G CUGGCCGC	1161	GCGGCCAG GCCGAAAGGCGAGUCAAGGUCU CUGGGCAG	3074
202	CCAGGCUG G CCGCCGCC	1162	GGCGGCGG GCCGAAAGGCGAGUCAAGGUCU CAGCCUGG	3075
211	CCGCCGCC G UGCCGAUG	1163	CAUCGGCA GCCGAAAGGCGAGUCAAGGUCU GGCGGCGG	3076
222	CCGAUGUA G CGGGCUCC	1164	GGAGCCCG GCCGAAAGGCGAGUCAAGGUCU UACAUCGG	3077
226	UGUAGCGG G CUCCGGAU	1165	AUCCGGAG GCCGAAAGGCGAGUCAAGGUCU CCGCUACA	3078
239	GGAUCCCA G CCUCUCCC	1166	GGGAGAGG GCCGAAAGGCGAGUCAAGGUCU UGGGAUCC	3079
256	CUGCUCCC G UGCUCUGC	1167	GCAGAGCA GCCGAAAGGCGAGUCAAGGUCU GGGAGCAG	3080
290	UCUCCACA G CCCGGACC	1168	GGUCCGGG GCCGAAAGGCGAGUCAAGGUCU UGUGGAGA	3081
304	ACCCGGGG G CUGGCCCA	1169	UGGGCCAG GCCGAAAGGCGAGUCAAGGUCU CCCCGGGU	3082
308	GGGGGCUG G CCCAGGGC	1170	GCCCUGGG GCCGAAAGGCGAGUCAAGGUCU CAGCCCCC	3083
315	GGCCCAGG G CCCUGCAG	1171	CUGCAGGG GCCGAAAGGCGAGUCAAGGUCU CCUGGGCC	3084
324	CCCUGCAG G CCCUGGCG	1172	CGCCAGGG GCCGAAAGGCGAGUCAAGGUCU CUGCAGGG	3085
330	AGGCCCUG G CGUCCUGA	1173	UCAGGACG GCCGAAAGGCGAGUCAAGGUCU CAGGGCCU	3086
332	GCCCUGGC G UCCUGAUG	1174	CAUCAGGA GCCGAAAGGCGAGUCAAGGUCU GCCAGGGC	3087
348	GCCCCCAA G CUCCCUCU	1175	AGAGGGAG GCCGAAAGGCGAGUCAAGGUCU UUGGGGGC	3088
365	CCUGAGAA G CCACCAGC	1176	GCUGGUGG GCCGAAAGGCGAGUCAAGGUCU UUCUCAGG	3089
372	AGCCACCA G CACCACCC	1177	GGGUGGUG GCCGAAAGGCGAGUCAAGGUCU UGGUGGCU	3090
391	ACUUGGGG G CAGGCGCC	1178	GGCGCCUG GCCGAAAGGCGAGUCAAGGUCU CCCCAAGU	3091
395	GGGGCAG G CGCCAGGG	1179	CCCUGGCG GCCGAAAGGCGAGUCAAGGUCU CUGCCCCC	3092
410	GGACGGAC G UGGGCCAG	1180	CUGGCCCA GCCGAAAGGCGAGUCAAGGUCU GUCCGUCC	3093
414	GGACGUGG G CCAGUGCG	1181	CGCACUGG GCCGAAAGGCGAGUCAAGGUCU CCACGUCC	3094
418	GUGGGCCA G UGCGAGCC	1182	GGCUCGCA GCCGAAAGGCGAGUCAAGGUCU UGGCCCAC	3095
424	CAGUGCGA G CCCAGAGG	1183	CCUCUGGG GCCGAAAGGCGAGUCAAGGUCU UCGCACUG	3096
433	CCCAGAGG G CCCGAAGG	1184	CCUUCGGG GCCGAAAGGCGAGUCAAGGUCU CCUCUGGG	3097
441	GCCCGAAG G CCGGGGCC	1185	GGCCCCGG GCCGAAAGGCGAGUCAAGGUCU CUUCGGGC	3098
447	AGGCCGGG G CCCACCAU	1186	AUGGUGGG GCCGAAAGGCGAGUCAAGGUCU CCCGGCCU	3099
457	CCACCAUG G CCCAAGCC	1187	GGCUUGGG GCCGAAAGGCGAGUCAAGGUCU CAUGGUGG	3100
463	UGGCCCAA G CCCUGCCC	1188	GGGCAGGG GCCGAAAGGCGAGUCAAGGUCU UUGGGCCA	3101
474	CUGCCCUG G CUCCUGCU	1189	AGCAGGAG GCCGAAAGGCGAGUCAAGGUCU CAGGGCAG	3102
491	GUGGAUGG G CGCGGGAG	1190	CUCCCGCG GCCGAAAGGCGAGUCAAGGUCU CCAUCCAC	3103
499	GCGCGGGA G UGCUGCCU	1191	AGGCAGCA GCCGAAAGGCGAGUCAAGGUCU UCCCGCGC	3104
515	UGCCCACG G CACCCAGC	1192	GCUGGGUG GCCGAAAGGCGAGUCAAGGUCU CGUGGGCA	3105
522	GGCACCCA G CACGGCAU	1193	AUGCCGUG GCCGAAAGGCGAGUCAAGGUCU UGGGUGCC	3106
527	CCAGCACG G CAUCOGGC	1194	GCCGGAUG GCCGAAAGGCGAGUCAAGGUCU CGUGCUGG	3107
534	GGCAUCCG G CUGCCCCU	1195	AGGGGCAG GCCGAAAGGCGAGUCAAGGUCU CGGAUGCC	3108
548	CCUGCGCA G CGGCCUGG	1196	CCAGGCCG GCCGAAAGGCGAGUCAAGGUCU UGCGCAGG	3109
551	GCGCAGCG G CCUGGGGG	1197	CCCCAGG GCCGAAAGGCGAGUCAAGGUCU CGCUGCGC	3110
560	CCUGGGGG G CGCCCCCC	1198	GGGGGGG GCCGAAAGGCGAGUCAAGGUCU CCCCCAGG	3111
573	CCCCIGGG G CUGCGGCU	1199	AGCCGCAG GCCGAAAGGCGAGUCAAGGUCU CCCAGGGG	3112
579	GGGCUGCG G CUGCCCCG	1200	CGGGGCAG GCCGAAAGGCGAGUCAAGGUCU CGCAGCCC	3113
	GACGAAGA G CCCGAGGA	1200	UCCUCGG GCCGAAAGGCGAGUCAAGGUCU UCUUCGUC	3114
603		1201	CGGCCGGG GCCGAAAGGCGAGUCAAGGUCU UCCUCGGG	3115
612	CCCGAGGA G CCCGGCCG		CCCUCCGG GCCGAAAGGCGAGUCAAGGUCU CGGGCUCC	3115
617	GGAGCCCG G CCGGAGGG	1203		3117
626	CCGGAGGG G CAGCUUUG	1204	CAAAGCUG GCCGAAAGGCGAGUCAAGGUCU CCCUCCGG	
629	GAGGGGCA G CUUUGUGG	1205	CCACAAAG GCCGAAAGGCGAGUCAAGGUCU UGCCCCUC	3118
643	UGGAGAUG G UGGACAAC	1206	GUUGUCCA GCCGAAAGGCGAGUCAAGGUCU CAUCUCCA	3119
659	CCUGAGGG G CAAGUCGG	1207	CCGACUUG GCCGAAAGGCGAGUCAAGGUCU CCCUCAGG	3120

Table 21

	The second secon	1208	UGCCCCGA GCCGAAAGGCGAGUCAAGGUCU UUGCCCCU	3121
663	AGGGGCAA G UCGGGGCA		UAGCCCUG GCCGAAAGGCGAGUCAAGGUCU CCCGACUU	3122
669	AAGUCGGG G CAGGGCUA	1209	CGUAGUAG GCCGAAAGGCGAGUCAAGGUCU CCUGCCCC	3123
674	GGGGCAGG G CUACUACG	1210	CAUCUCCA GCCGAAAGGCGAGUCAAGGUCU GUAGUAGC	3124
682	GCUACUAC G UGGAGAUG	1211	GCUGCCCA GCCGAAAGGCGAGUCAAGGUCU GGUCAUCU	3125
694	AGAUGACC G UGGGCAGC	1212		3126
698	GACCGUGG G CAGCCCCC	1213	GGGGGCUG GCCGAAAGGCGAGUCAAGGUCU CCACGGUC	3127
701	CGUGGGCA G CCCCCCGC	1214	GCGGGGG GCCGAAAGGCGAGUCAAGGUCU UGCCCACG	3127
727	ACAUCCUG G UGGAUACA	1215	UGUAUCCA GCCGAAAGGCGAGUCAAGGUCU CAGGAUGU	
737	GGAUACAG G CAGCAGUA	1216	UACUGCUG GCCGAAAGGCGAGUCAAGGUCU CUGUAUCC	3129
740	UACAGGCA G CAGUAACU	1217	AGUUACUG GCCGAAAGGCGAGUCAAGGUCU UGCCUGUA	3130
743	AGGCAGCA G UAACUUUG	1218	CAAAGUUA GCCGAAAGGCGAGUCAAGGUCU UGCUGCCU	3131
754	ACUUUGCA G UGGGUGCU	1219	AGCACCCA GCCGAAAGGCGAGUCAAGGUCU UGCAAAGU	3132
758	UGCAGUGG G UGCUGCCC	1220	GGGCAGCA GCCGAAAGGCGAGUCAAGGUCU CCACUGCA	3133
798	UACCAGAG G CAGCUGUC	1221	GACAGCUG GCCGAAAGGCGAGUCAAGGUCU CUCUGGUA	3134
801	CAGAGGCA G CUGUCCAG	1222	CUGGACAG GCCGAAAGGCGAGUCAAGGUCU UGCCUCUG	3135
809	GCUGUCCA G CACAUACC	1223	GGUAUGUG GCCGAAAGGCGAGUCAAGGUCU UGGACAGC	3136
833	CCGGAAGG G UGUGUAUG	1224	CAUACACA GCCGAAAGGCGAGUCAAGGUCU CCUUCCGG	3137
857	CACCCAGG G CAAGUGGG	1225	CCCACUUG GCCGAAAGGCGAGUCAAGGUCU CCUGGGUG	3138
861	CAGGGCAA G UGGGAAGG	1226	CCUUCCCA GCCGAAAGGCGAGUCAAGGUCU UUGCCCUG	3139
873	GAAGGGA G CUGGGCAC	1227	GUGCCCAG GCCGAAAGGCGAGUCAAGGUCU UCCCCUUC	3140
878	GGAGCUGG G CACCGACC	1228	GGUCGGUG GCCGAAAGGCGAGUCAAGGUCU CCAGCUCC	3141
889	CCGACCUG G UAAGCAUC	1229	GAUGCUUA GCCGAAAGGCGAGUCAAGGUCU CAGGUCGG	3142
893	CCUGGUAA G CAUCCCCC	1230	GGGGGAUG GCCGAAAGGCGAGUCAAGGUCU UUACCAGG	3143
905	CCCCCAUG G CCCCAACG	1231	CGUUGGGG GCCGAAAGGCGAGUCAAGGUCU CAUGGGGG	3144
913	GCCCCAAC G UCACUGUG	1232	CACAGUGA GCCGAAAGGCGAGUCAAGGUCU GUUGGGGC	3145
923	CACUGUGC G UGCCAACA	1233	UGUUGGCA GCCGAAAGGCGAGUCAAGGUCU GCACAGUG	3146
957	UCAGACAA G UUCUUCAU	1234	AUGAAGAA GCCGAAAGGCGAGUCAAGGUCU UUGUCUGA	3147
971	CAUCAACG G CUCCAACU	1235	AGUUGGAG GCCGAAAGGCGAGUCAAGGUCU CGUUGAUG	3148
986	CUGGGAAG G CAUCCUGG	1236	CCAGGAUG GCCGAAAGGCGAGUCAAGGUCU CUUCCCAG	3149
996	AUCCUGGG G CUGGCCUA	1237	UAGGCCAG GCCGAAAGGCGAGUCAAGGUCU CCCAGGAU	3150
	UGGGGCUG G CCUAUGCU	1238	AGCAUAGG GCCGAAAGGCGAGUCAAGGUCU CAGCCCCA	3151
1000	AUUGCCAG G CCUGACGA	1239	UCGUCAGG GCCGAAAGGCGAGUCAAGGUCU CUGGCAAU	3152
	UCCCUGGA G CCUUUCUU	1240	AAGAAAGG GCCGAAAGGCGAGUCAAGGUCU UCCAGGGA	3153
1038	ACUCUCUG G UAAAGCAG	1241	CUGCUUUA GCCGAAAGGCGAGUCAAGGUCU CAGAGAGU	3154
1057		1242	UGGGUCUG GCCGAAAGGCGAGUCAAGGUCU UUUACCAG	3155
1062	CUGGUAAA G CAGACCCA AGACCCAC G UUCCCAAC	1242	GUUGGGAA GCCGAAAGGCGAGUCAAGGUCU GUGGGUCU	3156
1072		1244	CCACAAAG GCCGAAAGGCGAGUCAAGGUCU UGCAGGGA	3157
1095	UCCCUGCA G CUUUGUGG	1245	AGCCAGCA GCCGAAAGGCGAGUCAAGGUCU CACAAAGC	3158
1103	GCUUUGUG G UGCUGGCU	1245	GGGGAAG GCCGAAAGGCGAGUCAAGGUCU CAGCACCA	3159
1109	UGGUGCUG G CUUCCCCC	1246	ACUUCAGA GCCGAAAGGCGAGUCAAGGUCU UGGUUGAG	3160
1125	CUCAACCA G UCUGAAGU	1248	GGCCAGCA GCCGAAAGGCGAGUCAAGGUCU UUCAGACU	3161
1132	AGUCUGAA G UGCUGGCC		GACAGAG GCCGAAAGGCGAGUCAAGGUCU CAGCACUU	3162
1138	AAGUGCUG G CCUCUGUC	1249	UGAUCAUG GCCGAAAGGCGAGUCAAGGUCU UCCCUCCG	3163
1154			GGUCGAUA GCCGAAAGGCGAGUCAAGGUCU CUCCAAUG	3164
1169		1251	AGAGACUG GCCGAAAGGCGAGUCAAGGUCU CUGUGUAC	3165
1193		1252	ACCAGAGA GCCGAAAGGCGAGUCAAGGUCU UGCCUGUG	3166
1196		1253	GGUGUAUA GCCGAAAGGCGAGUCAAGGUCU CAGAGACU	3167
1203		1254		3168
1218		1255	CACUCCCG GCCGAAAGGCGAGUCAAGGUCU CGGAUGGG	3169
1224		1256	UAAUACCA GCCGAAAGGCGAGUCAAGGUCU UCCCGCCG	3170
1227		1257	UCAUAAUA GCCGAAAGGCGAGUCAAGGUCU CACUCCCG	3170
1237	AUUAUGAG G UGAUCAUU	1258	AAUGAUCA GCCGAAAGGCGAGUCAAGGUCU CUCAUAAU	31/1

Table 21

			GAUCUCCA GCCGAAAGGCGAGUCAAGGUCU CCGCACAA	3172
1252	UUGUGCGG G UGGAGAUC	1259	UAGUUGUA GCCGAAAGGCGAGUCAAGGUCU UCCUUGCA	3173
1293	UGCAAGGA G UACAACUA	1260	CCACAAUG GCCGAAAGGCGAGUCAAGGUCU UCUUGUCA	3174
1310	UGACAAGA G CAUUGUGG	1261	UGGUGCA GCCGAAGGCGAGUCAAGGUCU UGUCCACA	3175
1322	UGUGGACA G UGGCACCA	1262	UGGUGGUG GCCGAAAGGCGAGUCAAGGUCU CACUGUCC	3176
1325	GGACAGUG G CACCACCA	1263		3177
1340	CAACCUUC G UUUGCCCA	1264	UGGGCAAA GCCGAAAGGCGAGUCAAGGUCU GAAGGUUG	3178
1354	CCAAGAAA G UGUUUGAA	1265	UUCAAACA GCCGAAAGGCGAGUCAAGGUCU UUUCUUGG	3179
1363	UGUUUGAA G CUGCAGUC	1266	GACUGCAG GCCGAAAGGCGAGUCAAGGUCU UUCAAACA	3180
1369	AAGCUGCA G UCAAAUCC	1267	GGAUUUGA GCCGAAAGGCGAGUCAAGGUCU UGCAGCUU	3181
1384	CCAUCAAG G CAGCCUCC	1268	GGAGGCUG GCCGAAAGGCGAGUCAAGGUCU CUUGAUGG	
1387	UCAAGGCA G CCUCCUCC	1269	GGAGGAGG GCCGAAAGGCGAGUCAAGGUCU UGCCUUGA	3182
1404	ACGGAGAA G UUCCCUGA	1270	UCAGGGAA GCCGAAAGGCGAGUCAAGGUCU UUCUCCGU	3183
1415	CCCUGAUG G UUUCUGGC	1271	GCCAGAAA GCCGAAAGGCGAGUCAAGGUCU CAUCAGGG	
1422	GGUUUCUG G CUAGGAGA	1272	UCUCCUAG GCCGAAAGGCGAGUCAAGGUCU CAGAAACC	3185
1431	CUAGGAGA G CAGCUGGU	1273	ACCAGCUG GCCGAAAGGCGAGUCAAGGUCU UCUCCUAG	3186
1434	GGAGAGCA G CUGGUGUG	1274	CACACCAG GCCGAAAGGCGAGUCAAGGUCU UGCUCUCC	3187
1438	AGCAGCUG G UGUGCUGG	1275	CCAGCACA GCCGAAAGGCGAGUCAAGGUCU CAGCUGCU	3188
1446	GUGUGCUG G CAAGCAGG	1276	CCUGCUUG GCCGAAAGGCGAGUCAAGGUCU CAGCACAC	3189
1450	GCUGGCAA G CAGGCACC	1277	GGUGCCUG GCCGAAAGGCGAGUCAAGGUCU UUGCCAGC	3190
1454	GCAAGCAG G CACCACCC	1278	GGGUGGUG GCCGAAAGGCGAGUCAAGGUCU CUGCUUGC	3191
1480	UUUUCCCA G UCAUCUCA	1279	UGAGAUGA GCCGAAAGGCGAGUCAAGGUCU UGGGAAAA	3192
1502	CCUAAUGG G UGAGGUUA	1280	UAACCUCA GCCGAAAGGCGAGUCAAGGUCU CCAUUAGG	3193
1507	UGGGUGAG G UUACCAAC	1281	GUUGGUAA GCCGAAAGGCGAGUCAAGGUCU CUCACCCA	3194
1518	ACCAACCA G UCCUUCCG	1282	CGGAAGGA GCCGAAAGGCGAGUCAAGGUCU UGGUUGGU	3195
1545	CUUCCGCA G CAAUACCU	1283	AGGUAUUG GCCGAAAGGCGAGUCAAGGUCU UGCGGAAG	3196
1557	UACCUGCG G CCAGUGGA	1284	UCCACUGG GCCGAAAGGCGAGUCAAGGUCU CGCAGGUA	3197
1561	UGCGGCCA G UGGAAGAU	1285	AUCUUCCA GCCGAAAGGCGAGUCAAGGUCU UGGCCGCA	3198
1573	AAGAUGUG G CCACGUCC	1286	GGACGUGG GCCGAAAGGCGAGUCAAGGUCU CACAUCUU	3199
1578	GUGGCCAC G UCCCAAGA	1287	UCUUGGGA GCCGAAAGGCGAGUCAAGGUCU GUGGCCAC	3200
1599	UGUUACAA G UUUGCCAU	1288	AUGGCAAA GCCGAAAGGCGAGUCAAGGUCU UUGUAACA	3201
1614	AUCUCACA G UCAUCCAC	1289	GUGGAUGA GCCGAAAGGCGAGUCAAGGUCU UGUGAGAU	3202
1625	AUCCACGG G CACUGUUA	1290	UAACAGUG GCCGAAAGGCGAGUCAAGGUCU CCGUGGAU	3203
1639	UUAUGGGA G CUGUUAUC	1291	GAUAACAG GCCGAAAGGCGAGUCAAGGUCU UCCCAUAA	3204
1655	CAUGGAGG G CUUCUACG	1292	CGUAGAAG GCCGAAAGGCGAGUCAAGGUCU CCUCCAUG	3205
1663	GCUUCUAC G UUGUCUUU	1293	AAAGACAA GCCGAAAGGCGAGUCAAGGUCU GUAGAAGC	3206
1678	UUGAUCGG G CCCGAAAA	1294	UUUUCGGG GCCGAAAGGCGAGUCAAGGUCU CCGAUCAA	3207
1694	ACGAAUUG G CUUUGCUG	1295	CAGCAAAG GCCGAAAGGCGAGUCAAGGUCU CAAUUCGU	3208
1706	UGCUGUCA G CGCUUGCC	1296	GGCAAGCG GCCGAAAGGCGAGUCAAGGUCU UGACAGCA	3209
1728	CACGAUGA G UUCAGGAC	1297	GUCCUGAA GCCGAAAGGCGAGUCAAGGUCU UCAUCGUG	3210
1738		1298	CACCGCUG GCCGAAAGGCGAGUCAAGGUCU CGUCCUGA	3211
1741	GGACGGCA G CGGUGGAA	1299	UUCCACCG GCCGAAAGGCGAGUCAAGGUCU UGCCGUCC	3212
1744		1300	GCCUUCCA GCCGAAAGGCGAGUCAAGGUCU CGCUGCCG	3213
1751		1301	CAAAAGGG GCCGAAAGGCGAGUCAAGGUCU CUUCCACC	3214
1784		1302	UGUUGUAG GCCGAAAGGCGAGUCAAGGUCU CACAGUCU	3215
1809		1303	AGGGUUGA GCCGAAAGGCGAGUCAAGGUCU UCAUCUGU	3216
1828		1304	GACAUAGG GCCGAAAGGCGAGUCAAGGUCU UAUGGUCA	3217
1840		1305	GAUGGCAG GCCGAAAGGCGAGUCAAGGUCU CAUGACAU	3218
1882		1306	CUGACACA GCCGAAAGGCGAGUCAAGGUCU CAUGAGGC	3219
1892		1307	CAGCGCCA GCCGAAAGGCGAGUCAAGGUCU UGACACAC	3220
1893		1308	AGGCAGCG GCCGAAAGGCGAGUCAAGGUCU CACUGACA	3221
1917		1309	UCAUGCUG GCCGAAAGGCGAGUCAAGGUCU UGGCGCAG	3222
191	COGCGCCA G CAGCAGGA	1307		

Table 21

1956 CUGCUGAA G URAGGAGG 1311 CCUCCUCA GCCGAAAGGCGAGUCAAGGUCU UUCAGCAG 3224 1964 GUGAGGAG C CCCAUGGG 1312 CCCAUGGG GCCGAAAGGCGAGUCAAGGUCU CUCCUCA 2225 1972 GCCCAUGG G CAGAAGAU 1313 AUCUUCUG GCCGAAAGGCGAGUCAAGGUCU CCAUGGGC 1226					
1975	1920	CGCCAGCA G CAUGAUGA	1310	UCAUCAUG GCCGAAAGGCGAGUCAAGGUCU UGCUGGCG	3223
	1956	CUGCUGAA G UGAGGAGG	1311	CCUCCUCA GCCGAAAGGCGAGUCAAGGUCU UUCAGCAG	3224
ACACCUCC GUGUINEC SUGUINEC 1314 GUGUACCA GCCGANAGGCGAGUICAGGUCU GGAGGUGU 3227	1964	GUGAGGAG G CCCAUGGG	1312	CCCAUGGG GCCGAAAGGCGAGUCAAGGUCU CUCCUCAC	3225
CCUCCEBUG & DUCKCUUU	1972	GCCCAUGG G CAGAAGAU	1313	AUCUUCUG GCCGAAAGGCGAGUCAAGGUCU CCAUGGGC	3226
	2006	ACACCUCC G UGGUUCAC	1314	GUGAACCA GCCGAAAGGCGAGUCAAGGUCU GGAGGUGU	3227
	2009	CCUCCGUG G UUCACUUU	1315	AAAGUGAA GCCGAAAGGCGAGUCAAGGUCU CACGGAGG	3228
2012 CACAGANG G CACCUGIG 1318 CACAGGUG GCCGANAGGCGAGUCANGGUC CAUCUGUG 2231 2051 CACCUGUG G CACAGAGCA 1319 UGCUCUGG GCCGANAGGCGAGUCANGGUCU CAUCUGUG 2323 2257 UGGCCAGA G CACCUCAG 1320 CUGAGGUG GCCGANAGGCGAGUCANGGUCU UCUGGCCA 3232 2257 UGGCCAGA G CACCUCAG 1320 CUGAGGUG GCCGANAGGCGAGUCANGGUCU UCUGGCCA 3232 2218 ANAGGCGG C CANAGGUG 1321 CUUGACCAG GCCGANAGGCGAGUCANAGGUCU UCUGGCCA 3232 2218 ANAGGCGG C CANAGGUG 1322 CUGACCAG GCCGANAGGCGAGUCANAGGUCU UCUGGCCA 2234 2218 ANAGGCGG C CANAGGUG 1322 CCACCUUG G CACAGAGAGGCGAGUCANAGGUCU CUUGCCA 2226 2227 CAAGGUGG G UCUCAGGAGG 1324 CCCUGGAA GCCGGANAGGCGAGUCANAGGUCU UCUGCCA 2226 2227 CAAGGUGG G UCUCAGGAG 1324 CCCUGGAA GCCGANAGGCGAGUCANAGGUCU UCUCCCUUG 2237 2227 ARAAGAA G CACUCUGC 1325 GCAGAGGUG GCCGANAGGCGAGUCANAGGUCU UCUCUUCU 3238 CUCUGCUG G CACAGAGG CAGGCAGAGAGCAGUCANAGGUCU UCUCUUCU 3238 UCUCUCUU G UCACCUCA 1326 UAUUUCCCG GCCGANAGGCGAGUCANAGGUCU UCACCAGAG 2329 UAUUUCUU G UCACCUCA 1327 UAUUUCCG GCCGANAGGCGAGUCANAGGUCU UCACCAGAG 2329 UAUUUCUU G UCACCUCA 1327 UAUUUCCG G GCCGANAGGCGAGUCANAGGUCU UCACCAGAG 2224 ANADUUCA G CCCUCAAAG 1328 UUUCCCGA GCCGANAGGCGAGUCANAGGUCU UUAAAUUU 2241 2424 ANADUUCA G CCCUCAAAG 1328 UUUCCCGA GCCGANAGGCGAGUCANAGGUCU UUAAAUUU 2242 2424 ANACUCA G CCCUCAAAG 1331 UUCCCAGA GCCGANAGGCGAGUCANAGGUCU UUAAAUUU 2243 2444 ANACUCA G CCCUCACAC 1331 UUCCCAGA GCCGANAGGCGAGUCANAGGUCU UUAAGAAA 3244 2324 UUUCCCAGA G UUCCAGCA 1332 UCCCCACUA GCCGANAGGCGAGUCANAGGUCU UUAAGAAA 3244 2324 ANAUCCUG G CAUCACAC 1333 UCCCCACUA GCCGANAGGCGAGUCANAGGUCU UUCCGAA 3242 1244 ANAUUCUG G CAUCACAC 1333 UCCCCACUA GCCGANAGGCGAGUCANAGGUCU UUCCGAAA 3244 2324 AUCCCCCAC G CUUCACAC 1335 GCACACAC GCCGANAGGCGAGUCANAGGUCU UUCCGAAA 3244 2324 ACCCCCAC G UUCCCCAC 1335 GCACACA GCCGANAGGCGAGUCANAGGUCU UCCCCACAGGU UCCCCACAGGCGAGCCACCCACAGGCCACCCCACGGCGAGCCCACAGGCCACCCCACGGCGAGCCCACAGGCCACCCCACGGCGAGC	2019	UCACUUUG G UCACAAGU	1316	ACUUGUGA GCCGAAAGGCGAGUCAAGGUCU CAAAGUGA	3229
	2026	GGUCACAA G UAGGAGAC	1317	GUCUCCUA GCCGAAAGGCGAGUCAAGGUCU UUGUGACC	3230
1920	2042	CACAGAUG G CACCUGUG	1318	CACAGGUG GCCGAAAGGCGAGUCAAGGUCU CAUCUGUG	3231
1321 AGGANAMG G CUSGCAMG 1321 CUSGCAGG GCCGANAGGCGAGUCAAGGUCU CUUUUCCU 3224	2051	CACCUGUG G CCAGAGCA	1319	UGCUCUGG GCCGAAAGGCGAGUCAAGGUCU CACAGGUG	3232
2213	2057	UGGCCAGA G CACCUCAG	1320	CUGAGGUG GCCGAAAGGCGAGUCAAGGUCU UCUGGCCA	3233
2127 CUGGENAG G IUGGUIUCC 1323 GGANACCA GCCGANAGGCGAUICANGGUCU CUUGCCAG 3226 2127 CAAGGUIGG G IUGCAGUG 1324 CCCUGGNA GCCGANAGGCGAUICANAGGUCU CUUGCCAG 3237 2128 CAAGGUIGG G IUGCAGUG 1325 GCAGAGUG GCCGANAGGCGAUCANGGUCU CCACCUUG 3237 2129 UACCUUGG G UCACCUCC 1325 GCAGAGUG GCCGANAGGCGAUCANGGUCU UCUUCCU 3238 2129 UACCUUGG G UCACCUCA 1326 UAUUCCCG GCCGANAGGCGAUCANAGGUCU UCUCUCCU 3237 2129 UACCUUGG G UCACCUCA 1326 UAUUCCCG GCCGANAGGCGAUCANAGGUCU UCACCAMAG 3239 2121 AAAUUTAA G UCAGGANA 1228 UTUCCCGA GCCGANAGGCGAUCANAGGUCU UTAAGAUGU 2424 2214 AAAUUTAA G UUUCAGAA 1328 UTUCCCGA GCCGANAGGCGAUCHAAGGUCU UTAAGAUTU 2424 2226 AACCUAGA G UAUUCCUC 1330 GAAGAAUA GCCGANAGGCGAUCHAAGGUCU UTAAGAATA 3244 2320 UTUUCUUTA G UUUCAGAA 1331 UUCUGAAA GCCGANAGGCGAUCHAAGGUCU UTAAGAATA 3244 2321 AUGUACAG G UAUCAGAC 1331 UUCUGAAA GCCGANAGGCGAUCHAAGGUCU UTAAGAATA 3244 2321 UTUCCUUG G G CAUCACAC 1331 UUCUGAAA GCCGANAGGCGAUCHAAGGUCU UTAAGAATA 3244 2321 UTUCCUUG G G CAUCACAC 1332 GUGUGAUG GCCGANAGGCGAUCHAAGGUCU UTAAGAATA 3244 2322 AUGUACCUG G GUUCAGGA 1332 UUCCCAGUA GCCGANAGGCGAUCHAAGGUCU UTAAGAATA 3244 2323 ACCUGGC G GUUCCCUU 1334 GUGUGAUG GCCGANAGGCGAUCHAAGGUCU UTAAGAATA 3244 2324 ACCUUGCG G GUGCCUU 1335 GACACAC GCCGANAGGCGAUCHAAGGUCU CAGUACU 3246 2334 ACCUUGCC G UGUGUCC 1336 GACACAC GCCGANAGGCGAUCHAAGGUCU CAGUACU 3246 2347 UUCCCUGUG G UACCCUUG 1337 CCAGGGUA GCCGANAGGCGAUCHAAGGUCU CACAGGU 3246 2347 ACCUUGCC G UGUGUCC 1336 GACACAC GCCGANAGGCGAUCHAAGGUCU CACAGGU 3250 2348 ACCUACAC G CUUGUCUCU 1339 CCAGGGAAGGCGAUCHAAGGUCU CACAGGUC 3251 2349 CACACCAC G CUUGUCUCU 1336 GAACACAG GCCGANAGGCGAUCHAAGGUCU CACAGGU 3251 2351 CACACCAG G UUCACAGA G CUUGACGAAGGCGAUCHAAGGUCU CACAGGC 3251 2352 GAACACAG CUUGUCUCU 1336 GAACACAG GCCGANAGGCGAUCHAAGGUCU CACAGGC 3251 2353 CACACCAG G UUCACAGG 3144 AUGUACGG GCCGANAGGCGAUCHAAGGUCU CACAGGC 3252	2114	AGGAAAAG G CUGGCAAG	1321	CUUGCCAG GCCGAAAGGCGAGUCAAGGUCU CUUUUCCU	3234
2227 CANGGUIGG & UUCCAGGG 1324 CCCUIGGAA. GCCRAAAGGCGAGUICAAGGICU CCACCUUG 2325 2172 AGAAAGA & CACUCUGC 1325 GCCAGAAAGGCGAGUICAAGGICU CCACCUUG 2327 2183 CUUGGCUG & CGGAAAIA 1326 UUUUCCCG GCCGAAAGGCGAGUICAAGGICU CAGCAGAG 3239 2183 CUUGGCUG & CCACCUCA 1327 UUAUUCCCG GCCGAAAGGCGAGUICAAGGUCU CAGGAGUA 3240 2184 AAAUUUCA & CUCKACUCA 1327 UUAUGCGGA GCCAAAGGCGAGUICAAGGUCU CAAGAGUA 3240 2241 AAAUUUCA & CCCUSAAC 1329 GUUCAGGG GCCGAAAGGCGAGUICAAGGUCU UGAAGGUU 3242 2288 AACCUACAA 1312 UUCCCGAA GCCAAAAGGCAGAUCAAGGUCU UGAAGAUU 3242 2326 HUULCUA & UULCAGAA 1331 UUCCGAAAAGGCGAGUCAAAGGCAGUUCU UAAAAAAA 2424 2314 AUUUCAGAA 13131 UUCCGAAAAGGCAGAUCAAAGGCAGUUCU UAAAAAAA 2242 2321 AUACUCUG 6 CAULCACA 1333 GUUCAGAGAAGGCAGUCAAAGGCAGUUCAAGGUCU UUCAAAAAA 2242 2324 UUACCUGAA 6 CAULCACAC 1333 GUUCAGUA 6 CACAAGGAAG	2118	AAAGGCUG G CAAGGUGG	1322	CCACCUUG GCCGAAAGGCGAGUCAAGGUCU CAGCCUUU	3235
2172 AGARAGAA G CACUCUEC 1325 GCAGAGUE G CCGRANAGGCGAGUCAAGGUCU UUCUUUUU 3238 2183 CUCUGUCU G G GGGAANA 1326 UUUUUCCG GCCGAAAGGCGAGUCAAGGUCU CAGCAGAA 3239 2198 UACUCUUG G UCACCUCA 1327 UUUCCGG GCCGAAAGGCGAGUCAAGGUCU CAGCAGAA 3240 2214 AAAUUUAA G UCGGGAAA 1328 UUUCCGGA GCCGAAAGGCGAGUCAAGGUCU UUAAGAUUU 3241 2243 AAACUUA G CCCUCAAAG 1329 GUUCAGG G GCCGAAAGGCGAGUCAAGGUCU UUAAGAUUU 3242 2385 AACCCAAA G UUUCAGAA 1329 GUUCAGG G GCCGAAAGGCGAGUCAAGGUCU UUUGGGUU 3243 2315 UUUUCUUA G UUUCAGAA 1331 UUCCGAAAA GCCGAAAGGCGAGUCAAGGUCU UUUGGGUU 3243 2316 UUUUCUUA G UUUCAGAA 1331 UUCCGAAAA GCCGAAAGGCGAGUCAAGGUCU UUUGGAAA 3245 2314 AAUUCUUG G GUUCAGCA 1333 UUCCCAAUAAGGCAGUCUAAGGUCU UUCUGAAA 3245 2320 AAGUACUG G GUUCACAC 1333 GUUGAGGA GCCGAAAGGCGAGUCAAGGUCU UUCUGAAA 3245 2313 ACACACAG G UUACACAC 1335 GACACAC G GCCGAAAGGCGAGUCAAGGUCU CAGGUGU 23266 2314 ACCUUGGC G UUGGUCC	2123	CUGGCAAG G UGGGUUCC	1323	GGAACCCA GCCGAAAGGCGAGUCAAGGUCU CUUGCCAG	3236
2198 LICUCUECTIG G CEGGANIII 1326	2127	CAAGGUGG G UUCCAGGG	1324	CCCUGGAA GCCGAAAGGCGAGUCAAGGUCU CCACCUUG	3237
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2288	2214	AAAUUUAA G UCGGGAAA	1328	UUUCCCGA GCCGAAAGGCGAGUCAAGGUCU UUAAAUUU	3241
2305 UUULCUUJA G UUUCAGAA 1331 UUUCAGAAA GCCGAAAGGCGAGUCAAGGICU UJAAGAAAA 2244 2314 UUUCAGAA G UACUDGCA 1332 UUCCAGAAA GCCGAAAGGCGAGUCAAGGICU UUCAGAAAA 2326 2320 AAGUACUG G CHUACCUG 1334 CAGGUAAGGCGAGUCAAGGUCU CAGUACUU 3246 2331 ACAGGUAAGGCGAAGGCGAGUCAAGGUCU CAGUACUU 3247 23242 UUACCUUG G CUUACCUG 1334 CAAGGUAA GCCGAAAGGCGAGUCAAGGUCU CAGGUAU 3247 2344 UACCUUG G G UACCUG 1336 GGACAACA GCCGAAAGGCGAGUCAAGGUCU CACAGGU 23260 2347 ACCUUGG G UACCCUG 1336 GGACAACA GCCGAAAGGCAGUCAAGGUCU CACAGGU 23260 2359 UCCCUUG G UACCCUG 1337 CCCAGGUA GCCGAAAGGCAGUCAAGGUCU CACAGGU 2327 2359 UCCCUCAG G CAGACAAAG 1338 CUUCUCUG GCCGAAAGGCAGUCAAGGUCU CACAGGUC 2328 2381 GAGACCAA G CUUGUUUU C 1339 CUUCUCUA GCCGAAAGGCAGUCAAGGUCU CACAGGC 2323 2403 UGGCCAAA GUCAGAGAGA G CUUGUUCUU C 1340 GACUUGG G GCCAAAGGCAGGUCUCAAGGUCU CACAGGC 2323 2403 UGGCCAAA GUCAGAAGGAGAGAGAGAGCAGGCAGAGGCAAAGGCAGGC	2243	AAACUUCA G CCCUGAAC	1329	GUUCAGGG GCCGAAAGGCGAGUCAAGGUCU UGAAGUUU	3242
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3233 AACURCTE G CHUCACAC 1334 GRUDBALE GECGRANGGGGGRUCANGRUCT CAGUACTU 2246 2333 ACAGGGAG G UULACUUG 1334 CANAGUUA GECGRANGGGGGRUCANGRUCT CAGUACTU 3247 2342 UULACUUG G GGUGUGUC 1335 GRACACAG GECGRANGGGGRUCANGGUCT CUGCGURU 3247 2344 ACCUUGGG G UUGGGCC 1336 GGRACACA GECGRANGGGGGGUCANGGUCT CAGGUAC 3249 2357 UCCCUUGG G URACCUUG 1336 GGRACACA GECGRANGGGGGGUCANGGUCT GCCANGGU 3249 2359 GUACCCUG G CAGAGANA 1338 CUUCUUG GCCANAGGGGGGGGCANGCANGGUCT CAGGGUAC 3251 2369 GUACCCUG G CAGAGANA 1338 CUUCUUG GCCANAGGGGAGGCANGCANGGGCU CAGGGUAC 3251 2361 GRACACA G CUUGUUTU 1339 GAACACAG GCCGANAGGGGAGUCANGGGUCT 2325 2362 CCUIGCUG G CCANAGUC 1340 GAACACAG GCCAANGGCGANGCANGGCUCT 2326 2463 GUACACAG G UUUGUUT 1340 GACUUTUG GCCGANAGGCAGUCANGGUCT 2326 2463 CAARGUCA G UUCGUGA 3441 CUUCUCUA GCCGANAGGGAGGUCANGGUCT 1346 2464 CAARGUCA G UUCGUGA 1342 CUUCUCUA GCCGANAGGGGAGUCANGGUCT 1366 2465 AUBACACA G CUUCHACUA 1344 AUBACACAA GCCGANAGGGAGGUCTANGGUCT 1366 2466 AUBACACA G CUUCACACA 1344 AUBUUAGA GCCGANAGGGGAGGUCANGGCANGUCTUUTUU 3256 2461 AUBACACA G CUCACACA 1344 AUBUUAGA GCCGANAGGGGAGGGGAGCACGCUCANGGGCUC 1366 2461 AUBACACA G CUCACACA 1344 AUBUUAGA GCCGANAGGGCANGCCANGGCCC 1344 2461 AUBACACA G CUCACACA 1344 AUBUUAGA GCCGANAGGGGAGGGCACCCCANGGCCC 1344 2461 AUBACACA G CUCACACA 1344 AUBUUAGA GCCGANAGGGCANGCCANGGCCC 1344 2461 AUBACACA G CUCACACA 1344 AUBUUAGA GCCGANAGGGCANGCCANGCCC 1344 2461 AUBACACA G CUCACACA 1344 AUBUAGAG GCCCANAGGGCANGCCANGCCC 1344 2461 AUBACACA G CUCACACA 1344 AUBUAGAG GCCCANAGGGCANGCCANGCCCANGCCC 1344 2461 AUBACACA G CUCACACA 1344 AUBUAGAG GCCCANAGGGCANGCCANGCCCANGCCC 1344 2461 AUBACACA G CUCACACA 1344 AUBUAGAG GCCCANAGGCANGCCCANGCCCC 1344 2461 AUBACACAC G CUCACACAC 1344 AUBUAGAG GCCCANAGGCANGCCCANGCCCC 1344 2461 AUBACACAC G CUCACACACCCC 1344 1344 1344 1344 1344 1344 1344 134	2305	UUUUCUUA G UUUCAGAA	1331	UUCUGAAA GCCGAAAGGCGAGUCAAGGUCU UAAGAAAA	3244
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2357 UCCCUGUG G LACCCUGO 1337 CCAGGGUA GCCGRAAGGCGCGUCAAGGIUC CACAGGGA 2250 2365 GUACCCUG G CAGAGAMG 1338 CUUUUUUG GCCGAAAGGCGGGUCAAGGIUC CAGGGUAC 2351 2381 GAGACCAA G CUUGUTUC 1339 GAAACAAG GCCGGAAAGGCGGGUCAAGGIUC AGGGUC 3252 2397 CCCUGUG G CCCAAAGGC 1410 GACUUGG GCCGAAAGGCGAGUCAAGGGUC UUGGCUC 3253 2401 UGGCCAAA G UCCAGUAG 1411 CCUCUCA GCCGAAAGGCGAGUCAAGGUC UUGCCC 2324 2407 CAAAGUCA G UUGCUAU 1342 CUCUCCA GCCGAAAGGCGAGUCAAGGUC UUGCCAU 3255 2424 GAUGCACA G UUGCUAU 1343 AUGCCACA G CUCGCAAGGCGGAGUCAAGGCCGUUUGUUUGUCAUC 2325 2463 AUAAACAA G CCCCAAACGCAGGCGGCGCGCCCCACGCCACGCCAGGCCACGCCACGCCAGGCCACGCCACCCCCACCCCCC	2342	UUACCUUG G CGUGUGUC	1335	GACACACG GCCGAAAGGCGAGUCAAGGUCU CAAGGUAA	3248
2365 GUACCCUG G CAGAGAAG 1338 CUUCUCUG GCCGAAAGGCGAGUCAAGGUCU CAGGGUAC 3251 2391 GAGACCAA G CUUGUUUC 1339 GAAACAAG GCCGAAAGGCGAGUCAAGGUCU UUGGUCUC 3252 2492 CCUGUCUG G CCCAAAGUC 1340 GACUUUGG GCCAAAGGCAGUCUCAAGGUCU UCACAGGCC 3252 2403 UGGCCAAA G UCAGUAGG 1341 CCUACUGA GCCGAAAGGCGAGUCAAGGUCU UUUGGCCA 3254 2407 CAAAGUCA G UAGGAGAG 1342 CUCUCCUA GCCGAAAGGCGAGUCAAGGUCU UGACUUUG 3255 2424 GAUGCACA G UUUGCUAU 1343 AUAGCAAA GCCGAAAGGCGAGAAGGCCAGUCAAGGUCU UUGUCULC 2263 2463 AUAAACAA G CCUACAU 1344 AUGUUAGG GCCGAAAGGCGGAGUCAAGGUCU UUGUUUAU 3257	2344	ACCUUGGC G UGUGUCCC	1336	GGGACACA GCCGAAAGGCGAGUCAAGGUCU GCCAAGGU	3249
2381 GAGACCAA G CUUGUUUC 1339 GAAACAAG GCCGGAAAGGCGAGUCAAGGUCU UUGGUCUC 3252 2397 CCCUGCUG G CCRAAGUC 1340 GACUUUGG GCCGAAAGGCGAGUCAAGGUCU CACCAGG 3253 2401 UGGCCAAA G UCAGUAGG 1341 CCULXCUGA GCCGAAAGGCGAGUCAAGGUCU UGACUUGG 3254 2407 CAAAGUCA G UUGCUAU 1342 CUCUCCUA GCCGAAAGGGGAGUCAAGGUCU UGACUUGG 3255 2424 GAUGCACA G UUUGCUAU 1343 AUJAGCAAA GCCGAAAGGCGAGUCAAGGUCU UGACUUG 2356 2463 AURAACAA G CCUACAU 1344 AUGUUAGG GCCGAAAGGCGAGUCAAGGUCU UGACUUG 2356	2357	UCCCUGUG G UACCCUGG	1337	CCAGGGUA GCCGAAAGGCGAGUCAAGGUCU CACAGGGA	3250
2397 CCCUGCUG G CCRAAGUC 1340 GACUUUGG GCCGAAAGGCGAGUCAAGGUCU CAGCAGGG 3253 2403 UGGCCAAA G UCKGUAGG 1341 CCUACUGA GCCGAAAGGCGAGUCAAGGUCU UUUGACCA 3254 2407 CAAAGUCA G UAGGAGAG 1342 CUUUCCUA GCCGAAAGGCGAGUCAAGGUCU UGACUUUG 3256 2424 GAUGCACA G UUUGCUAU 1343 AUGACAAA GCCGAAAGGCGAGUCAAGGUCU UGUGCAUC 3256 2463 AUAAACAA G CCUAACAU 1344 AUGUUAGG GCCGAAAGGCGAGUCAAGGUCU UUGUUUAU 3257	2365	GUACCCUG G CAGAGAAG	1338	CUUCUCUG GCCGAAAGGCGAGUCAAGGUCU CAGGGUAC	3251
2403 UGGCCAAA G UCAGUAGG 1341 CCUACUGA GCCGAAAGGCGAGUCAAGGUCU UJUGGCCA 3254 2407 CAAAGUCA G UAGGAGAG 1342 CUCUCCUA GCCGAAAGGCGAGUCAAGGUCU UGACUUUG 3255 2426 GAUGACA G UJUGCAUA 1343 AUGACAAA GCCABAAGGCGAGUCAAGGUCU UGAGUCUC 2366 2463 AUGACAA G CCUCACAU 1344 AUGUUAGG GCCGAAAGGCGAGUCAAGGUCU UUGUUUAU 3257	2381	GAGACCAA G CUUGUUUC	1339	GAAACAAG GCCGAAAGGCGAGUCAAGGUCU UUGGUCUC	3252
2407 CAAAGUCA G UMGGAGG 1342 CUCUCCILA GCCGAAAGGGCGAGUCAAGGICU UGACUUUG 1325 2424 GUUGECAC G UUUGECUAU 1343 AUINGENAA GCCGAAAGGCGAGUCAAGGUCU UGUGCAU 23256 2463 AUAAACAA G CCUAACAU 1344 AUGUUMAG GCCGAAAGGCGAGUCAAGGUCU UUGUGCAU 3256	2397	CCCUGCUG G CCAAAGUC	1340	GACUUUGG GCCGAAAGGCGAGUCAAGGUCU CAGCAGGG	3253
2424 GAUGCACA G UUUGCUAU 1343 AUAGCAAA GCCGAAAGGCGAGUCAAGGUCU UGUGCAUC 3256 2463 AUAAACAA G CCUAACAU 1344 AUGUUAGG GCCGAAAGGCGAGUCAAGGUCU UUGUUUAU 3257	2403	UGGCCAAA G UCAGUAGG	1341	CCUACUGA GCCGAAAGGCGAGUCAAGGUCU UUUGGCCA	3254
2463 AUAAACAA G CCUAACAU 1344 AUGUUAGG GCCGAAAGGCGAGUCAAGGUCU UUGUUUAU 3257	2407	CAAAGUCA G UAGGAGAG	1342	CUCUCCUA GCCGAAAGGCGAGUCAAGGUCU UGACUUUG	3255
	2424	GAUGCACA G UUUGCUAU	1343	AUAGCAAA GCCGAAAGGCGAGUCAAGGUCU UGUGCAUC	3256
2474 UAACAUUG G UGCAAAGA 1345 UCUUUGCA GCCGAAAGGCGAGUCAAGGUCU CAAUGUUA 3258	2463	AUAAACAA G CCUAACAU	1344	AUGUUAGG GCCGAAAGGCGAGUCAAGGUCU UUGUUUAU	3257
	2474	UAACAUUG G UGCAAAGA	1345	UCUUUGCA GCCGAAAGGCGAGUCAAGGUCU CAAUGUUA	3258

Input Sequence = AF190725. Cut Site = G/. Stem Length = 8 . Core Sequence = GCcgaaagGCGaGuCaaGGuCu AF190725 (Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA; 2526 bp)

Table 22: Human BACE DNAzyme and Target Sequence

Pos	Substrate	Seq ID	Ribozyme	Rz Seq
48	GCUGGAUU A UGGUGGCC	3	GGCCACCA GGCTAGCTACAACGA AATCCAGC	3259
677	GCAGGGCU A CUACGUGG	27	CCACGTAG GGCTAGCTACAACGA AGCCCTGC	3260
680	GGGCUACU A CGUGGAGA	28	TCTCCACG GGCTAGCTACAACGA AGTAGCCC	3261
733	UGGUGGAU A CAGGCAGC	31	GCTGCCTG GGCTAGCTACAACGA ATCCACCA	3262
788	GCAUCGCU A CUACCAGA	38	TCTGGTAG GGCTAGCTACAACGA AGCGATGC	3263
791	UCGCUACU A CCAGAGGC	39	GCCTCTGG GGCTAGCTACAACGA AGTAGCGA	3264
815	CAGCACAU A CCGGGACC	41	GGTCCCGG GGCTAGCTACAACGA ATGTGCTG	3265
839	GGGUGUGU A UGUGCCCU	43	AGGGCACA GGCTAGCTACAACGA ACACACCC	3266
848	UGUGCCCU A CACCCAGG	44	CCTGGGTG GGCTAGCTACAACGA AGGGCACA	3267
1004	GCUGGCCU A UGCUGAGA	58	TCTCAGCA GGCTAGCTACAACGA AGGCCAGC	3268
1171	UUGGAGGU A UCGACCAC	85	GTGGTCGA GGCTAGCTACAACGA ACCTCCAA	3269
1187	CUCGCUGU A CACAGGCA	88	TGCCTGTG GGCTAGCTACAACGA ACAGCGAG	3270
1205	UCUCUGGU A UACACCCA	91	TGGGTGTA GGCTAGCTACAACGA ACCAGAGA	3271
1207	UCUGGUAU A CACCCAUC	92	GATGGGTG GGCTAGCTACAACGA ATACCAGA	3272
1229	GGAGUGGU A UUAUGAGG	94	CCTCATAA GGCTAGCTACAACGA ACCACTCC	3273
1232	GUGGUAUU A UGAGGUGA	96	TCACCTCA GGCTAGCTACAACGA AATACCAC	3274
1295	CAAGGAGU A CAACUAUG	101	CATAGTTG GGCTAGCTACAACGA ACTCCTTG	3275
1301	GUACAACU A UGACAAGA	102	TCTTGTCA GGCTAGCTACAACGA AGTTGTAC	. 3276
1493	CUCACUCU A CCUAAUGG	130	CCATTAGG GGCTAGCTACAACGA AGAGTGAG	3277
1510	GUGAGGUU A CCAACCAG	133	CTGGTTGG GGCTAGCTACAACGA AACCTCAC	3278
1550	GCAGCAAU A CCUGCGGC	141	GCCGCAGG GGCTAGCTACAACGA ATTGCTGC	3279
1595	CGACUGUU A CAAGUUUG	144	CAAACTTG GGCTAGCTACAACGA AACAGTCG	3280
1633	GCACUGUU A UGGGAGCU	152	AGCTCCCA GGCTAGCTACAACGA AACAGTGC	3281
1645	GAGCUGUU A UCAUGGAG	154	CTCCATGA GGCTAGCTACAACGA AACAGCTC	3282
1661	GGGCUUCU A CGUUGUCU	158	AGACAACG GGCTAGCTACAACGA AGAAGCCC	3283
1787	CUGUGGCU A CAACAUUC	176	GAATGTTG GGCTAGCTACAACGA AGCCACAG	3284
1832	CAUAGCCU A UGUCAUGG	182	CCATGACA GGCTAGCTACAACGA AGGCTATG	3285
2141	GGGACUGU A CCUGUAGG	212	CCTACAGG GGCTAGCTACAACGA ACAGTCCC	3286
2191	GCGGGAAU A CUCUUGGU	215	ACCAAGAG GGCTAGCTACAACGA ATTCCCGC	3287
2290	CCCAAAGU A UUCUUCUU	240	AAGAAGAA GGCTAGCTACAACGA ACTTTGGG	3288
2316	UCAGAAGU A CUGGCAUC	254	GATGCCAG GGCTAGCTACAACGA ACTTCTGA	3289
2336	CGCAGGUU A CCUUGGCG	257	CGCCAAGG GGCTAGCTACAACGA AACCTGCG	3290
2359	CCUGUGGU A CCCUGGCA	260	TGCCAGGG GGCTAGCTACAACGA ACCACAGG	3291
2431	AGUUUGCU A UUUGCUUU	269	AAAGCAAA GGCTAGCTACAACGA AGCAAACT	3292
2455	GGGACUGU A UAAACAAG	275	CTTGTTTA GGCTAGCTACAACGA ACAGTCCC	3293
140	AAGCCGCC A CCGGCCCG	322	CGGGCCGG GGCTAGCTACAACGA GGCGGCTT	3294
151	GGCCCGCC A UGCCCGCC	327	GGCGGGCA GGCTAGCTACAACGA GGCGGGCC	3295
287	CGCUCUCC A CAGCCCGG	380	CCGGGCTG GGCTAGCTACAACGA GGAGAGCG	3296
368	GAGAAGCC A CCAGCACC	412	GGTGCTGG GGCTAGCTACAACGA GGCTTCTC	3297
374	CCACCAGC A CCACCCAG	415	CTGGGTGG GGCTAGCTACAACGA GCTGGTGG	3298
377	CCAGCACC A CCCAGACU	417	AGTCTGGG GGCTAGCTACAACGA GGTGCTGG	3299
451	CGGGGCCC A CCAUGGCC	435	GGCCATGG GGCTAGCTACAACGA GGGCCCCG	3300
454	GGCCCACC A UGGCCCAA	437	TTGGGCCA GGCTAGCTACAACGA GGTGGGCC	3301
512	GCCUGCCC A COGCACCC	456	GGGTGCCG GGCTAGCTACAACGA GGGCAGGC	3302
517	CCCACGGC A CCCAGCAC	457	GTGCTGGG GGCTAGCTACAACGA GCCGTGGG	3303
524	CACCCAGC A CGGCAUCC	461	GGATGCCG GGCTAGCTACAACGA GCTGGGTG	3304
529	AGCACGGC A UCCGGCUG	462	CAGCCGGA GGCTAGCTACAACGA GCCGTGCT	3305

			CACCAGGA GGCTAGCTACAACGA GTTGAGCG	3306
721	CGCUCAAC A UCCUGGUG	508	GGAAGGG GGCTAGCTACAACGA GGGGGGCA	3307
770	UGCCCCCC A CCCCUUCC	522	AGTAGCGA GGCTAGCTACAACGA GCAGGAAG	3308
782	CUUCCUGC A UCGCUACU	529		3309
811	UGUCCAGC A CAUACCGG	538	CCGGTATG GGCTAGCTACAACGA GCTGGACA	3310
813	UCCAGCAC A UACCGGGA	539	TCCCGGTA GGCTAGCTACAACGA GTGCTGGA	3311
850	UGCCCUAC A CCCAGGGC	547	GCCCTGGG GGCTAGCTACAACGA GTAGGGCA	3312
880	AGCUGGGC A CCGACCUG	553	CAGGTCGG GGCTAGCTACAACGA GCCCAGCT	3313
895	UGGUAAGC A UCCCCCAU	557	ATGGGGGA GGCTAGCTACAACGA GCTTACCA	3313
902	CAUCCCCC A UGGCCCCA	562	TGGGGCCA GGCTAGCTACAACGA GGGGGATG	3314
916	CCAACGUC A CUGUGCGU	567	ACGCACAG GGCTAGCTACAACGA GACGTTGG	3316
931	GUGCCAAC A UUGCUGCC	571	GGCAGCAA GGCTAGCTACAACGA GTTGGCAC	3317
940	UUGCUGCC A UCACUGAA	574	TTCAGTGA GGCTAGCTACAACGA GGCAGCAA	3317
943	CUGCCAUC A CUGAAUCA	575	TGATTCAG GGCTAGCTACAACGA GATGGCAG	
964	AGUUCUUC A UCAACGGC	580	GCCGTTGA GGCTAGCTACAACGA GAAGAACT	3319
988	GGGAAGGC A UCCUGGGG	586	CCCCAGGA GGCTAGCTACAACGA GCCTTCCC	3320
1070	GCAGACCC A CGUUCCCA	610	TGGGAACG GGCTAGCTACAACGA GGGTCTGC	
1156	GAGGGAGC A UGAUCAUU	638	AATGATCA GGCTAGCTACAACGA GCTCCCTC	3322
1162	GCAUGAUC A UUGGAGGU	639	ACCTCCAA GGCTAGCTACAACGA GATCATGC	3323
1178	UAUCGACC A CUCGCUGU	641	ACAGCGAG GGCTAGCTACAACGA GGTCGATA	3324
1189	CGCUGUAC A CAGGCAGU	644	ACTGCCTG GGCTAGCTACAACGA GTACAGCG	3325
1209	UGGUAUAC A CCCAUCCG	649	CGGATGGG GGCTAGCTACAACGA GTATACCA	3326
1213	AUACACCC A UCCGGCGG	652	CCGCCGGA GGCTAGCTACAACGA GGGTGTAT	3327
1243	AGGUGAUC A UUGUGCGG	654	CCGCACAA GGCTAGCTACAACGA GATCACCT	3328
1312	ACAAGAGC A UUGUGGAC	663	GTCCACAA GGCTAGCTACAACGA GCTCTTGT	3329
1327	ACAGUGGC A CCACCAAC	665	GTTGGTGG GGCTAGCTACAACGA GCCACTGT	3330
1330	GUGGCACC A CCAACCUU	667	AAGGTTGG GGCTAGCTACAACGA GGTGCCAC	3331
1378	UCAAAUCC A UCAAGGCA	679	TGCCTTGA GGCTAGCTACAACGA GGATTTGA	3332
1396	CCUCCUCC A CGGAGAAG	687	CTTCTCCG GGCTAGCTACAACGA GGAGGAGG	3333
1456	AAGCAGGC A CCACCCCU	698	AGGGGTGG GGCTAGCTACAACGA GCCTGCTT	3334
1459	CAGGCACC A CCCCUUGG	700	CCAAGGGG GGCTAGCTACAACGA GGTGCCTG	3335
1471	CUUGGAAC A UUUUCCCA	705	TGGGAAAA GGCTAGCTACAACGA GTTCCAAG	3336
1483	UCCCAGUC A UCUCACUC	709	GAGTGAGA GGCTAGCTACAACGA GACTGGGA	3337
1488	GUCAUCUC A CUCUACCU	711	AGGTAGAG GGCTAGCTACAACGA GAGATGAC	3338
1528	CCUUCCGC A UCACCAUC	723	GATGGTGA GGCTAGCTACAACGA GCGGAAGG	3339
1531	UCCGCAUC A CCAUCCUU	724	AAGGATGG GGCTAGCTACAACGA GATGCGGA	3340
1534	GCAUCACC A UCCUUCCG	726	CGGAAGGA GGCTAGCTACAACGA GGTGATGC	3341
1576	AUGUGGCC A CGUCCCAA	737	TTGGGACG GGCTAGCTACAACGA GGCCACAT	3342
1606	AGUUUGCC A UCUCACAG	744	CTGTGAGA GGCTAGCTACAACGA GGCAAACT	3343
1611	GCCAUCUC A CAGUCAUC	746	GATGACTG GGCTAGCTACAACGA GAGATGGC	3344
1617	UCACAGUC A UCCACGGG	748	CCCGTGGA GGCTAGCTACAACGA GACTGTGA	3345
1621	AGUCAUCC A CGGGCACU	750	AGTGCCCG GGCTAGCTACAACGA GGATGACT	3346
1627	CCACGGC A CUGUUAUG	751	CATAACAG GGCTAGCTACAACGA GCCCGTGG	3347
1648	CUGUUAUC A UGGAGGGC	754	GCCCTCCA GGCTAGCTACAACGA GATAACAG	3348
1715		765	CGTGCACA GGCTAGCTACAACGA GGCAAGCG	3349
1721		766	ACTCATCG GGCTAGCTACAACGA GCACATGG	3350
1762	CUUUUGUC A CCUUGGAC	772	GTCCAAGG GGCTAGCTACAACGA GACAAAAG	3351
1771		775	GTCTTCCA GGCTAGCTACAACGA GTCCAAGG	3352
1792		779	CTGTGGAA GGCTAGCTACAACGA GTTGTAGC	3353
1797		781	TCTGTCTG GGCTAGCTACAACGA GGAATGTT	3354
1819		788	TATGGTCA GGCTAGCTACAACGA GAGGGTTG	3355
1825		790	ATAGGCTA GGCTAGCTACAACGA GGTCATGA	3356
1023				

Table 22

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1837	CCUAUGUC A UGGCUGCC	793	GGCAGCCA GGCTAGCTACAACGA GACATAGG	3357
1846	UGGCUGCC A UCUGCGCC	796	GGCGCAGA GGCTAGCTACAACGA GGCAGCCA	3358
1861	CCCUCUUC A UGCUGCCA	802	TGGCAGCA GGCTAGCTACAACGA GAAGAGGG	3359
1869	AUGCUGCC A CUCUGCCU	805	AGGCAGAG GGCTAGCTACAACGA GGCAGCAT	3360
1879	UCUGCCUC A UGGUGUGU	810	ACACACCA GGCTAGCTACAACGA GAGGCAGA	3361
1922	CCAGCAGC A UGAUGACU	822	AGTCATCA GGCTAGCTACAACGA GCTGCTGG	3362
1942	CUGAUGAC A UCUCCCUG	825	CAGGGAGA GGCTAGCTACAACGA GTCATCAG	3363
1968	GGAGGCCC A UGGGCAGA	833	TCTGCCCA GGCTAGCTACAACGA GGGCCTCC	3364
1998	CCUGGACC A CACCUCCG	840	CGGAGGTG GGCTAGCTACAACGA GGTCCAGG	3365
2000	UGGACCAC A CCUCCGUG	841	CACGGAGG GGCTAGCTACAACGA GTGGTCCA	3366
2013	CGUGGUUC A CUUUGGUC	845	GACCAAAG GGCTAGCTACAACGA GAACCACG	3367
2022	CUUUGGUC A CAAGUAGG	847	CCTACTTG GGCTAGCTACAACGA GACCAAAG	3368
2035	UAGGAGAC A CAGAUGGC	849	GCCATCTG GGCTAGCTACAACGA GTCTCCTA	3369
2044	CAGAUGGC A CCUGUGGC	851	GCCACAGG GGCTAGCTACAACGA GCCATCTG	3370
2059	GCCAGAGC A CCUCAGGA	856	TCCTGAGG GGCTAGCTACAACGA GCTCTGGC	3371
2076	CCCUCCCC A CCCACCAA	866	TTGGTGGG GGCTAGCTACAACGA GGGGAGGG	3372
2080	CCCCACCC A CCAAAUGC	869	GCATTTGG GGCTAGCTACAACGA GGGTGGGG	3373
2174	AAAGAAGC A CUCUGCUG	885	CAGCAGAG GGCTAGCTACAACGA GCTTCTTT	3374
2201	UCUUGGUC A CCUCAAAU	891	ATTTGAGG GGCTAGCTACAACGA GACCAAGA	3375
2260	CUUUGUCC A CCAUUCCU	906	AGGAATGG GGCTAGCTACAACGA GGACAAAG	3376
2263	UGUCCACC A UUCCUUUA	908	TAAAGGAA GGCTAGCTACAACGA GGTGGACA	3377
2322	GUACUGGC A UCACACGC	922	GCGTGTGA GGCTAGCTACAACGA GCCAGTAC	3378
2325	CUGGCAUC A CACGCAGG	923	CCTGCGTG GGCTAGCTACAACGA GATGCCAG	3379
2327	GGCAUCAC A CGCAGGUU	924	AACCTGCG GGCTAGCTACAACGA GTGATGCC	3380
2421	GAGGAUGC A CAGUUUGC	945	GCAAACTG GGCTAGCTACAACGA GCATCCTC	3381
2470	AGCCUAAC A UUGGUGCA	954	TGCACCAA GGCTAGCTACAACGA GTTAGGCT	3382
11	ACGCGUCC G CAGCCCGC	960	GCGGGCTG GGCTAGCTACAACGA GGACGCGT	3383
18	CGCAGCCC G CCCGGGAG	961	CTCCCGGG GGCTAGCTACAACGA GGGCTGCG	3384
29	CGGGAGCU G CGAGCCGC	962	GCGGCTCG GGCTAGCTACAACGA AGCTCCCG	3385
36	UGCGAGCC G CGAGCUGG	964	CCAGCTCG GGCTAGCTACAACGA GGCTCGCA	3386
69	CAGCCAAC G CAGCCGCA	967	TGCGGCTG GGCTAGCTACAACGA GTTGGCTG	3387
75	ACGCAGCC G CAGGAGCC	968	GGCTCCTG GGCTAGCTACAACGA GGCTGCGT	3388
94	GAGCCCUU G CCCCUGCC	969	GGCAGGGG GGCTAGCTACAACGA AAGGGCTC	3389
100	UUGCCCCU G CCCGCGCC	970	GGCGCGGG GGCTAGCTACAACGA AGGGGCAA	3390
104	CCCUGCCC G CGCCGCCG	971	CGGCGGCG GGCTAGCTACAACGA GGGCAGGG	3391
106	CUGCCCGC G CCGCCGCC	972	GGCGGCGG GGCTAGCTACAACGA GCGGGCAG	3392
109	CCCGCGCC G CCGCCCGC	973	GCGGGCGG GGCTAGCTACAACGA GGCGCGGG	3393
112	GCGCCGCC G CCCGCCGG	974	CCGGCGGG GGCTAGCTACAACGA GGCGGCGC	3394
116	CGCCGCCC G CCGGGGGG	975	CCCCCCGG GGCTAGCTACAACGA GGGCGGCG	3395
137	GGGAAGCC G CCACCGGC	976	GCCGGTGG GGCTAGCTACAACGA GGCTTCCC	3396
148	ACCEGCCC G CCAUGCCC	977	GGGCATGG GGCTAGCTACAACGA GGGCCGGT	3397
153	CCCGCCAU G CCCGCCCC	978	GGGGCGGG GGCTAGCTACAACGA ATGGCGGG	3398
157	CCAUGCCC G CCCCUCCC	979	GGGAGGG GGCTAGCTACAACGA GGGCATGG	3399
172	CCAGCCCC G CCGGGAGC	980	GCTCCCGG GGCTAGCTACAACGA GGGGCTGG	3400
183	GGGAGCCC G CGCCCGCU	981	AGCGGGCG GGCTAGCTACAACGA GGGCTCCC	3401
185	GAGCCCGC G CCCGCUGC	982	GCAGCGGG GGCTAGCTACAACGA GCGGGCTC	3402
189	CCGCGCCC G CUGCCCAG	983	CTGGGCAG GGCTAGCTACAACGA GGGCGCGG	3403
192	CGCCCGCU G CCCAGGCU	984	AGCCTGGG GGCTAGCTACAACGA AGCGGGCG	3404
205	GGCUGGCC G CCGCCGUG	985	CACGGCGG GGCTAGCTACAACGA GGCCAGCC	3405
208	UGGCCGCC G CCGUGCCG	986	CGGCACGG GGCTAGCTACAACGA GGCGGCCA	3406
213	GCCGCCGU G CCGAUGUA	987	TACATCGG GGCTAGCTACAACGA ACGGCGGC	3407

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250	UCUCCCCU G CUCCCGUG	989	CACGGGAG GGCTAGCTACAACGA AGGGGAGA	3408
258	GCUCCCGU G CUCUGCGG	990	CCGCAGAG GGCTAGCTACAACGA ACGGGAGC	3409
263	CGUGCUCU G CGGAUCUC	991	GAGATOCG GGCTAGCTACAACGA AGAGCACG	3410
280	CCCUGACC G CUCUCCAC	993	GTGGAGAG GGCTAGCTACAACGA GGTCAGGG	3411
320	AGGGCCCU G CAGGCCCU	994	AGGGCCTG GGCTAGCTACAACGA AGGGCCCT	3412
340	GUCCUGAU G CCCCCAAG	996	CTTGGGGG GGCTAGCTACAACGA ATCAGGAC	3413
397	GGGCAGGC G CCAGGGAC	998	GTCCCTGG GGCTAGCTACAACGA GCCTGCCC	3414
420	GGGCCAGU G CGAGCCCA	999	TGGGCTCG GGCTAGCTACAACGA ACTGGCCC	3415
468	CAAGCCCU G CCCUGGCU	1002	AGCCAGGG GGCTAGCTACAACGA AGGGCTTG	3416
480	UGGCUCCU G CUGUGGAU	1003	ATCCACAG GGCTAGCTACAACGA AGGAGCCA	3417
493	GGAUGGGC G CGGGAGUG	1004	CACTCCCG GGCTAGCTACAACGA GCCCATCC	3418
501	GCGGGAGU G CUGCCUGC	1005	GCAGGCAG GGCTAGCTACAACGA ACTCCCGC	3419
504	GGAGUGCU G CCUGCCCA	1006	TGGGCAGG GGCTAGCTACAACGA AGCACTCC	3420
508	UGCUGCCU G CCCACGGC	1007	GCCGTGGG GGCTAGCTACAACGA AGGCAGCA	3421
537	AUCCGGCU G CCCCUGCG	1008	CGCAGGGG GGCTAGCTACAACGA AGCCGGAT	3422
543	CUGCCCCU G CGCAGCGG	1009	CCGCTGCG GGCTAGCTACAACGA AGGGGCAG	3423
545	GCCCCUGC G CAGCGGCC	1010	GGCCGCTG GGCTAGCTACAACGA GCAGGGGC	3424
562	UGGGGGC G CCCCCUG	1011	CAGGGGG GGCTAGCTACAACGA GCCCCCCA	3425
576	CUGGGGCU G CGGCUGCC	1012	GGCAGCCG GGCTAGCTACAACGA AGCCCCAG	3426
582	CUGCGGCU G CCCCGGGA	1013	TCCCGGGG GGCTAGCTACAACGA AGCCGCAG	3427
708	AGCCCCC G CAGACGCU	1019	AGCGTCTG GGCTAGCTACAACGA GGGGGGCT	3428
714	CCGCAGAC G CUCAACAU	1020	ATGTTGAG GGCTAGCTACAACGA GTCTGCGG	3429
751	GUAACUUU G CAGUGGGU	1021	ACCCACTG GGCTAGCTACAACGA AAAGTTAC	3430
760	CAGUGGGU G CUGCCCCC	1022	GGGGCAG GGCTAGCTACAACGA ACCCACTG	3431
763	UGGGUGCU G CCCCCCAC	1023	GTGGGGG GGCTAGCTACAACGA AGCACCCA	3432
780	CCCUUCCU G CAUCGCUA	1024	TAGCGATG GGCTAGCTACAACGA AGGAAGGG	3433
785	CCUGCAUC G CUACUACC	1025	GGTAGTAG GGCTAGCTACAACGA GATGCAGG	3434
843	GUGUAUGU G CCCUACAC	1026	GTGTAGGG GGCTAGCTACAACGA ACATACAC	3435
921	GUCACUGU G CGUGCCAA	1028	TTGGCACG GGCTAGCTACAACGA ACAGTGAC	3436
925	CUGUGCGU G CCAACAUU	1029	AATGTTGG GGCTAGCTACAACGA ACGCACAG	3437
934	CCAACAUU G CUGCCAUC	1030	GATGGCAG GGCTAGCTACAACGA AATGTTGG	3438
937	ACAUUGCU G CCAUCACU	1031	AGTGATGG GGCTAGCTACAACGA AGCAATGT	3439
1006	UGGCCUAU G CUGAGAUU	1033	AATCTCAG GGCTAGCTACAACGA ATAGGCCA	3440
1015	CUGAGAUU G CCAGGCCU	1035	AGGCCTGG GGCTAGCTACAACGA AATCTCAG	3441
1092	UUCUCCCU G CAGCUUUG	1039	CARAGCTG GGCTAGCTACAACGA AGGGAGAA	3442
1105	UUUGUGGU G CUGGCUUC	1040	GAAGCCAG GGCTAGCTACAACGA ACCACAAA	3443
1134	UCUGAAGU G CUGGCCUC	1042	GAGGCCAG GGCTAGCTACAACGA ACTTCAGA	3444
1182	GACCACUC G CUGUACAC	1045	GTGTACAG GGCTAGCTACAACGA GAGTGGTC	3445
1248	AUCAUUGU G CGGGUGGA	1048	TCCACCCG GGCTAGCTACAACGA ACAATGAT	3446
1286	AAUGGACU G CAAGGAGU	1050	ACTCCTTG GGCTAGCTACAACGA AGTCCATT	3447
1344	CUUCGUUU G CCCAAGAA	1052	TTCTTGGG GGCTAGCTACAACGA AAACGAAG	3448
1366	UUGAAGCU G CAGUCAAA	1054	TTTGACTG GGCTAGCTACAACGA AGCTTCAA	3449
1442	GCUGGUGU G CUGGCAAG	1056	CTTGCCAG GGCTAGCTACAACGA ACACCAGC	3450
1526	GUCCUUCC G CAUCACCA	1058	TGGTGATG GGCTAGCTACAACGA GGAAGGAC	3451
1542	AUCCUUCC G CAGCAAUA	1059	TATTGCTG GGCTAGCTACAACGA GGAAGGAT	3452
1554	CAAUACCU G CGGCCAGU	1060	ACTGGCCG GGCTAGCTACAACGA AGGTATTG	3453
1603	ACAAGUUU G CCAUCUCA	1062	TGAGATGG GGCTAGCTACAACGA AAACTTGT	3454
1699	UUGGCUUU G CUGUCAGC	1066	GCTGACAG GGCTAGCTACAACGA AAAGCCAA	3455
1708	CUGUCAGC G CUUGCCAU	1067	ATGGCAAG GGCTAGCTACAACGA GCTGACAG	3456
1712	CAGCGCUU G CCAUGUGC	1068	GCACATGG GGCTAGCTACAACGA AAGCGCTG	3457
1719	UGCCAUGU G CACGAUGA	1069	TCATCGTG GGCTAGCTACAACGA ACATGGCA	3458
1,19	OGCCAOGO G CACGAOGA	1 1003	TOATEGTO GOCTAGCTACAACGA ACATGGCA	_ 3230

Table 22

1843	UCAUGGCU G CCAUCUGC	1074	GCAGATGG GGCTAGCTACAACGA AGCCATGA	3459
1850	UGCCAUCU G CGCCCUCU	1075	AGAGGGCG GGCTAGCTACAACGA AGATGGCA	3460
1852	CCAUCUGC G CCCUCUUC	1076	GAAGAGGG GGCTAGCTACAACGA GCAGATGG	3461
1863	CUCUUCAU G CUGCCACU	1077	AGTGGCAG GGCTAGCTACAACGA ATGAAGAG	3462
1866	UUCAUGCU G CCACUCUG	1078	CAGAGTGG GGCTAGCTACAACGA AGCATGAA	3463
1874	GCCACUCU G CCUCAUGG	1079	CCATGAGG GGCTAGCTACAACGA AGAGTGGC	3464
1895	UCAGUGGC G CUGCCUCC	1080	GGAGGCAG GGCTAGCTACAACGA GCCACTGA	3465
1898	GUGGCGCU G CCUCCGCU	1081	AGCGGAGG GGCTAGCTACAACGA AGCGCCAC	3466
1904	CUGCCUCC G CUGCCUGC	1082	GCAGGCAG GGCTAGCTACAACGA GGAGGCAG	3467
1907	CCUCCGCU G CCUGCGCC	1083	GGCGCAGG GGCTAGCTACAACGA AGCGGAGG	3468
1911	CGCUGCCU G CGCCAGCA	1084	TGCTGGCG GGCTAGCTACAACGA AGGCAGCG	3469
1913	CUGCCUGC G CCAGCAGC	1085	GCTGCTGG GGCTAGCTACAACGA GCAGGCAG	3470
1933	AUGACUUU G CUGAUGAC	1088	GTCATCAG GGCTAGCTACAACGA AAAGTCAT	3471
1950	AUCUCCCU G CUGAAGUG	1091	CACTTCAG GGCTAGCTACAACGA AGGGAGAT	3472
2087	CACCAAAU G CCUCUGCC	1094	GGCAGAGG GGCTAGCTACAACGA ATTTGGTG	3473
2093	AUGCCUCU G CCUUGAUG	1095	CATCAAGG GGCTAGCTACAACGA AGAGGCAT	3474
2179	AGCACUCU G CUGGCGGG	1097	CCCGCCAG GGCTAGCTACAACGA AGAGTGCT	3475
2227	GAAAUUCU G CUGCUUGA	1098	TCAAGCAG GGCTAGCTACAACGA AGAATTTC	3476
2230	AUUCUGCU G CUUGAAAC	1099	GTTTCAAG GGCTAGCTACAACGA AGCAGAAT	3477
2329	CAUCACAC G CAGGUUAC	1102	GTAACCTG GGCTAGCTACAACGA GTGTGATG	3478
2393	GUUUCCCU G CUGGCCAA	1103	TTGGCCAG GGCTAGCTACAACGA AGGGAAAC	3479
2419	GAGAGGAU G CACAGUUU	1104	AAACTGTG GGCTAGCTACAACGA ATCCTCTC	3480
2428	CACAGUUU G CUAUUUGC	1105	GCAAATAG GGCTAGCTACAACGA AAACTGTG	3481
2428	UGCUAUJU G CUJUAGAG	1106	CTCTAAAG GGCTAGCTACAACGA AAATAGCA	3482
2435	ACAUUGGU G CAAAGAUU	1107	AATCTTTG GGCTAGCTACAACGA ACCAATGT	3483
2485	CAAAGAUU G CCUCUUGA	1108	TCAAGAGG GGCTAGCTACAACGA AATCTTTG	3484
219	GUGCCGAU G UAGCGGGC	1110	GCCCGCTA GGCTAGCTACAACGA ATCGGCAC	3485
483	CUCCUGCU G UGGAUGGG	1111	CCCATCCA GGCTAGCTACAACGA AGCAGGAG	3486
634	GCAGCUUU G UGGAGAUG	1112	CATCTCCA GGCTAGCTACAACGA AAAGCTGC	3487
804	AGGCAGCU G UCCAGCAC	1113	GTGCTGGA GGCTAGCTACAACGA AGCTGCCT	3488
835	GGAAGGGU G UGUAUGUG	1114	CACATACA GGCTAGCTACAACGA ACCCTTCC	3489
837	AAGGGUGU G UAUGUGCC	1115	GGCACATA GGCTAGCTACAACGA ACACCCTT	3490
841	GUGUGUAU G UGCCCUAC	1116	GTAGGGCA GGCTAGCTACAACGA ATACACAC	3491
919	ACGUCACU G UGCGUGCC	1117	GGCACGCA GGCTAGCTACAACGA AGTGACGT	3492
	GCAGCUUU G UGGUGCUG	1118	CAGCACCA GGCTAGCTACAACGA AAAGCTGC	3493
1100	UGGCCUCU G UCGGAGGG	1119	CCCTCCGA GGCTAGCTACAACGA AGAGGCCA	3494
1144	CACUCGCU G UACACAGG	1120	CCTGTGTA GGCTAGCTACAACGA AGCGAGTG	3495
1185	UGAUCAUU G UGCGGGUG	1121	CACCCGCA GGCTAGCTACAACGA AATGATCA	3496
1245	AGAGCAUU G UGGACAGU	1122	ACTGTCCA GGCTAGCTACAACGA AATGCTCT	3497
1315	AAGAAAGU G UUUGAAGC	1123	GCTTCAAA GGCTAGCTACAACGA ACTTTCTT	3498
1356	CAGCUGGU G UGCUGGCA	1124	TGCCAGCA GGCTAGCTACAACGA ACCAGCTG	3499
1440	UGGAAGAU G UGGCCACG	1125	CGTGGCCA GGCTAGCTACAACGA ATCTTCCA	3500
1570	AGACGACU G UUACAAGU	1125	ACTTGTAA GGCTAGCTACAACGA AGTCGTCT	3501
1592	CGGGCACU G UUAUGGGA	1127	TCCCATAA GGCTAGCTACAACGA AGTGCCCG	3502
1630	UGGGAGCU G UUAUCAUG	1128	CATGATAA GGCTAGCTACAACGA AGCTCCCA	3503
1642	UCUACGUU G UCUUUGAU	1129	ATCAAAGA GGCTAGCTACAACGA AACGTAGA	3504
1666	GCUUUGCU G UCAGCGCU	1130	AGCGCTGA GGCTAGCTACAACGA AGCAAAGC	3505
1702		1131	ATCGTGCA GGCTAGCTACAACGA ATGGCAAG	3506
1717	CUUGCCAU G UGCACGAU	1131	CAAGGTGA GGCTAGCTACAACGA AAAAGGGC	3507
1759	GCCCUUUU G UCACCUUG	1133	TGTAGCCA GGCTAGCTACAACGA AGTCTTCC	3508
1781	GGAAGACU G UGGCUACA	1133	AGCCATGA GGCTAGCTACAACGA ATAGGCTA	3509
1834	UAGCCUAU G UCAUGGCU	1134	AGCCATOR COCTACOTACARCON TIMES	

Table 22

			CACTGACA GGCTAGCTACAACGA ACCATGAG	3510
1884	CUCAUGGU G UGUCAGUG	1135	GCCACTGA GGCTAGCTACAACGA ACACCATG	3511
1886	CAUGGUGU G UCAGUGGC	1136	TCTGGCCA GGCTAGCTACAACGA AGGTGCCA	3512
2048	UGGCACCU G UGGCCAGA	1137	TACAGGTA GGCTAGCTACAACGA AGTCCCTG	3513
2139	CAGGGACU G UACCUGUA	1138	GTTTCCTA GGCTAGCTACAACGA AGGTACAG	3514
2145	CUGUACCU G UAGGAAAC	1139	ATGGTGGA GGCTAGCTACAACGA AAAGGTTC	3515
2256	GAACCUUU G UCCACCAU	1140	CAGGGACA GGCTAGCTACAACGA AAGGGTTC	3516
2346	CUUGGCGU G UGUCCCUG	1141	CAGGGACA GGCTAGCTACAACGA ACGCCAAG CACAGGGA GGCTAGCTACAACGA ACACGCCA	3517
2348	UGGCGUGU G UCCCUGUG	1142	GGGTACCA GGCTAGCTACAACGA ACGGACAC	3518
2354	GUGUCCCU G UGGUACCC	1143	CAGGGAAA GGCTAGCTACAACGA AGGCTAGG	3519
2385	CCAAGCUU G UUUCCCUG	1144		3520
2453	CAGGGACU G UAUAAACA	1145	TGTTTATA GGCTAGCTACAACGA AGTCCCTG	3521
14	CGUCCGCA G CCCGCCCG	1146	CGGGCGGG GGCTAGCTACAACGA TGCGGACG	3522
26	GCCCGGGA G CUGCGAGC	1147	GCTCGCAG GGCTAGCTACAACGA TCCCGGGC	3523
33	AGCUGCGA G CCGCGAGC	1148	GCTCGCGG GGCTAGCTACAACGA TCGCAGCT	3523
40	AGCCGCGA G CUGGAUUA	1149	TAATCCAG GGCTAGCTACAACGA TCGCGGCT	
51	GGAUUAUG G UGGCCUGA	1150	TCAGGCCA GGCTAGCTACAACGA CATAATCC	3525 3526
54	UUAUGGUG G CCUGAGCA	1151	TGCTCAGG GGCTAGCTACAACGA CACCATAA	
60	UGGCCUGA G CAGCCAAC	1152	GTTGGCTG GGCTAGCTACAACGA TCAGGCCA	3527
63	CCUGAGCA G CCAACGCA	1153	TGCGTTGG GGCTAGCTACAACGA TGCTCAGG	3528
72	CCAACGCA G CCGCAGGA	1154	TCCTGCGG GGCTAGCTACAACGA TGCGTTGG	3529
81	CCGCAGGA G CCCGGAGC	1155	GCTCCGGG GGCTAGCTACAACGA TCCTGCGG	3530
88	AGCCCGGA G CCCUUGCC	1156	GGCAAGGG GGCTAGCTACAACGA TCCGGGCT	3531
134	CCAGGGAA G CCGCCACC	1157	GGTGGCGG GGCTAGCTACAACGA TTCCCTGG	3532
144	CGCCACCG G CCCGCCAU	1158	ATGGCGGG GGCTAGCTACAACGA CGGTGGCG	3533
167	CCCUCCCA G CCCCGCCG	1159	CGGCGGG GGCTAGCTACAACGA TGGGAGGG	3534
179	CGCCGGGA G CCCGCGCC	1160	GGCGCGGG GGCTAGCTACAACGA TCCCGGCG	3535
198	CUGCCCAG G CUGGCCGC	1161	GCGGCCAG GGCTAGCTACAACGA CTGGGCAG	3536
202	CCAGGCUG G CCGCCGCC	1162	GGCGGCGG GGCTAGCTACAACGA CAGCCTGG	3537
211	CCGCCGCC G UGCCGAUG	1163	CATCOGCA GGCTAGCTACAACGA GGCGGCGG	3538
222	CCGAUGUA G CGGGCUCC	1164	GGAGCCCG GGCTAGCTACAACGA TACATCGG	3539
226	UGUAGCGG G CUCCGGAU	1165	ATCCGGAG GGCTAGCTACAACGA CCGCTACA	3540
239	GGAUCCCA G CCUCUCCC	1166	GGGAGAGG GGCTAGCTACAACGA TGGGATCC	3541
256	CUGCUCCC G UGCUCUGC	1167	GCAGAGCA GGCTAGCTACAACGA GGGAGCAG	3542
290	UCUCCACA G CCCGGACC	1168	GGTCCGGG GGCTAGCTACAACGA TGTGGAGA	3543
304	ACCCGGGG G CUGGCCCA	1169	TGGGCCAG GGCTAGCTACAACGA CCCCGGGT	3544
308	GGGGGCUG G CCCAGGGC	1170	GCCCTGGG GGCTAGCTACAACGA CAGCCCCC	3545
315	GGCCCAGG G CCCUGCAG	1171	CTGCAGGG GGCTAGCTACAACGA CCTGGGCC	3546
324	CCCUGCAG G CCCUGGCG	1172	CGCCAGGG GGCTAGCTACAACGA CTGCAGGG	3547
330	AGGCCCUG G CGUCCUGA	1173	TCAGGACG GGCTAGCTACAACGA CAGGGCCT	3548
332	GCCCUGGC G UCCUGAUG	1174	CATCAGGA GGCTAGCTACAACGA GCCAGGGC	3549
348	GCCCCCAA G CUCCCUCU	1175	AGAGGGAG GGCTAGCTACAACGA TTGGGGGC	3550
365	CCUGAGAA G CCACCAGC	1176	GCTGGTGG GGCTAGCTACAACGA TTCTCAGG	3551
372	AGCCACCA G CACCACCC	1177	GGGTGGTG GGCTAGCTACAACGA TGGTGGCT	3552
391	ACUUGGG G CAGGCGCC	1178	GGCGCCTG GGCTAGCTACAACGA CCCCAAGT	3553
395	GGGGCAG G CGCCAGGG	1179	CCCTGGCG GGCTAGCTACAACGA CTGCCCCC	3554
410	GGACGGAC G UGGGCCAG	1180	CTGGCCCA GGCTAGCTACAACGA GTCCGTCC	3555
414	GGACGUGG G CCAGUGCG	1181	CGCACTGG GGCTAGCTACAACGA CCACGTCC	3556
418	GUGGGCCA G UGCGAGCC	1182	GGCTCGCA GGCTAGCTACAACGA TGGCCCAC	3557
424	CAGUGCGA G CCCAGAGG	1183	CCTCTGGG GGCTAGCTACAACGA TCGCACTG	3558
433	CCCAGAGG G CCCGAAGG	1184	CCTTCGGG GGCTAGCTACAACGA CCTCTGGG	3559
441	GCCCGAAG G CCGGGGCC	1185	GGCCCCGG GGCTAGCTACAACGA CTTCGGGC	3560
441				

Table 22

4677 CACCOURGE & COCCARGOCC 1187 GGCTTOGG GGCTMGCTMGAAGGA CHTGGTGGG A 554 4631 UBGGCCCRA & CCCUGCCC 1188 GGGCTGG GGCTMGCTMGAAGGA CHTGGGCCA 354 474 CUGCCCUG & CUCCUCCCU 1199 AGCAGGAG GGCTMGCTMCAAGGA CHTGGGCCA 354 474 CUGCCCUG & CUCCUCCCU 1199 AGCAGGAG GGCTMGCTMCAAGGA CHTGGGCCA 354 479 GGCGGGGG & GUGCGGGG 1190 CTCCCGGG GGCTMGCTMCAAGGA CAGCGAG 354 479 GGCGGGGG & GUGCGGGC 1190 CTCCCGGG GGCTMGCTMCAAGGA CCATCGAC 354 571 CACACACG & CACCGCAC 1192 CTCCGGG GGCTMGCTMCAAGGA CCATCGAC 354 572 CACACACG & CACCGCGG 1194 CCCGGGGTG GGCTMGCTMCAAGGA CCGTGGGC 354 573 CACACACG & CACCGCGG 1194 CCCGGGGTG GGCTMGCTMCAAGGA CCGTGGGG 354 574 CACACACG & CACCGCGGC 1194 CCCGGGGTG GGCTMGCTMCAAGGA CCGTGCTG 355 575 CACACACG & CACCGCGG 1195 AGGGGGGG GGCTMGCTMCAAGGA CGGTGCTG 355 576 CCCGGGGG & GUGCGGCC 1195 AGGGGGGG GGCTMGCTMCAAGGA CGGTGCTG 355 578 CCCCCGGGG & GUGCGGCC 1195 AGGGGGGG GGCTMGCTMCAAGGA CGGTGCTG 355 579 CCCCCGGGG & GUGCGGCC 1195 AGGGGGGG GGCTMGCTMCAAGGA CGGTGCGG 355 570 CCCCCGGGG & GUGCGCCC 1195 AGGGGGGG GGCTMGCTMCAACGA CCGCCGG 355 570 CCCCCGGGG & GUGCGCCC 1195 AGGGGGGG GGCTMGCTMCAACGA CCGCCGGG 355 570 CCCCCGGGG & GUGCGCCC 1159 AGGGGGGG GGCTMGCTMCAACGA CCCCCGGG 355 571 CCCCCGGGG & GUGCGCCC 1159 AGGGGGGG GGCTMGCTMCAACGA CCCCCGGG 355 572 CCCCCGGGG & GUGCCCCC 1159 AGGGGGGG GGCTMGCTMCAACGA CCCCAGGGG 355 573 CCCCCGGGG & GUGCCCCC 1159 AGGGGGGG GGCTMGCTMCAACGA CCCCAGGGG 355 574 CCCCCGGGGG & CUGCCCCC 1159 AGGGGGGG GCCTMCCTMCAACGA CCCCAGGGG 355 575 QGCCUCCG & GUGCCCCC 1200 CCGGGGCAG GCCTMCCTMCAACGA CCCCAGGGG 355 576 CCCGAGGA & CCCGCGGG 1200 CCGGGGCAG GCCTMCCTMCAACGA CCCCAGGGG 355 577 QGCCUCCG & GUGCCCCC 1200 CCGGGGCAG GCCTMCCTMCAACGA CCCCCAGGG 355 578 QGCCCCCC & CCCAGGGG CCCCCCCG & CCCAGGGG GCCTMCCTMCAACGA CCCCCCGG 355 579 QGCCUCCAG GCCAGGGG CCCCCCCG & CCCAGGGG GCCTMCCTMCAACGA CCCCCCGG 355 579 QGGCCGGG CAGGCCG CCCCCCGGGGGGCCG GCCCCCCCGG GCCTMCCTMCAACGA CCCCCCGGG GCCCCCCCCGGGGGCCG CCCCCCGGGGGCCGCC				ATGGTGGG GGCTAGCTACAACGA CCCGGCCT	3561
18	447	AGGCCGGG G CCCACCAU	1186		3562
1999 GOGGOGO G COCCOGO 1189 AGCAGGA GOTTACCTACACGA CAGGAGA 354					
1990 COUGROUND COUCRESS 1190 CTCCCCCC GOTTACTACARCIA CONTCCAC 349					
					3565
515 UGCCCACG G CACCCAGC 1192 GCCGGGTG GSCTANCTACAACA COTGGGGCA 315 522 GGCACCCA G CACGGCGC 1193 ATGCCGTG GGCTANCTACAACCA COTGGGGCA 356 527 CCACACCG G CACGGCGC 1194 GCCGGGTG GGCTACCTACAACCA COTGCTGG 356 534 GGCALCCG G CUGCCCU 1195 AGGGGGG GGCTACCTACAACCA COTGCTGG 356 548 CCUGCACCA G GGCCCCUGG 1196 CCAGGCCG GGCTACCTACAACCA TGGGCAGG 357 551 GCGCAGCG G CCCCCCC 1198 AGGGGGGG GCTACCTACAACCA CCCCCAGG 357 573 GCCCCUGGG G CUGCCCC 1199 AGCGGCAG GGCTACCTACAACCA CCCCAGGG 25 573 GCCCCCGAGGA 1201 CCGGGGCAG GCCTACCTACAACCA CCCCAGGG 35 573 GCCCCGAGGA 1201 TCCTCGGGG GCTACCTACAACCA CCCCAGGG 25 573 GGCGCAGAGA G CCGCGACG 1202 CGGGGCAG GCTACCTACAACCA CCCCAGGG 25 630 GACGAGGAG 1201 TCCTCGGGG GCTACCTACAACCA CCCCACGGG 35 512 CCCCAAGAGA G CCCCGACGG 1202 CGGCCGGG GCCTACCTACAACCA CCCCCCCC 35 <td< td=""><td></td><td></td><td></td><td></td><td></td></td<>					
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196					3570
SECTION SECT	534				
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1986 COURGAGE & COLOCICCO 1199 AGCOGGAG GOTTACTRACACOA COCAGGGG 15	551				3573
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579 GAGCOLOG C. COCCCCC 1201 TCCTCGGG GGCTAGCTACAACGA TCTTCGTC 151 CCCCGAGGA G CCCCGGCGG 1202 CGGGCGGG GGCTAGCTACAACGA TCTTCGTC 152 CCCCCAACGA G CCCCGGCGG 1203 CCCCCCGG GGCTAGCTACAACGA TCCTCCGGG GGCTAGCTACAACGA TCCTCCGGG GGCTAGCTACAACGA TCCTCCGG GGCTAGCTACAACGA CGCCTCCGG 1203 CCCCCCGG GGCTAGCTACAACGA CGCCTCCGG GGCTAGCTACAACGA CGCCTCCGG GGCTAGCTACAACGA CGCCTCCGG GGCTAGCTACAACGA CGCCTCCGG GGCTAGCTACAACGA CGCCTCCGG GGCTAGCTACAACGA CGCCTCCGG GGCTAGCTACAACGA CACCTCCA 1204 CAAAAGCTG GGCTAGCTACAACGA CACCTCCCA 1205 CCCCAACAGA GGCTAACCTACAACGA CACCTCCA 1205 CCCCACAAGA GGCTAACCTACAACGA CACCTCCA 1205 CCCCACATA GGCTAACCTACAACGA CACCTCCA 1205 CCCCACATA GGCTAGCTACAACGA CTCCCCA 1205 CCCCACATA GGCTAGCTACAACGA CTCCCCA 1205 CCCCACATA GGCTAGCTACAACGA CTCCCCA 1205 CCCCACATA GGCTAGCTACAACGA CTCCCCCC 1205 CCCCACATA GGCTAGCTACAACGA CTCCCCC 1205 CCCCACATA GGCTAGCTACAACGA CGCTACCTACAACGA CTCCCCC 1205 CCCCACATA GGCTAGCTACAACGA CGCCCCCC 1205 CCCCCCCCC 1205 CCCCCCCC 1205 CCCCCCCCC 1205 CCCCCCCCCC 1205 CCCCCCCCC 1205	573				
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	603				
1973 GANACICU COURGING 1204 CARAGETG GETTACTRARACIA CECTCOGG 55 629 GAGGGGCA C CUUUGUGG 1204 CARAGETG GETTACTRARACIA CECTCOGG 55 629 GAGGGGCA C CUUUGUGG 1205 CACCAMAG GETTACTRARACIA CECTCOGG 56 631 GAGGGCA C CUUUGUGG 1206 CTTOTTCCA GETTACTRARACIA CACCCTCCA 55 652 CCUGARGG C CARAGUGG 1207 CTGCARTTG GETTACTRARACIA CECTCACA 55 653 AAGUGGG C AGAGGCGA 1208 TOCCCCA GETTACTRARACIA CECTCAC 35 654 AAGUGGG C CAGAGCUA 1209 TOCCCCA GETTACTRARACIA CECTCACG 35 6574 GGGGCAA G UCAGGACA 1209 CACCATCA GETTACTRARACIA CECCCC 35 6582 GCULCUAC G UGAGGAUG 1211 CATCTCCA GETTACTRARACIA CECCCCC 15 6594 AAGUGGC G UGAGGACA 1212 CATCTCCA GETTACTRARACIA CECCCCC 15 6596 GACCOGG G CACCCCC 1213 GAGGGCTG GETTACTRARACIA CONTECCC 15 6596 GACCOGG G CACCCCC 1214 GAGGGGGG GETTACTRARACIA CONTECCC 15 6596 GACCOGG G CACCCCC 1214 GAGGGGGG GETTACTRARACIA CONTECCCAC 15 701 CUUGAGCA G CUCCCCC 1214 GAGGGGGG GETTACTRARACIA CONTECCCAC 15 702 CACCAGG G CACCAGUA 1215 TOTATCCA GETTACTRARACIA CONTECCCAC 15 703 GARINACIA G CACCAGUA 1216 TOTACCCA GETTACTRARACIA CONTECCCAC 15 704 UACAGGG G CACCAGUA 1216 TOTACCCA GETTACTRARACIA CONTECCCAC 15 705 GARINACIA G CACCAGUA 1216 TOTACCCA GETTACTRARACIA CONTECCCAC 15 706 UACAGGG G CACCAGUA 1216 TOTACCCA GETTACTRARACIA TOTACCAC 15 707 CACCAGGG G CACCAGUA 1216 TOTACCCA GETTACTRARACIA TOTACCAC 15 708 UACCAGGG G CACCAGUA 1217 AOTTACTO GOCTACCACAGA TOCCACTOTA 15 709 UACCAGGG G CACCAGUC 1219 ACCACCCA GETTACTRACACGA TOCCACCTOTA 15 701 UACAGGGG G CACCUGCC 1220 GOGCAGCA GETTACTRACACGA TOCCACCTOTA 15 702 UACCAGGG G CACCUGCC 1220 GOGCAGCA GETTACTRACACGA TOCCACCTOTA 15 703 UACCAGGG G CACCUGCC 1220 GOGCAGCA GETTACTRACACGA TOCCACCTOTA 15 704 UACCAGGG G CACCUGCC 1220 GOGCAGCA GETTACTRACACGA TOCCACCTOTA 15 705 UACCAGGG G CACCUGCC 1220 GOGCAGCA GETTACTRACACGA TOCCACCTOTA 15	612				
229 GAGGAGA G CUUTURURG 1205 CACADARG GGCTAGCTACAAGA TGCCCCTC 15	617				
639 GAGGIGAN G UGGIGACAAC 1206 TTOTICCA GICTAGATCAACGA CATCTCCA 35 6 6 12 0 CCUGAGGG CAAGUGGG 1207 CCGACTTG GICTAGACGA CATCTCCA 35 6 6 12 0 CCUGAGGG CAAGUGGG 1207 TGCCCA GICTAGATGAACGA CATCTCCA 35 6 12 0 CCUGAGGG CAAGUGGG 1208 TGCCCCG GICTAGATGAACGA CCCCCCT 35 6 12 0 AGGGCAGC 1208 TGCCCCG GICTAGATGAACGA CCCCCC 35 6 12 0 AGGGCAGCA GICTAGACGA CCCCCC 35 6 12 0 AGGGCAGCAGCAACGA CCCCCCC 35 6 12 0 AGGGCAGCAGCAACGA CCCCCC 35 6 12 0 AGGGCAGCAGCAACGA CCCCCCC 35 6 12 0 AGGGCAGCAGCAACGA CCCCCC 35 6 12 0 AGGGCAGCAGCAACGA CCCCCCC 35 6 12 0 AGGGCAGCAGCAACGA CCCCCCC 35 6 12 0 AGGGCAGCACAACGA CCCCCCC 35 6 12 0 AGGCCACCC 35 6 12 0 AGGCCACCC 35 6 12 0 AGGCCACCC 35 6 12 0 AGGCCACCCC 35 6 12 0 AGGCCACCC 35 6 12 0 AGGCCACCCC 35 6 12 0 AGGCCACCC 35 6 12 0 AGGCCACCCC 35 7 0 AGGCCACCC 35 7 0 AGGCCACCCACCACCACCACCACCACCACCACCACCACCA	626	CCGGAGGG G CAGCUUUG			3579
CUIDASSG 6 CAMBURGE 1207 CORACTTG GETRACTRACKGN CECTEGRG	629				3580
653 AGGGGGA & UCCGGGGGA 1208 TOCCCCCA GGCTAGCTACAACGA TYGCCCT 35 659 AAGUCGGG & CAGGGCGA 1208 TOCCCCCA GGCTAGCTACAACGA TYGCCCT 35 659 AAGUCGGG & CAGGGCGA 1209 TAGGCCTG GGCTAGCTACAACGA CTGCCCC 35 652 GAGGAGG & CUUCAGG 1210 COTACTAG GGCTAGCTACACGA CCCCCACTT 35 652 GCUACUAC & UGCGAGAGG 1211 CATCTCCA GGCTAGCTACACGA GTAGTAGC 35 654 AAGUCGG & UGCGAGAGG 1211 CATCTCCA GGCTAGCTACACGA GTAGTAGC 35 658 GACCGUGG & CAGCCCCC 1213 GGGGGGT GGCTAACCTACACGA GTAGTAGC 35 701 CGUGGGCA & CCCCCCCC 1214 GCGGGGGG GGCTAGCTACAACGA CACGGGTC 35 727 ACCUCCUG & UGGANACA 1215 TOTATCCA GGCTAGCTACAACGA CACGGTC 35 727 ACCUCCUG & UGGANACA 1216 ACCUCCCA GGCTAGCTACAACGA CACGGTC 35 740 UACCAGGGG & CAGUACU 1217 ACTTACTC GGCTAGCTACAACGA CACGGTTC 35 740 UACCAGGGG & CAUACU 1218 CAAAGTTA GGCTAACCTACAACGA TCCCTACTA 35 740 UACCAGGGG & CAUACU 1218 CAAAGTTA GGCTAACCTACAACGA TCCTACTA 35 754 ACUUCGA & UGGGGGC 1220 GGCAGCGACGTACAACGA TCCTACTA 35 758 UACCAGGG & UACCUUCC 1220 GGCAACGTACAACGA TCCTACCAACGT 125 759 UACCAGGG & CACCUCCC 1220 GGCAACGTACAACGA TCCTACCAACGT 125 800 CAGAGGGA & CACUUCCA 1221 CACACCAG GGCTAACCTACAACGA TCCTACTAC 35 810 CAGAGGGA & CACUUCCA 1222 CTCGACAG GGCTAACCTACAACGA CTCTCCTG 35 810 CAGAGGGA & CACUUCCA 1222 CTCGACAG GGCTAACCTACAACGA CTCCTCTG 35 811 CAGAGGGA & CAUCUCCA 1222 CTCGACAG GGCTAACCTACAACGA CTCTCCTG 35 812 CACCCAGG & CACUGAC 1224 CACACACA GGCTAACCTACAACGA CTCCTCTG 36 813 CCGGAGAG & CUUCUCA 1224 CACACACA GGCTAACCTACAACGA CTCCTCTG 36 814 CAGGGCAA & CUCGGAGGG 1256 CCCTCCCA GGCTAACCTACAACGA CTCCTCTG 36 815 CAGCGCAA & CACGGAGG &	643				3581
669 ANGUEGGA G CONSCIUL 1209 TRACCCORT GESTRACTRACAGA COCCINETT 35 669 ANGUEGGA G CARGECUA 1209 TRACCCORT GESTRACTRACAGA COCCINETT 35 669 ANGUEGGA G CUACURAGA 1210 TRACCCORT GESTRACTRACAGA COCCINETT 35 682 GULCULCA G URGAGAUS 1211 CATCTECA GESTRACTRACAGA COCCINETAGA GESTRACTRACAGA COCCINETAGA GESTRACTRACAGA COCCINETAGA GESTRACTRACAGA COCCINETAGA GESTRACTRACAGA COCCINETAGA GESTRACTRACAGA CACCINETAGA GESTRACTRACAGA CACCINETA	659	CCUGAGGG G CAAGUCGG	1207		3582
674 GGGGCAGG G CUACUNG 1210 COTAGTAG GGCTAGCTACAACGA CCTGCCCC 156 682 GCUACUNG G UGGGAGAU 1211 CATCTCCA GGCTAGCTACAACGA CCTGCCCC 156 683 AGAGGGC UGGGGCAG 1212 CATCTCCA GGCTAGCTACAACGA GTAGTAGC 156 684 AGAGGGC G UGGGCAGC 1212 GCTGCCCA GGCTAGCTACAACGA GTAGTACT 157 685 GACGGUGG G CAGCCCCC 1213 GGGGGCTG GGCTAGCTACAACGA CACCGGCTC 1214 686 GACGGUGG G CAGCCCCC 1214 GGGGGGGG GGCTAGCTACAACGA CACCGGCTC 1215 727 ACAUCCUG G UGGANACA 1215 TOTATCCA GGCTAGCTACAACGA CACCGGCTC 1216 728 AGAGCCACA G UGACACCC 1217 AGATACTACAACGA CACCGACCA 1217 737 GGANACAG G CAGCAGUA 1216 TACTCCTG GGCTAGCTACAACGA CACCGACCC 1217 740 UACCAGGCA G CAUNACCU 1217 AGATACTAC GGCTAGCTACAACGA TCCCTGCT 1218 754 AGUUGCA G UGAGGGCU 1219 AGACACCA GGCTAGCTACAACGA TCCACGACCA CACCGACCACCA CACCGACCA GGCTAGCTACAACGA CACCGACCACCACCACCACCACCACCACCACCACCACCAC	663	AGGGGCAA G UCGGGGCA	1208		3583
	669	AAGUCGGG G CAGGGCUA	1209		3584
	674	GGGGCAGG G CUACUACG			3585
998 ALCOGUEG & CAGCECCC 1213 GGGGGCTG GGCTAGCTACAACGA CCACGGTC 1568 CACCGGGGG & CACCCCCC 1214 GGGGGGCTG GGCTAGCTACAACGA CCACGGTC 1572 CACCGGGGGGG GGCTAGCTACAACGA CCACGGTC 1572 CACCGGGGGGG GGCTAGCTACAACGA CCACGGTC 1572 CACCGGGGGGG GGCTAGCTACAACGA CCACGGTC 1573 GGAUACAG C CACCGGGGGGG GGCTAGCTACAACGA CCACGGTC 1574 CACCGGGGGGG GGCTAGCTACAACGA CCACGGTC 1217 ACTTACTC GGCTAGCTACAACGA CCGTACTCAACGA CCACGGTC 1218 CAAAGTTA GGCTAGCTACAACGA TCCTCTA 1574 ACUTUGCA G UGGGUGCU 1218 CAAAGTTA GGCTAGCTACAACGA TCCTCTA 1578 UACCACGG G UAACGUUC 1218 CAAAGTTA GGCTAGCTACAACGA TCCTCTA 1578 UACCACGG G CACGGCGCC 1220 GGCAGCA GGCTAGCTACAACGA TCCTCTCA 1578 UACCACGA G CACGGUC 1221 CACAGCTG GGCTAGCTACAACGA CCCTCTGCA 1578 UACCACGA G CACGUUC 1221 CACAGCTG GGCTAGCTACAACGA CCCTCTGGTA 1580 CAGAGGGG G CACGUUC 1221 CACAGCTG GGCTAGCTACAACGA CCCTCTGGTA 1580 CAGAGGGG G CACGUUC 1222 CTUGACAC GGCTAGCTACAACGA CTCCTCTG 1580 CAGAGGG G CACGUUC 1222 CTUGACAC GGCTAGCTACAACGA CTCCTCTG 1580 CAGGGAGG G CAUGUUM 1224 CATACACA GGCTAGCTACAACGA CCCTCTGG 1580 CAGGGCAA G UGGGAAGG UCUGUUM 1224 CATACACA GGCTAGCTACAACGA CCCTCTGG 1580 CAGGGCAA G UGGGAAGG CACGGGGGGG 1225 CCCTCCCA GGCTAGCTACAACGA CCCCTGGGG 1580 CAGGGCAA G UGGGAAGG CACGGAAGG CACGGAAGGAA	682	GCUACUAC G UGGAGAUG	1211		3586
976 GRUGGGCA G CCCCCCGC 1214 GCGGGGGG GGCTAGCTACAACGA TCCCCACC 35	694		1212		3587
121 COURGER O COCCOCC 1225 TOTATICCA GICTACTARACIA CAGGATGT 35	698	GACCGUGG G CAGCCCCC			3588
177	701		1214		3589
1216 GORGIACHA C PARLUNACU 1217 AGTRACTE GOCTAGCTACAACGA TOCCTGTA 35 1740 UACAGGGA G CARUMACU 1217 AGTRACTE GOCTAGCTACAACGA TOCCTGTA 35 1741 AGGCAGCA G UAACUUUG 1218 CAAAGTTA GOCTAGCTACAACGA TOCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	727		1215		3590
143	737				3591
1218 AGGERGEA D DIACULUS 1218 AGGERGEA GENERAL TRANSPORT 1219 AGGERGEA GENERAL TRANSPORT 1210 AGGERGEA GENERAL GENERAL TRANSPORT 1210 AGGERGEA GENERAL GENERAL TRANSPORT 1210 AGGERGEA GENERAL GENERAL GENERAL TRANSPORT 1210 AGGERGEA GENERAL GEN	740	UACAGGCA G CAGUAACU			3592
123	743				3593
1788	754		1219		3594
798	758				3595
123 GOTAGCTACAACGA CACGALGACC 1223 GOTAGCTACCAACGA CACGACACC 1833 CCGGAAGG G GUGUGUAUG 1224 CATACACA GGCTAGCTACAACGA CCTTCCGG 35	798	UACCAGAG G CAGCUGUC			3596
809 GCUGUCA G EXCAURACE 1224 CATACACA GGCTAGCTACACCA CCTTCCGG 35 833 CCGGAAGG G GUGUADUG 1224 CATACACA GGCTAGCTACACCA CCTTCCGG 35 857 CACCCAGG G CAAGUGGG 1225 CCCTTCCG GGCTAAGCTACACCA CCTGGGTC G 861 CAGGGCAA G UGGGAGG 1225 CCTTCCGA GGCTAAGCTACACGA TICCCCTT 36 873 GAAGGGGA G CUGGGCAC 1227 GTGCCCAG GGCTAAGCTACAACGA TICCCCTT 36 876 GGACCUGG G CACCGACC 1228 GGTCGCTA GGCTAAGCTACAACGA CCAGCTCC 126 877 GGACCUGG GACCACCC 1228 GGTCGCTA GGCTAAGCTACAACGA CCAGCTCC 126 878 CGACCUGG GUAAGCACC 1229 GATGCTTA GGCTAGCTACAACCA CAGGTCGG 36 878 CGACCUGG GUAAGCACC 1229 GATGCTTA GGCTAGCTACAACCA CAGGTCGG 36	801				3597
837 CCGGARGG G GUGUGAUG 1224 CCCACTTG GGCTAGCTACAACGA CCTGGGTG 56	809	GCUGUCCA G CACAUACC			3598
125	833				
861 CAGGGCAA G UGGGAGG 1228 GTGCCCAG GGCTAGCTACAACGA TCCCCTTC 36	857	CACCCAGG G CAAGUGGG			3600
873 GAAGGUGG G CUGSSCAC 1228 GGTCGGTG GGCTMGCTACAAGGA CCAGCTCC 36 878 GGAGCUGG G CACCGACC 1228 GGTCGGTG GGCTMGCTACAAGGA CCAGCTCC 36 889 CCGACCUG G UAAGCAUC 1229 GATGCTTA GGCTMGCTACAAGGA CAGGTCGG 36	861				3601
878 GGAGCUGG G CACCGACC 1228 GGTCGGTG GGCTAGCTACAACGA CAGGTCGG 36	873				3602
889 CCGACCUG G DAAGCAUC 1229 GATGCTTA GGCTAGCTACGATCGT	878				3603
ACCOUNTS COUNTRY COUNTRY CANAGE TRACCAGE 31	889				3604
893 CCUGGUAA G CAUCCCC 1230 GGGGGATG GGCTAGCTACCTAC	893	CCUGGUAA G CAUCCCCC	1230	GGGGGATG GGCTAGCTACAACGA TTACCAGG	3605
905 CCCCCAUG G CCCCAACG 1231 CGTTGGGG CCCTAGCTTGGTGGG	905	CCCCCAUG G CCCCAACG			3606
913 GCCCCAAC G UCACUGUG 1232 CACAGIGA GGCIAGCIACACCAI CITOGGGG	913	GCCCCAAC G UCACUGUG	1232		3607
923 CACUGUGC G UGCCAACA 1233 IGTTGGCA GGCTAGCTTCATCGT	923		1233		3608
957 UCAGACAA G UUCUUCAU 1234 AIGAAGAA GGCIAGCIACAACGA IIGIGIA	957	UCAGACAA G UUCUUCAU	1234		3609
971 CAUCAACG G CUCCAACU 1235 AGTIGGAG GGCIAGCTACAACGT COTTO	971	CAUCAACG G CUCCAACU	1235		3610
986 CUGGGAAG G CAUCCUGG 1236 CCAGGATG GGCTAGCTACAACGA CTTCCCAG 36	986	CUGGGAAG G CAUCCUGG	1236	CCAGGATG GGCTAGCTACAACGA CTTCCCAG	3611

		ī	able 22	
996	AUCCUGGG G CUGGCCUA	1237	TAGGCCAG GGCTAGCTACAACGA CCCAGGAT	3612
1000	UGGGGCUG G CCUAUGCU	1238	AGCATAGG GGCTAGCTACAACGA CAGCCCCA	3613
1020	AUUGCCAG G CCUGACGA	1239	TCGTCAGG GGCTAGCTACAACGA CTGGCAAT	3614
1038	UCCCUGGA G CCUUUCUU	1240	AAGAAAGG GGCTAGCTACAACGA TCCAGGGA	3615
1057	ACUCUCUG G UAAAGCAG	1241	CTGCTTTA GGCTAGCTACAACGA CAGAGAGT	3616
1062	CUGGUAAA G CAGACCCA	1242	TGGGTCTG GGCTAGCTACAACGA TTTACCAG	3617
1072	AGACCCAC G UUCCCAAC	1243	GTTGGGAA GGCTAGCTACAACGA GTGGGTCT	3618
1095	UCCCUGCA G CUUUGUGG	1244	CCACAAAG GGCTAGCTACAACGA TGCAGGGA	3619
1103	GCUUUGUG G UGCUGGCU	1245	AGCCAGCA GGCTAGCTACAACGA CACAAAGC	3620
1109	UGGUGCUG G CUUCCCCC	1246	GGGGGAAG GGCTAGCTACAACGA CAGCACCA	3621
1125	CUCAACCA G UCUGAAGU	1247	ACTTCAGA GGCTAGCTACAACGA TGGTTGAG	3622
1132	AGUCUGAA G UGCUGGCC	1248	GGCCAGCA GGCTAGCTACAACGA TTCAGACT	3623
1138	AAGUGCUG G CCUCUGUC	1249	GACAGAGG GGCTAGCTACAACGA CAGCACTT	3624
1154	CGGAGGGA G CAUGAUCA	1250	TGATCATG GGCTAGCTACAACGA TCCCTCGG	3625
1169	CAUUGGAG G UAUCGACC	1251	GGTCGATA GGCTAGCTACAACGA CTCCAATG	, 3626
1193	GUACACAG G CAGUCUCU	1252	AGAGACTG GGCTAGCTACAACGA CTGTGTAC	3627
1196	CACAGGCA G UCUCUGGU	1253	ACCAGAGA GGCTAGCTACAACGA TGCCTGTG	3628
1203	AGUCUCUG G UAUACACC	1254	GGTGTATA GGCTAGCTACAACGA CAGAGACT	3629
1218	CCCAUCCG G CGGGAGUG	1255	CACTCCCG GGCTAGCTACAACGA CGGATGGG	3630
1224	CGGCGGGA G UGGUAUUA	1256	TAATACCA GGCTAGCTACAACGA TCCCGCCG	3631
1227	CGGGAGUG G UAUUAUGA	1257	TCATAATA GGCTAGCTACAACGA CACTCCCG	3632
1237	AUUAUGAG G UGAUCAUU	1258	AATGATCA GGCTAGCTACAACGA CTCATAAT	3633
1252	UUGUGCGG G UGGAGAUC	1259	GATCTCCA GGCTAGCTACAACGA CCGCACAA	3634
1293	UGCAAGGA G UACAACUA	1260	TAGTTGTA GGCTAGCTACAACGA TCCTTGCA	3635
1310	UGACAAGA G CAUUGUGG	1261	CCACAATG GGCTAGCTACAACGA TCTTGTCA	3636
1322	UGUGGACA G UGGCACCA	1262	TGGTGCCA GGCTAGCTACAACGA TGTCCACA	3637
1325	GGACAGUG G CACCACCA	1263	TGGTGGTG GGCTAGCTACAACGA CACTGTCC	3638
1340	CAACCUUC G UUUGCCCA	1264	TGGGCAAA GGCTAGCTACAACGA GAAGGTTG	3639
1354	CCAAGAAA G UGUUUGAA	1265	TTCAAACA GGCTAGCTACAACGA TTTCTTGG	3640
1363	UGUUUGAA G CUGCAGUC	1266	GACTGCAG GGCTAGCTACAACGA TTCAAACA	3641
1369	AAGCUGCA G UCAAAUCC	1267	GGATTTGA GGCTAGCTACAACGA TGCAGCTT	3642
1384	CCAUCAAG G CAGCCUCC	1268	GGAGGCTG GGCTAGCTACAACGA CTTGATGG	3643
1387	UCAAGGCA G CCUCCUCC	1269	GGAGGAGG GGCTAGCTACAACGA TGCCTTGA	3644
1404	ACGGAGAA G UUCCCUGA	1270	TCAGGGAA GGCTAGCTACAACGA TTCTCCGT	3645
1415	CCCUGAUG G UUUCUGGC	1271	GCCAGAAA GGCTAGCTACAACGA CATCAGGG	3646
1422	GGUUUCUG G CUAGGAGA	1272	TCTCCTAG GGCTAGCTACAACGA CAGAAACC	3647
1431	CUAGGAGA G CAGCUGGU	1273	ACCAGCTG GGCTAGCTACAACGA TCTCCTAG	3648
1434	GGAGAGCA G CUGGUGUG	1274	CACACCAG GGCTAGCTACAACGA TGCTCTCC	3649
1438	AGCAGCUG G UGUGCUGG	1275	CCAGCACA GGCTAGCTACAACGA CAGCTGCT	3650
1446	GUGUGCUG G CAAGCAGG	1276	CCTGCTTG GGCTAGCTACAACGA CAGCACAC	3651
1450	GCUGGCAA G CAGGCACC	1277	GGTGCCTG GGCTAGCTACAACGA TTGCCAGC	3652 3653
1454	GCAAGCAG G CACCACCC	1278	GGGTGGTG GGCTAGCTACAACGA CTGCTTGC TGAGATGA GGCTAGCTACAACGA TGGGAAAA	3654
1480	UUUUCCCA G UCAUCUCA	1279	TAACCTCA GGCTAGCTACAACGA TGGGAAAA TAACCTCA GGCTAGCTACAACGA CCATTAGG	3655
1502	CCUAAUGG G UGAGGUUA	1280	TAACCTCA GGCTAGCTACAACGA CCATTAGG GTTGGTAA GGCTAGCTACAACGA CTCACCCA	3656
1507	UGGGUGAG G UUACCAAC	1281	GTTGGTAA GGCTAGCTACAACGA CTCACCCA CGGAAGGA GGCTAGCTACAACGA TGGTTGGT	3657
1518	ACCAACCA G UCCUUCCG	1282	AGGTATTG GGCTAGCTACAACGA TGGTTGGT	3658
1545	CUUCCGCA G CAAUACCU	1283	TCCACTGG GGCTAGCTACAACGA TGCGGAAG TCCACTGG GGCTAGCTACAACGA CGCAGGTA	3659
1557	UACCUGCG G CCAGUGGA	1284	ATCTTCCA GGCTAGCTACAACGA CGCAGGTA ATCTTCCA GGCTAGCTACAACGA TGGCCGCA	3660
1561	UGCGGCCA G UGGAAGAU	1285	GGACGTGG GGCTAGCTACAACGA TGGCCGCA	3661
1573	AAGAUGUG G CCACGUCC	1286	TCTTGGGA GGCTAGCTACAACGA CACATCTT TCTTGGGA GGCTAGCTACAACGA GTGGCCAC	3662
1578	GUGGCCAC G UCCCAAGA	128/	TOTTOGON GOCTAGOTACANCON GIGGOCAC	1 3000

Table 22

1599	UGUUACAA G UUUGCCAU	1288	ATGGCAAA GGCTAGCTACAACGA TTGTAACA	3663
1614	AUCUCACA G UCAUCCAC	1289	GTGGATGA GGCTAGCTACAACGA TGTGAGAT	3664
1625	AUCCACGG G CACUGUUA	1290	TAACAGTG GGCTAGCTACAACGA CCGTGGAT	3665
1639	UUAUGGGA G CUGUUAUC	1291	GATAACAG GGCTAGCTACAACGA TCCCATAA	3666
1655	CAUGGAGG G CUUCUACG	1292	CGTAGAAG GGCTAGCTACAACGA CCTCCATG	3667
1663	GCUUCUAC G UUGUCUUU	1293	AAAGACAA GGCTAGCTACAACGA GTAGAAGC	3668
1678	UUGAUCGG G CCCGAAAA	1294	TTTTCGGG GGCTAGCTACAACGA CCGATCAA	3669
1694	ACGAAUUG G CUUUGCUG	1295	CAGCAAAG GGCTAGCTACAACGA CAATTCGT	3670
1706	UGCUGUCA G CGCUUGCC	1296	GGCAAGCG GGCTAGCTACAACGA TGACAGCA	3671
1728	CACGAUGA G UUCAGGAC	1297	GTCCTGAA GGCTAGCTACAACGA TCATCGTG	3672
1738	UCAGGACG G CAGCGGUG	1298	CACCGCTG GGCTAGCTACAACGA CGTCCTGA	3673
1741	GGACGGCA G CGGUGGAA	1299	TTCCACCG GGCTAGCTACAACGA TGCCGTCC	3674
1744	CGGCAGCG G UGGAAGGC	1300	GCCTTCCA GGCTAGCTACAACGA CGCTGCCG	3675
1751	GGUGGAAG G CCCUUUUG	1301	CAAAAGGG GGCTAGCTACAACGA CTTCCACC	3676
1784	AGACUGUG G CUACAACA	1302	TGTTGTAG GGCTAGCTACAACGA CACAGTCT	3677
1809	ACAGAUGA G UCAACCCU	1303	AGGGTTGA GGCTAGCTACAACGA TCATCTGT	3678
1828	UGACCAUA G CCUAUGUC	1304	GACATAGG GGCTAGCTACAACGA TATGGTCA	3679
1840	AUGUCAUG G CUGCCAUC	1305	GATGGCAG GGCTAGCTACAACGA CATGACAT	3680
1882	GCCUCAUG G UGUGUCAG	1306	CTGACACA GGCTAGCTACAACGA CATGAGGC	3681
1890	GUGUGUCA G UGGCGCUG	1307	CAGCGCCA GGCTAGCTACAACGA TGACACAC	3682
1893	UGUCAGUG G CGCUGCCU	1308	AGGCAGCG GGCTAGCTACAACGA CACTGACA	3683
1917	CUGCGCCA G CAGCAUGA	1309	TCATGCTG GGCTAGCTACAACGA TGGCGCAG	3684
1920	CGCCAGCA G CAUGAUGA	1310	TCATCATG GGCTAGCTACAACGA TGCTGGCG	3685
1956	CUGCUGAA G UGAGGAGG	1311	CCTCCTCA GGCTAGCTACAACGA TTCAGCAG	3686
1964	GUGAGGAG G CCCAUGGG	1312	CCCATGGG GGCTAGCTACAACGA CTCCTCAC	3687
1972	GCCCAUGG G CAGAAGAU	1313	ATCTTCTG GGCTAGCTACAACGA CCATGGGC	3688
2006	ACACCUCC G UGGUUCAC	1314	GTGAACCA GGCTAGCTACAACGA GGAGGTGT	3689
2009	CCUCCGUG G UUCACUUU	1315	AAAGTGAA GGCTAGCTACAACGA CACGGAGG	3690
2019	UCACUJUG G UCACAAGU	1316	ACTTGTGA GGCTAGCTACAACGA CAAAGTGA	3691
2026	GGUCACAA G UAGGAGAC	1317	GTCTCCTA GGCTAGCTACAACGA TTGTGACC	3692
2042	CACAGAUG G CACCUGUG	1318	CACAGGTG GGCTAGCTACAACGA CATCTGTG	3693
2051	CACCUGUG G CCAGAGCA	1319	TGCTCTGG GGCTAGCTACAACGA CACAGGTG	3694
2057	UGGCCAGA G CACCUCAG	1320	CTGAGGTG GGCTAGCTACAACGA TCTGGCCA	3695
2114	AGGAAAAG G CUGGCAAG	1321	CTTGCCAG GGCTAGCTACAACGA CTTTTCCT	3696
2118	AAAGGCUG G CAAGGUGG	1322	CCACCTTG GGCTAGCTACAACGA CAGCCTTT	3697
2123	CUGGCAAG G UGGGUUCC	1323	GGAACCCA GGCTAGCTACAACGA CTTGCCAG	3698
2127	CAAGGUGG G UUCCAGGG	1324	CCCTGGAA GGCTAGCTACAACGA CCACCTTG	3699
2172	AGAAAGAA G CACUCUGC	1325	GCAGAGTG GGCTAGCTACAACGA TTCTTTCT	3700
2183	CUCUGCUG G CGGGAAUA	1326	TATTCCCG GGCTAGCTACAACGA CAGCAGAG	3701
2198	UACUCUUG G UCACCUCA	1327	TGAGGTGA GGCTAGCTACAACGA CAAGAGTA	3702
2214	AAAUUUAA G UCGGGAAA	1328	TTTCCCGA GGCTAGCTACAACGA TTAAATTT	3703
2243	AAACUUCA G CCCUGAAC	1329	GTTCAGGG GGCTAGCTACAACGA TGAAGTTT	3704
2288	AACCCAAA G UAUUCUUC	1330	GAAGAATA GGCTAGCTACAACGA TTTGGGTT	3705
2305	UUUUCUUA G UUUCAGAA	1331	TTCTGAAA GGCTAGCTACAACGA TAAGAAAA	3706
2314	UUUCAGAA G UACUGGCA	1332	TGCCAGTA GGCTAGCTACAACGA TTCTGAAA	3707
2320	AAGUACUG G CAUCACAC	1333	GTGTGATG GGCTAGCTACAACGA CAGTACTT	3708
2333	ACACGCAG G UUACCUUG	1334	CAAGGTAA GGCTAGCTACAACGA CTGCGTGT	3709
2342	UUACCUUG G CGUGUGUC	1335	GACACACG GGCTAGCTACAACGA CAAGGTAA	3710
2344	ACCUUGGC G UGUGUCCC	1336	GGGACACA GGCTAGCTACAACGA GCCAAGGT	3711
2357	UCCCUGUG G UACCCUGG	1337	CCAGGGTA GGCTAGCTACAACGA CACAGGGA	3712
2365	GUACCCUG G CAGAGAAG	1338	CTTCTCTG GGCTAGCTACAACGA CAGGGTAC	3713

Table 22

			aoic 22	
2381	GAGACCAA G CUUGUUUC	1339	GAAACAAG GGCTAGCTACAACGA TTGGTCTC	3714
2397	CCCUGCUG G CCAAAGUC	1340	GACTTTGG GGCTAGCTACAACGA CAGCAGGG	3715
2403	UGGCCAAA G UCAGUAGG	1341	CCTACTGA GGCTAGCTACAACGA TTTGGCCA	3716
2407	CAAAGUCA G UAGGAGAG	1342	CTCTCCTA GGCTAGCTACAACGA TGACTTTG	3717
2424	GAUGCACA G UUUGCUAU	1343	ATAGCAAA GGCTAGCTACAACGA TGTGCATC	3718
2463	AUAAACAA G CCUAACAU	1344	ATGTTAGG GGCTAGCTACAACGA TTGTTTAT	3719
2474	UAACAUUG G UGCAAAGA	1345	TCTTTGCA GGCTAGCTACAACGA CAATGTTA	3720
45	CGAGCUGG A UUAUGGUG	1346	CACCATAA GGCTAGCTACAACGA CCAGCTCG	3721
67	AGCAGCCA A CGCAGCCG	1347	CGGCTGCG GGCTAGCTACAACGA TGGCTGCT	3722
125	CCGGGGG A CCAGGGAA	1348	TTCCCTGG GGCTAGCTACAACGA CCCCCCGG	3723
217	CCGUGCCG A UGUAGCGG	1349	CCGCTACA GGCTAGCTACAACGA CGGCACGG	3724
233	GGCUCCGG A UCCCAGCC	1350	GGCTGGGA GGCTAGCTACAACGA CCGGAGCC	3725
267	CUCUGCGG A UCUCCCCU	1351	AGGGGAGA GGCTAGCTACAACGA CCGCAGAG	3726
277	CUCCCCUG A CCGCUCUC	1352	GAGAGCGG GGCTAGCTACAACGA CAGGGGAG	3727
296	CAGCCCGG A CCCGGGGG	1353	CCCCCGGG GGCTAGCTACAACGA CCGGGCTG	3728
338	GCGUCCUG A UGCCCCCA	1354	TGGGGGCA GGCTAGCTACAACGA CAGGACGC	3729
383	CCACCCAG A CUUGGGGG	1355	CCCCCAAG GGCTAGCTACAACGA CTGGGTGG	3730
404	CGCCAGGG A CGGACGUG	1356	CACGTCCG GGCTAGCTACAACGA CCCTGGCG	3731
408	AGGGACGG A CGUGGGCC	1357	GGCCCACG GGCTAGCTACAACGA CCGTCCCT	3732
487	UGCUGUGG A UGGGCGCG	1358	CGCGCCCA GGCTAGCTACAACGA CCACAGCA	3733
592	CCCGGGAG A CCGACGAA	1359	TTCGTCGG GGCTAGCTACAACGA CTCCCGGG	3734
596	GGAGACCG A CGAAGAGC	1360	GCTCTTCG GGCTAGCTACAACGA CGGTCTCC	3735
640	UUGUGGAG A UGGUGGAC	1361	GTCCACCA GGCTAGCTACAACGA CTCCACAA	3736
647	GAUGGUGG A CAACCUGA	1362	TCAGGTTG GGCTAGCTACAACGA CCACCATC	3737
650	GGUGGACA A CCUGAGGG	1363	CCCTCAGG GGCTAGCTACAACGA TGTCCACC	3738
688	ACGUGGAG A UGACCGUG	1364	CACGGTCA GGCTAGCTACAACGA CTCCACGT	3739
691	UGGAGAUG A CCGUGGGC	1365	GCCCACGG GGCTAGCTACAACGA CATCTCCA	3740
712	CCCCGCAG A CGCUCAAC	1366	GTTGAGCG GGCTAGCTACAACGA CTGCGGGG	3741
719	GACGCUCA A CAUCCUGG	1367	CCAGGATG GGCTAGCTACAACGA TGAGCGTC	3742
731	CCUGGUGG A UACAGGCA	1368	TGCCTGTA GGCTAGCTACAACGA CCACCAGG	3743
746	CAGCAGUA A CUUUGCAG	1369	CTGCAAAG GGCTAGCTACAACGA TACTGCTG	3744
821	AUACCGGG A CCUCCGGA	1370	TCCGGAGG GGCTAGCTACAACGA CCCGGTAT	3745
884	GGGCACCG A CCUGGUAA	1371	TTACCAGG GGCTAGCTACAACGA CGGTGCCC	3746
911	UGGCCCCA A CGUCACUG	1372	CAGTGACG GGCTAGCTACAACGA TGGGGCCA	3747
929	GCGUGCCA A CAUUGCUG	1373	CAGCAATG GGCTAGCTACAACGA TGGCACGC	3748
948	AUCACUGA A UCAGACAA	1374	TTGTCTGA GGCTAGCTACAACGA TCAGTGAT	3749
953	UGAAUCAG A CAAGUUCU	1375	AGAACTTG GGCTAGCTACAACGA CTGATTCA	3750
968	CUUCAUCA A CGGCUCCA	1376	TGGAGCCG GGCTAGCTACAACGA TGATGAAG	3751
977	CGGCUCCA A CUGGGAAG	1377	CTTCCCAG GGCTAGCTACAACGA TGGAGCCG	3752
1012	AUGCUGAG A UUGCCAGG	1378	CCTGGCAA GGCTAGCTACAACGA CTCAGCAT	3753
1025	CAGGCCUG A CGACUCCC	1379	GGGAGTCG GGCTAGCTACAACGA CAGGCCTG	3754
1028	GCCUGACG A CUCCCUGG	1380	CCAGGGAG GGCTAGCTACAACGA CGTCAGGC	3755
1049	UUUCUUUG A CUCUCUGG	1381	CCAGAGAG GGCTAGCTACAACGA CAAAGAAA	3756
1066	UAAAGCAG A CCCACGUU	1382	AACGTGGG GGCTAGCTACAACGA CTGCTTTA	3757
1079	CGUUCCCA A CCUCUUCU	1383	AGAAGAGG GGCTAGCTACAACGA TGGGAACG	3758
1121	CCCCCUCA A CCAGUCUG	1384	CAGACTGG GGCTAGCTACAACGA TGAGGGGG	3759
1159	GGAGCAUG A UCAUUGGA	1385	TCCAATGA GGCTAGCTACAACGA CATGCTCC	3760
1175	AGGUAUCG A CCACUCGC	1386	GCGAGTGG GGCTAGCTACAACGA CGATACCT	3761
1240	AUGAGGUG A UCAUUGUG	1387	CACAATGA GGCTAGCTACAACGA CACCTCAT	3762
1258	GGGUGGAG A UCAAUGGA	1388	TCCATTGA GGCTAGCTACAACGA CTCCACCC	3763
1262	GGAGAUCA A UGGACAGG	1389	CCTGTCCA GGCTAGCTACAACGA TGATCTCC	3764
1202	GUAGAUCA A GUGACAGG	1303		

Table 22

1000	AUCAAUGG A CAGGAUCU	1390	AGATCCTG GGCTAGCTACAACGA CCATTGAT	3765
1266	UGGACAGG A UCUGAAAA	1391	TTTTCAGA GGCTAGCTACAACGA CCTGTCCA	3766
1271	AUCUGAAA A UGGACUGC	1392	GCAGTCCA GGCTAGCTACAACGA TTTCAGAT	3767
	GAAAAUGG A CUGCAAGG	1393	CCTTGCAG GGCTAGCTACAACGA CCATTTTC	3768
1283	GGAGUACA A CUAUGACA	1394	TGTCATAG GGCTAGCTACAACGA TGTACTCC	3769
1298	CAACUAUG A CAAGAGCA	1395	TGCTCTTG GGCTAGCTACAACGA CATAGTTG	3770
1304	CAUUGUGG A CAGUGGCA	1396	TGCCACTG GGCTAGCTACAACGA CCACAATG	3771
1319	CACCACCA A CCUUCGUU	1397	AACGAAGG GGCTAGCTACAACGA TGGTGGTG	3772
1334	GCAGUCAA A UCCAUCAA	1398	TTGATGGA GGCTAGCTACAACGA TTGACTGC	3773
1374	GUUCCCUG A UGGUUUCU	1399	AGAAACCA GGCTAGCTACAACGA CAGGGAAC	3774
1412	CCCUUGGA A CAUUUUCC	1400	GGAAAATG GGCTAGCTACAACGA TCCAAGGG	3775
1469		1401	CTCACCCA GGCTAGCTACAACGA TAGGTAGA	3776
1498	UCUACCUA A UGGGUGAG	1402	AGGACTGG GGCTAGCTACAACGA TGGTAACC	3777
1514	GGUUACCA A CCAGUCCU	1403	CGCAGGTA GGCTAGCTACAACGA TGCTGCGG	3778
1548	CCGCAGCA A UACCUGCG	1404	TGGCCACA GGCTAGCTACAACGA CTTCCACT	3779
1568	AGUGGAAG A UGUGGCCA	1405	AACAGTCG GGCTAGCTACAACGA CTTGGGAC	3780
1586	GUCCCAAG A CGACUGUU	1405	TGTAACAG GGCTAGCTACAACGA CGTCTTGG	3781
1589	CCAAGACG A CUGUUACA	1405	GGGCCGA GGCTAGCTACAACGA CAAAGACA	3782
1673	UGUCUUUG A UCGGGCCC	1407	CCAATTCG GGCTAGCTACAACGA TTTCGGGC	3783
1686	GCCCGAAA A CGAAUUGG		AAAGCCAA GGCTAGCTACAACGA TCGTTTTC	3784
1690	GAAAACGA A UUGGCUUU	1409	TGAACTCA GGCTAGCTACAACGA CGTGCACA	3785
1724	UGUGCACG A UGAGUUCA	1410	CGCTGCCG GGCTAGCTACAACGA CCTGAACT	3786
1735	AGUUCAGG A CGGCAGCG	1411	CTTCCATG GGCTAGCTACAACGA CCAAGGTG	3787
1769	CACCUUGG A CAUGGAAG	1412	AGCCACAG GGCTAGCTACAACGA CTTCCATG	3788
1778	CAUGGAAG A CUGUGGCU	1413	GTGGAATG GGCTAGCTACAACGA TGTAGCCA	3789
1790	UGGCUACA A CAUUCCAC	1414	CTCATCTG GGCTAGCTACAACGA CTGTGGAA	3790
1801	UUCCACAG A CAGAUGAG	1415	TTGACTCA GGCTAGCTACAACGA CTGTCTGT	3791
1805	ACAGACAG A UGAGUCAA	1416	CATGAGGG GGCTAGCTACAACGA TGACTCAT	3792
1813	AUGAGUCA A CCCUCAUG	1413	GGCTATGG GGCTAGCTACAACGA CATGAGGG	3793
1822	CCCUCAUG A CCAUAGCC	1419	CAAAGTCA GGCTAGCTACAACGA CATGCTGC	3794
1925	GCAGCAUG A UGACUUUG	1419	CAGCAAAG GGCTAGCTACAACGA CATCATGC	3795
1928	GCAUGAUG A CUUUGCUG	1421	AGATGTCA GGCTAGCTACAACGA CAGCAAAG	3796
1937	CUUUGCUG A UGACAUCU	1422	GGGAGATG GGCTAGCTACAACGA CATCAGCA	3797
1940	UGCUGAUG A CAUCUCCC	1422	AATCTCTA GGCTAGCTACAACGA CTTCTGCC	3798
1979	GGCAGAAG A UAGAGAUU	1423	CAGGGGAA GGCTAGCTACAACGA CTCTATCT	3799
1985	AGAUAGAG A UUCCCCUG	1424	AGGTGTGG GGCTAGCTACAACGA CCAGGGGA	3800
1995	UCCCCUGG A CCACACCU	1425	CATCTGTG GGCTAGCTACAACGA CTCCTACT	3801
2033	AGUAGGAG A CACAGAUG	1425	AGGTGCCA GGCTAGCTACAACGA CTGTGTCT	3802
2039	AGACACAG A UGGCACCU	1427	GGGGAGGG GGCTAGCTACAACGA CCTGAGGT	3803
2067	ACCUCAGG A CCCUCCCC	1429	CAGAGGCA GGCTAGCTACAACGA TTGGTGGG	3804
2085	CCCACCAA A UGCCUCUG	1429	CTTCTCCA GGCTAGCTACAACGA CAAGGCAG	3805
2099	CUGCCUUG A UGGAGAAG		AGGTACAG GGCTAGCTACAACGA CCCTGGAA	3806
2136	UUCCAGGG A CUGUACCU	1431	CTTTTCTG GGCTAGCTACAACGA TTCCTACA	3807
2152	UGUAGGAA A CAGAAAAG	1432	CAAGAGTA GGCTAGCTACAACGA TCCCGCCA	3808
2189	UGGCGGGA A UACUCUUG	1433	GACTTAAA GGCTAGCTACAACGA TTGAGGTG	3809
2208	CACCUCAA A UUUAAGUC	1434	CAGCAGAA GGCTAGCTACAACGA TTCCCGAC	3810
2222	GUCGGGAA A UUCUGCUG	1435	GGCTGAAG GGCTAGCTACAACGA TTCAAGCA	3811
2237	UGCUUGAA A CUUCAGCC		GACAAAGG GGCTAGCTACAACGA TCAGGGCT	3812
2250	AGCCCUGA A CCUUUGUC	1437	TTGGAGAA GGCTAGCTACAACGA TTAAAGGA	3813
2273	UCCUUUAA A UUCUCCAA	1438	ACTITIGG GGCTAGCTACAACGA TGAGGAAT	3814
2281	AUUCUCCA A CCCAAAGU	1439	AAGCTTGG GGCTAGCTACAACGA CTCTTCTC	3815
2376	GAGAAGAG A CCAAGCUU	1440	Anderros decradering	

Table 22

2417	AGGAGAGG A UGCACAGU	1441	ACTGTGCA GGCTAGCTACAACGA CCTCTCCT	3816
2444	CUUUAGAG A CAGGGACU	1442	AGTCCCTG GGCTAGCTACAACGA CTCTAAAG	3817
2450	AGACAGGG A CUGUAUAA	1443	TTATACAG GGCTAGCTACAACGA CCCTGTCT	3818
2459	CUGUAUAA A CAAGCCUA	1444	TAGGCTTG GGCTAGCTACAACGA TTATACAG	3819
2468	CAAGCCUA A CAUUGGUG	1445	CACCAATG GGCTAGCTACAACGA TAGGCTTG	3820
2482	GUGCAAAG A UUGCCUCU	1446	AGAGGCAA GGCTAGCTACAACGA CTTTGCAC	3821
2494	CCUCUUGA A UUAAAAAA	1447	TTTTTTAA GGCTAGCTACAACGA TCAAGAGG	3822
2507	AAAAAAAA A CUAGAAAA	1448	TTTTCTAG GGCTAGCTACAACGA TTTTTTTT	3823

Input Sequence = AF190725. Cut Site = G/.
Stem Length = 8. Core Sequence = GGCTAGCTACAACGA
AF190725 (Homo sapiens beta-site APP Cleaving enzyme (BACE) MRNA; 2525 bp)

Table 23: Human BACE Amberzyme Ribozyme and Target Sequence

POS	Substrate	T Tac		A
2	SOSCIECT & CAGCCCGC	096	GCGGGCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGACGCGU	3260
:	CCASCOC G CCCGGGAG	196	CUCCCGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCUGCG	3261
9	0 0	962	GCGGCUCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCUCCCG	3262
67	COCOCCO D COCCOCCO	063	HEREGER GEAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCAGCUCC	3263
31	SCHOOL & MACCOCK	964	CCAGCUCG GGAGGAAACUCC CU UCAAGGACAUCGUCGGG GGCUCGCA	3264
000	CGAGCCGC G AGCUGGAU	965	AUCCAGOU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCGGCUCG	3265
28	GGUGGCCU G AGCAGCCA	996	UBGCUGCU GGAGGAANCUCC CU UCAAGGACAUCGUCCGGG AGGCCACC	3266
69	CAGCCAAC G CAGCCGCA	196	UGCEGCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCEGG GUUGGCUG	3267
75	ACGCAGCC G CAGGAGCC	968	GGCUCCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCUGCGU	3268
9.4	GAGCCCUU G CCCCUGCC	696	GGCAGGGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AAGGGCUC	3269
100	UNGCCCCU G CCCGCGCC	970	GGCGCGGG GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AGGGGCAA	32/0
104	50050050 5 00050000	971	CGGCGGCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCAGGG	3271
106	CUGCCGC G CCGCCGCC	972	GGCGGCGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCGGGCAG	3272
100	2022202 9 22025222	973	GCGGGCGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCGCGGG	3273
112	95005000 0 00000000	974	CCGGCGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCGGCGC	3274
116	55555500 5 00050000	975	CCCCCCGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCGGCG	3275
137	GGGAAGCC G CCACCGGC	926	GCCGGUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCUUCCC	3276
148	ACCRECACE G CCAUGCCC	277	GGGCAUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCCGGU	3277
22	22225020 8 118225020	978	GGGGCGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGGCGGG	3278
200	DOUDDO D DOUBLED	979	GGGAGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCAUGG	3279
122	JENESCO D JOJONGO	980	GCUCCOSS GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGGCUGG	3280
183	GGGAGCCC G CGCCCGCU	981	AGCGGGCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCUCCC	3281
100	DENICOUR & JUJULIAN	982	GCAGCGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCGGGCUC	3282
081	CORPECTOR G CUGCCCAG	983	CUBBECAG GEAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCGCGG	3283
100	Canada a cochagadu	984	AGCCUGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCGGGCG	3284
300	prediction of concount	985	CACGGCGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCCAGCC	3285
208	ndeccece a ccauecos	986	CBGCACBB GBAGGAAACUCC CU UCAAGGACAUCGUCCBBG BGCBBCCA	3286
213	φ	987	UACAUCGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGGCGGC	3287
216	GCCGUGCC G AUGUAGCG	886	CGCUACAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCACGGC	3288
			ADADOCA DOCUMENTACION OF THE PROPERTY OF THE P	3289

25.8	aminonell a minisciss	990	CCGCAGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGGGAGC	3290
000	Congenien a Cocanonia	166	GAGAUCCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAGCACG	3291
226	ITCHIOCOCCI G ACCIGCING	992	AGAGOGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGGAGA	3292
000	Contain B. Containon	566	GUGGAGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGUCAGGG	3293
300	c	994	AGGGCCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGCCCU	3294
337	0	995	GGGGGCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGACGCC	3295
340	יט	966	CUUGGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCAGGAC	3296
360	CCUCUCCU G AGAAGCCA	664	UGGCUUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGAGAGG	3297
397	GGGCAGGC G CCAGGGAC	966	GUCCCUGG GGAGGAACUCC CU UCAAGGACAUCGUCOGGG GCCUGCCC	3298
420	GGGCCAGU G CGAGCCCA	666		3299
422	GCCAGUGC G AGCCCAGA	1000	UCUGGGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCACUGGC	3300
437	GAGGGCCC G AAGGCCGG	1001	CCGGCCUU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GGGCCCUC	3301
468	O	1002	AGCCAGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGCUUG	3302
480	UGGCUCCU G CUGUGGAU	1003		3303
493	GGAUGGGC G CGGGAGUG	1004		3304
201	GCGGGAGU G CUGCCUGC	1005		3305
504	GGAGUGCU G CCUGCCCA	1006	UGGGCAGG GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG AGCACUCC	3306
805	DECLIGION G COCACGGC	1007	GCCGUGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGCAGCA	3307
537	U	1008	CGCAGGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCCGGAU	3308
543	U	1009	CCGCUGCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGGCAG	3309
545	CCCCCUGC G CAGCGGCC	1010	GOCCOCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCAGGGGC	3310
562	ngggggg g cccccng	1011	CAGGGGGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GCCCCCCA	3311
576	CUGGGGCU G CGGCUGCC	1012		3312
582	CUGCGGCU G CCCCGGGA	1013	UCCCGGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCCGCAG	3313
595	ю	1014	CUCUUCGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGUCUCCC	3314
598	O	1015	GGGCUCUT GGAGGANACUCC CU UCAAGGACAUCGUCCGGG GUCGGUCU	3315
607	AAGAGCCC G AGGAGCCC	1016	GGCCUCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCUCUU	3316
654	GACAACCU G AGGGGCAA	1017		3317
9	GUGGAGAU G ACCGUGGG	1018		3318
708	AGCCCCC G CAGACGCU	1019	AGCGUCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGGGGCU	3319
714	CCGCAGAC G CUCAACAU	1020	AUGUUGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUCUGCGG	3320
751	GUAACUUU G CAGUGGGU	1021	ACCCACUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAGUUAC	3321
760	O	1022	GGGGGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCCACUG	3322
763	UGGGUGCU G CCCCCCAC	1023	GUGGGGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCACCCA	3323

3324	3325	3326	3327	3328	3329	3330	3331	3332	3333	3334	3335	3336	3337	3338	3339	3340	3341	3342	3343	3344	3345	3346	3347	3348	3349	3350	3351	3352	3353	3354	3355	3356	3357
TRECCOATE GGAGGAAACTICC CIT UCAAGGACAUCGUCCGGG AGGAAGGG	GOUAGUAG GGAGGAAACUCC CU UCNAGGACAUGGUCGGG GAUGCAGG	GUGUAGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAUACAC	UACCAGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGUGCCCA	UNGGCACG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAGUGAC	AAUGUUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGCACAG	GAUGGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUGUUGG	AGUGAUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCAAUGU	GUCUGAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUGAUGG	AAUCUCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAGGCCA	GGCAAUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCAUAGG	AGGCCUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUCUCAG	GGAGUCGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGCCUGG	CAGGGAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUCAGGCC	CAGAGAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAGAAAG	CAAAGCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGAGAA	GAAGCCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCACAAA	CAGCACUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGACUGGU	GAGGCCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUUCAGA	CCAAUGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGCUCCC	CGAGUGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAUACCUC	GUGUACAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAGUGGUC	GAUCACCU GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AUAAUACC	ACAAUGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCUCAUA	UCCACCCG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG ACAAUGAU	UCCAUUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAUCCUG	ACUCCUUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUCCAUU	GCUCUUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAGUUGU	UNCUUGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAACGAAG	UCCAGCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAACACUU	UTUGAÇUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCUUCAA	GAAACCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGAACU	CUUGCCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACACCAGC	GGUAACCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCCAUUA
1024	1025	1026	1027	1028	1029	1030	1031	1032	1033	1034	1035	1036	1037	1038	1039	1040	1041	1042	1043	1044	1045	1046	1047	1048	1049	1050	1001	1052	1053	1054	1055	1056	1057
ALTOCATION O HOSTINGO	CONGRATIO G CHACIBOC	GUGUAUGU G CCCUACAC	ugggggg g Accuggua	O	CUGUGOGU G CCAACAUU	CCAACAUU G CUGCCAUC	ACAUJGCU G CCAUCACU	CCAUCACU G MAUCAGAC	UGGCCUAU G CUGAGAUU	CCUAUGCU G AGAUUGCC	CUGAGAUU G CCAGGCCU	CCAGGCCU G ACGACUCC	GGCCUGAC G ACUCCCUG	CUUTCUUT G ACUCUCUG	UNCUCCCU G CAGCUUUG	unuenden e cuedenuc	ACCAGUCU G AAGUGCUG	UCUGAAGU G CUGGCCUC	GGGAGCAU G AUCAUUGG	GAGGUAUC G ACCACUCG	GACCACUC G CUGUACAC	GGURUUAU G AGGUGAUC	UAUGAGGU G AUCAUUGU	AUCAUUGU G CGGGUGGA	CAGGAUCU G AAAAUGGA	AAUGGACU G CAAGGAGU	ACAACUAU G ACAAGAGC	CUUCGUUU G CCCAAGAA	AAGUGUUU G AAGCUGCA	UUGAAGCU G CAGUCAAA	AGUUCCCU G AUGGUUUC	GCUGGUGU G CUGGCAAG	UAAUGGGU G AGGUUACC
001	785	843	883	921	925	934	937	946	1006	1009	1015	1024	1027	1048	1092	1105	1129	1134	1158	1174	1182	1234	1239	1248	1275	1286	1303	1344	1360	1366	1411	1442	1504

3358	3359	3360	3361	3362	3363	3364	3365	3366	3367	3368	3369	3370	3371	3372	3373	3374	3375	3376	3377	3378	3379	3380	3381	3382	3383	3384	3385	3386	3387	3388	3389	3390
HAGHGAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGAAGGAC	UAUTIGCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGAAGGAU	ACUGGCCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGUAUUG	GUANCAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUCUUGGG		CU UCAAGGACAUCGUCCGGG	CU UCANGGACAUCGUCGGGG	AGCCAAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUUUUCGG	GCUGACAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAGCCAA	AUGGCAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCUGACAG	GCACAUGG GCAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGCGCUG	UCAUCGUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAUGGCA	GAACUCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUGCACAU		GGUUGACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCUGUCU	GCUAUGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGAGGGU	GCAGAUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCCAUGA	AGAGGGCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAUGGCA	GAAGAGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCAGAUGG	AGUGGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGAAGAG	CAGAGUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCAUGAA		GGAGGCAG GCAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCCACUGA	AGCGGAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCGCCAC	GCAGGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGAGGCAG	GGCGCAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCGGAGG	UGCUGGCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGCAGCG	GCUGCUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCAGGCAG	AAAGUCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGCUGCU	AGCAAAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCAUGCU	GUCAUCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAGUCAU	GAUGUCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCAAAGU	GGAGALIGII GGAGGAAGUCC CU UCAAGGACAUCGUCCGGG AUCAGCAA
1058	1059	1060	1001	1062	1063	1064	1065	1066	1067	1068	1069	1070	101	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090
CONTROL O CONTROLLO	, e	0	CCCAAGAC G ACUGUUAC	ACANGINIT G CCAUCUCA	INVESTIGATION OF AUGGGGGC			o c	0	Change of the Change	TIGGGAIGH G CAGGAIIGA	AUGUSCAC G AUGAGUUC	UGCACGAU G AGUUCAGG	U	U	neaugedu e ceaucuge	U	CCAUCUGE G CCCUCUUC	CICINICAL G CUGCCACU	INCALLECTI G CCACUCUG	GCCACUCU G CCUCAUGG	TICAGIGGE G CUGECUCE	C		CONCORD & CONGORCO	CGCUGCCU G CGCCAGCA	CUGCCUGC G CCAGCAGC	AGCAGCAU G AUGACUUU	AGCAUGAU G ACUTUGCU	O	ACUUDGCU G AUGACAUC	CONTROL S LIABILIZATION
2025	1520	1554	15.88	1603	1672	1682	0071	1600	1200	1712	1710	1723	1726	1807	1821	1843	1850	1852	1863	1866	1874	200	1808	1904	1907	1911	1913	1924	1927	1933	1936	

GGCCUCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUUCAGC
GGCAGAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUUUGGUG
CAUCAAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG 'AGAGGCAU
UNCUCCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGGCAGA
CCCGCCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAGUGCU
UCAAGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAAUUUC
GUUUCAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCAGAAU
UGAAGUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGCAGCA
CAAAGGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGCUGA
GUAACCUG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GUGUGAUG
UNGGCCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGAAAC
AAACUGUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCCUCUC
GCANAUNG GGAGGANACUCC CU UCANGGACAUCGUCCGGG NAACUGUG
CUCUADAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAUAGCA
AAUCUUUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCAAUGU
UCAAGAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUCUUUG
UUUUAAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGAGGCA
GCCCGCUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCGGCAC
CCCAUCCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCAGGAG
CAUCUCCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAGCUGC
GUGCUGGA GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AGCUGCCU
CACAUACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCCUUCC
GGCACAUA GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG ACACCCUU
GUAGGGCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUACACAC
GECACGCA GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG AGUGACGU
CAGCACCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAGCUGC
CCCUCCGA GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AGAGGCCA
CCUGUGUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCGAGUG
CACCCGCA GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AAUGAUCA
ACUGUCCA GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AAUGCUCU
GCUUCAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUUUCUU
UGCCAGCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCAGCUG
COLLIGATE CONCESSION OF STREET

3426	3427	3428	3429	3430	3431	3432	3433	3434	3435	3436	3437	3438	3439	3440	3441	3442	3443	3444	3445	3446	3447	3448	3449	3450	3451	3452	3453	3454	3455	3456	3457	3458	3459
AGUCGUCU	AGUGCCCG	AGCUCCCA	AACGUAGA	AGCAAAGC	AUGGCAAG	AAAAGGGC	AGUCUUCC	AUAGGCUA	ACCAUGAG	ACACCAUG	AGGUGCCA	AGUCCCUG	AGGUACAG	AAAGGUUC	ACGCCAAG	ACACGCCA	AGGGACAC	AAGCUUGG	AGUCCCUG	UGCGGACG	UCCCGGGC	UCGCAGCU		CAUAAUCC	CACCAUAA	UCAGGCCA	UGCUCAGG	UGCGUUGG	uccueces	UCCGGGCU	UUCCCUGG	CGGUGGCG	UGGGAGGG
CU UCAAGGACAUCGUCCGGG		AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	CU UCAAGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	CU UCAAGGACAUCGUCCGGG AAAGGUUC	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	CU UCAAGGACAUCGUCCGGG UCGCAGCU	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	CU UCAAGGACAUCGUCCGGG UCCGGGCU	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG	AGGACAUCGUCCGGG
GGAAACUCC CU UCAA	UCCCAUNA GGAGGANACUCC CU UCNAGGACAUCGUCCGGG	CAUGADAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCUCCCA	AUCAAAGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACGUAGA	GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCAAAGC	GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGGCAAG	GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG	GGAGGAAACUCC CU UCA	AGCCAUGA GGAGGAACUCC CU UCAAGGACAUCGUCCGGG	CACUGACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG	GCCACUGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACACCAUG	GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGUGCCA	GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUCCCUG	GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGUACAG		CAGGGACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG	CACAGGGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACACGCCA	OGGUACCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGACAC	CAGGGAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGCUUGG	UGUIULAUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUCCCUG	CGGGCGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCGGACG	GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCCGGGC	AGGARACUCC CU UCA	DAAUCCAG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG	UCAGGCCA GGAGGMAACUCC CU UCAAGGACAUCGUCCGGG	JECUCAGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CACCAUAA	SUNGGOUG GGAGGAAACUCC OU UCAAGGACAUCGUCOGGG UCAGGCCA	USCGUUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCUCAGG	UCCUGOGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCGUUGG	GGAGGAAACTUCC CU UCAAGGACAUCGUCCGGG UCCUGCGG	GGAGGAAACUCC CU UCA	GEUGGCOG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG	AUGGOGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGUGGCG	COUCOOR GANGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGGAGGG
ACUUGUAA GGAGGAAACUCC	UCCCAUNA GGA	CAUGAUAA GGA	AUCAAAGA GGA	AGCGCUGA GGA	AUCGUGCA GGA	CAAGGUGA GGA	UGUAGCCA GGA	AGCCAUGA GGA	CACUGACA GGA	GCCACUGA GGA	UCUGGCCA GGA	UACAGGUA GGA	GUUUCCUA GGP	AUGGUGGA GGAGGAAACUCC	CAGGGACA GGA	CACAGGGA GGZ	GGGUACCA GGF	CAGGGAAA GG	UGUUUAUA GG	190 99939993 191	GCUCGCAG GG	GCUCGCGG GGAGGAAACUCC	UNAUCCAG GG	UCAGGCCA GG	UGCUCAGG GG	GUUGGCUG GG	nacennae ee	100 00000000 001	ecuccage ger	GGCAAGGG GG	GGUGGCGG GG	AUGGCGGG GG	CGGCGGGG GG
1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	1136	1137	1138	1139	1140	1141	1142	1143	1144	1145	1146	1147	1148	1149	1150	1151	1152	1153	1154	1155	1156	1157	1158	1159
AGACGACU G UDACAAGU	CGGGCACU G UDAUGGGA	UGGGAGCU G UUAUCAUG	UCUACGUU G UCUUUGAU	GCUUUGCU G UCAGCGCU	CUUGCCAU G UGCACGAU	GCCCUUUU G UCACCUUG	GGAAGACU G UGGCUACA	UAGCCUAU G UCAUGGCU	CUCAUGGU G UGUCAGUG	CAUGGUGU G UCAGUGGC	UGGCACCU G UGGCCAGA	CAGGGACU G UACCUGUA	CUGUACCU G UAGGAAAC	GAACCUUU G UCCACCAU	CUNGGCGU G UGUCCCUG	uggeguen e uccenana	GUGUCCCU G UGGUACCC	CCAAGCUU G UUUCCCUG	CAGGGACU G UAUAAACA	CGUCCGCA G CCCGCCCG	GCCCGGGA G CUGCGAGC	AGCUGCGA G CCGCGAGC	AGCCGCGA G CUGGAUUA	GGAUDAUG G UGGCCUGA	UNAUGGUG G CCUGAGCA	UGGCCUGA G CAGCCAAC	CCUGAGCA G CCAACGCA	CCAACGCA G CCGCAGGA	CCGCAGGA G CCCGGAGC	AGCCCGGA G CCCUUGCC	CCAGGGAA G CCGCCACC	CGCCACCG G CCCGCCAU	CCCUCCCA G CCCCGCCG
1592	1630	1642	1666	1702	1717	1759	1781	1834	1884	1886	2048	2139	2145	2256	2346	2348	2354	2385	2453	14	26	33	40	21	5.4	9	63	72	81	88	134	144	167

1160 GREGIGES GRAGANARUCC 1117 GROGICORS GRAGANARUCC 1118 GROCIOCORS GRAGANARUCC 1118 GRACIOCORS GRAGANARUCC 1117 GRACIOCORS GRAGANARUCC 1117 GRACIOCORS GRAGANARUCC 1117 GRACIOCORS GRAGANARUCC 1117 GRACIOCORS GRAGANARUCC 1118 GRACIOCORS GRAC	3460								H			-		-						-	_	3481	_		-	-		-			-	3491	
1160 1163 1163 1164 1165 1166 1166 1166 1167 1170 1170 1170 1170	AAACUCC CU UCAAGGACAUCGUCCGGG UCCCGGCG	AAACUCC CU UCAAGGACAUCGUCCGGG CUGGGCAG	AAACUCC CU UCAAGGACAUCGUCCGGG CAGCCUGG	AMACUCC CU UCAAGGACAUCGUCCGGG GGCGGCGG	AAACUCC CU UCAAGGACAUCGUCCGGG UACAUCGG	AAACUCC CU UCAAGGACAUCGUCCGGG CCGCUACA	AAACUCC CU UCAAGGACAUCGUCCGGG UGGGAUCC	AAACUCC CU UCAAGGACAUCGUCCGGG GGGAGCAG	AAACUCC CU UCAAGGACAUCGUCCGGG UGUGGAGA	AAACUCC CU UCAAGGACAUCGUCCGGG CCCCGGGU	AAACUCC CU UCAAGGACAUCGUCCGGG CAGCCCCC	MANACUCC CU UCANGGACAUCGUCCGGG CCUGGGCC	PAACUCC CU UCAAGGACAUCGUCCGGG CUGCAGGG	NAACUCC CU UCAAGGACAUCGUCCGGG CAGGGCCU	MANACUCC CU UCAAGGACAUCGUCCGGG GCCAGGGC	PAACUCC CU UCAAGGACAUCGUCCGGG UUGGGGGC	PARACUCO CU UCARGRACAUCGUCCGGG UUCUCAGG	MANACUCE OU UCAAGGACAUCGUCCGGG UGGUGGCU	SANACUCC CU UCAAGGACAUCGUCCGGG CCCCAAGU	MANACUCC CU UCAAGGACAUCGUCCGGG CUGCCCCC	SAAACUCC CU UCAAGGACAUCGUCCGGG GUCCGUCC	MANACUCC CU UCANGGACAUCGUCCGGG CCACGUCC	MANACUCC CU UCANGGACAUCGUCCGGG UGGCCCAC	SANACUCC CU UCANGGACAUCGUCCGGG UCGCACUG	SAMACUCC CU UCAAGGACAUCGUCCGGG CCUCUGGG	SANACUCC CU UCAAGGACAUCGUCCGGG CUUCGGGC	SAMACUCO CU UCAAGGACAUCGUCCGGG CCCGGCCU	SAMACUCC CU UCAAGGACAUCGUCCGGG CAUGGUGG	SAAACUCC CU UCAAGGACAUCGUCCGGG UUGGGCCA	SAAACUCC CU UCAAGGACAUCGUCCGGG CAGGGCAG	BAAACUCC CU UCAAGGACAUCGUCCGGG CCAUCCAC	AGGCAGCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCCGCGC	
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	CAPTIGORA G COGOGOCO	CUGCCCAG G CUGGCCGC		O	CCGAUGUA G CGGGCUCC	UGUAGEGG G CUCCGGAU	GGAUCCCA G CCUCUCCC	CHECUCCE & DECUCIOR	UCUCCACA G CCCGGACC	ACCCGGGG G CUGGCCCA	GGGGGUG G CCCAGGGC	GGCCCAGG G CCCUGCAG	CCCUGCAG G CCCUGGCG	AGGCCCUG G CGUCCUGA	GCCCUGGC G UCCUGAUG	GCCCCCAA G CUCCCUCU	CCUGAGAA G CCACCAGC	AGCCACCA G CACCACCC	Acundada a cadacacc	GGGGGCAG G CGCCAGGG	GGACGGAC G UGGGCCAG	GGACGUGG G CCAGUGCG	GUGGGCCA G UGCGAGCC	CAGUGCGA G CCCAGAGG	CCCAGAGG G CCCGAAGG		AGGCCGGG G CCCACCAU	O	0	cueccue e cuccuecu	U	gcecege a uccueccu	

3494	3495	3496	3497	3498	3499	3500	3501	3502	3503	3504	3505	3506	3507	3508	3509	3510	3511	3512	3513	3514	3515	3516	3517	3518	3519	3520	3521	3522	3523	3524	3525	3526	3527
GCCGGAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGUGCUGG	AGGGGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGAUGCC	CCAGGCCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCGCAGG	CCCCCAGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CGCUGCGC	GGGGGGCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCCCAGG	AGCCGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCAGGGG	CGGGGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGCAGCCC	UCCUCGGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UCUUCGUC	CGCCCGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCUCGGG	CCCUCCGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGGCUCC	CAAAGCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCUCCGG	CCACADAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCCCCUC	GUUGUCCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUCUCCA	CCGACUUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCUCAGG	UGCCCCGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGCCCCU	UAGCCCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCGACUU	CGUAGUAG GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG CCUGCCCC		GCUGCCCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGUCAUCU	GGGGGCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCACGGUC	GCGGGGGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UGCCCACG	UGUAUCCA GGAGGAAACUCC OU UCAAGGACAUCGUCCGGG CAGGAUGU	UACUGCUG GGAGGAAACUCC CU UCAAGGACAJCGJCCGGG CUGUAJCC	AGUUACUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCCUGUA	CAAAGUUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCUGCCU	AGCACCCA GGAGGAAACUCC CU UCAAGGACAUCQUCCGGG UGCAAAGU	GGGCAGCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCACUGCA	GACAGCUG GEAGGAAACUCC CU UCAAGGACAUCGUCGGGG CUCUGGUA	CUGGACAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCCUCUG	GGUAUGUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGACAGC	CAUACACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUUCCGG	CCCACUUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUGGGUG	CCUUCCCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGCCCUG	GUGCCCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCCCUUC
1194	1195	1196	1197	1198	1199	1200	1201	1202	1203	1204	1205	1206	1207	1208	1209	1210	1211	1212	1213	1214	1215	1216	1217	1218	1219	1220	1221	1222	1223	1224	1225	1226	1227
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AANUULAA G UGGGGAAA 1328 UUUCCGA GGAGGAAACUCC CU UGAAGACAUCGUCCGGG UDAAAUUU AAAUUULAA G UGGGGAAA 1329 CIIIICAGG GGAGGAAACUCC CU UGAAGACAUGGUCGGG UGAAGUU	0010	magneting a newconca	1327	UGAGGIGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAGAGUA	3627
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3630	3631	3632	3633	3634	3635	3636	3637	3638	3639	3640	3641	3642	3643	3644	3645	3646	3647	3648	3649	3650	3651	3652	3653	3654	3655	3656	3657	3658	3659	3660	3661	3662	3663
າກຕອອວກກ	UNAGARAA	UUCUGAAA	CAGUACUU	CUGCGUGU	CAAGGUAA	GCCAAGGU	CACAGGGA	CAGGGUAC	ungenchc	CAGCAGGG	UUUGGCCA	UGACUUUG	UGUGCAUC	UUGUUUAU	CAAUGUUA	GGGCGGC	ceacceee	CCGGGCGG	AGCUCGCG	CAGCUCGC	AUAAUCCA	ACCAURAU	DECEGANG	cugcegen	GGGCUCCU	ceeecncc	93099936	CGGCGGGC	CCGGCGGG	CCCGGCGG	50550000	വാധവാ	nggucccc
CAAGGACAUCGUCCGGG (CAAGGACAUCGUCCGGG 1	CAAGGACAUCGUCCGGG	CAAGGACAUCGUCCGGG	CAAGGACAUCGUCGGG	CAAGGACAUCGUCCGGG	CAAGGACAUCGUCCGGG	CAAGGACAUCGUCCGGG	CAAGGACAUCGUCCGGG	CAAGGACAUCGUCCGGG	CAAGGACAUCGUCCGGG	CU UCAAGGACAUCGUCCGGG UUUGGCCA	CAAGGACAUCGUCCGGG	CAAGGACAUCGUCCGGG	CAAGGACAUCGUCCGGG	JCAAGGACAUCGUCCGGG	JCAAGGACAUCGUCCGGG	CAAGGACAUCGUCCGGG	JCAAGGACAUCGUCCGGG	JCAAGGACAUCGUCCGGG	JCAAGGACAUCGUCCGGG	JCAAGGACAUCGUCCGGG	JCAAGGACAUCGUCCGGG	JCAAGGACAUCGUCCGGG	JCAAGGACAUCGUCCGGG	JCAAGGACAUCGUCCGGG	JCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG
GAAGAADA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUGGGUU	UUCUGAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAAGAAAA	UGCCAGUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCUGAAA	GUGUGAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGUACUU	CAAGGUAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG	GACACACG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG	GGGACACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG	CCAGGGUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACAGGGA	CUUCUCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGGGUAC	GAMACAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGGUCUC	GACUUUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGCAGGG	CCUACUGA GGAGGAAACUCC CU U	CUCUCCUA GCAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGACUUUG	AUAGCANA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUGCAUC	AUGUUAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGUUUAU	UCULUGCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAUGUUA	GCAGCUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCGGGC	CECAGCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG	UCGCAGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG	CCAUAAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCUCGCG	ACCAUMAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGCUCGC	CAGGCCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAAUCCA	GCUCAGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCAUAAU	CCGGGCUC GGAGGAAACUCC CU UCAAGGACAUCSUCCGGG UGCGGCUG	UCCOGGCU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CUGCGGCU	AAGGCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCUCCU	CAAGGGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGGCUCC	GGUCCCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCGGGCG	UBGUCCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGCGGGC	CUGGUCCC GGAGGANACUCC CU UCAAGGACAUCGUCCGGG CCGGCGGG	CCUGGUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG	CCCUGGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCCGGCG	UCCCUGGIJ GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCCCGGC	CGGCUUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGUCCCC
GAAGAAU	UUCUGAA	UGCCAGE	GUGUGAL	CAAGGUP	GACACAC	GGGACAC	CCAGGG	CUUCUCI	GAMACAI	GACUUUC	CCUACUC	CUCUCCI	AUAGCA	AUGUUA	DCDDDGG	GCAGCUI	CGCAGCI	UCGCAG	CCAURA	ACCAUA	CAGGCC	GCUCAG	099900	nccede	AAGGGC	CAAGGG	CGUCCC	DOGGOCC	CUGGUC	CCUGGU	CCCUGG	ncccne	CGGCUU
1330	1331	1332	1333	1334	1335	1336	1337	1338	1339	1340	1341	1342	1343	1344	1345	1449	1450	1451	1452	1453	1454	1455	1456	1457	1458	1459	1460	1461	1462	1463	1464	1465	1466
G UAUUCUUC	G UUUCAGAA	G UACUGGCA	0	ACACGCAG G UNACCUNG	maccinia a cauguanc	ACCHINGGE G UGUGUECE	ucccuque a uacccuda	GUACCCUG G CAGAGAAG	G CUUGUUUC	CCCUGCUG G CCAAAGUC	UGGCCAAA G UCAGUAGG	CAAAGUCA G UAGGAGAG	GAUGCACA G UNUGCUAU	G CCUNACAU	UNACAUUG G UGCANAGA	GCCCGCCC G GGAGCUGC	CCCGCCCG G GAGCUGCG	CCGCCCGG G AGCUGCGA	G GAUTUAUGG	G AUUAUGGU	g guggccug	AUDAUGGU G GCCUGAGC	CAGCCGCA G GAGCCCGG	AGCCGCAG G AGCCCGGA	AGGAGCCC G GAGCCCUU	G AGCCCUUG	CGCCCGCC G GGGGGACC	GCCCGCCG G GGGGACCA	CCCGCCGG G GGGACCAG	CCGCCGGG G GGACCAGG	G GACCAGGG	G ACCAGGGA	GGGGACCA G GGAAGCCG
AACCCAAA	UUUUCUUA	UUUCAGAA	AAGUACUG	ACACICAG	DINACCING	ACCITIGGO	UCCCUGUG	GUACCCUG	GAGACCAA G	CCCUGCUG	UGGCCAAA	CAAAGUCA	GAUGCACA	AUABACAA	UAACAUUG	GCCCGCCC	CCCGCCCG	55000000	CGCGAGCU G	GCGAGCUG	UGGAUUAU	AUUAUGGU	CAGCCGCA	AGCCGCAG	AGGAGCCC	GGAGCCCG G	2202222	BCCCGCCG	SSCCGCCGG	CCGCCGG	0 00000000	9 99999009	GGGGACCA
2288	2305	2314	2320	2333	2342	2344	2357	2365	2381	2397	2403	2407	2424	2463	2474	22	23	24	43	44	20	23	7.8	4	85	98	119	120	121	122	123	124	129

3664	3665	3666	3667	3668	3669	3670	3671	3672	3673	3674	3675	3676	3677	3678	3679	3680	3681	3682	3683	3684	3685	3686	3687	3688	3689	3690	3691	3692	3693	_	_	3696
GCGGCUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGGUCCC	GGCGGCUU GGAGGAAGUCC CU UCAAGGACAUCGUCCGGG CCUGGUCC	UGGCGGGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GGUGGCGG	CGGGCUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCGGGGC	GCGGGCUC GBAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGCGGGG	COCCOGCU GCAGGAACUCC CU UCAAGGACAUCGUCGGG CCGGCGGG	CGGCCAGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UGGCCAGC	GCGGCGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCCUGGG	CCGGAGCC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GCUACAUC	UCCGGAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGCUACAU	CUGGGAUC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GGAGCCCG	GCUGGGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGAGCCC	GGGAGAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCAGAGCA	GGGGAGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGCAGAGC	CCCGGGUC GCAGGRAACUCC CU UCAAGGACAUCGUCCGGG GGGCUGUG	CCCCGGGU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CGGGCUGU	CCAGCCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGUCCGG	GCCAGCCC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CGGGUCCG	GECCAGCE GGAGGAAACUCE EU UCAAGGACAUCGUCGGG CCGGGUCE	GGGCCAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCGGGUC	CCCUGGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCCCCCG	GCAGGGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGGCCAG	UGCAGGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGGGCCA	GCCAGGGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UGCAGGGC	CAGGACGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGCCUG	GOUGGOUU GCAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCAGGAGA	CCCCAAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGGUGGU	CCUGCCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGUCUGG	GCCUGCCC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CAAGUCUG	CGCCUGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAAGUCU	GOGCCUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCAAGUC	CCUGGCGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UGCCCCCA	GUCCGUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGCGCCU
1467	1468	1469	1470	1471	1472	1473	1474	1475	1476	1477	1478	1479	1480	1481	1482	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	1493	1494	1495	1496	1497	1498	1499
GGGACCAG G GAAGCCGC	GGACCAGG G AAGCCGCC	CCGCCACC G GCCCGCCA	GCCCCGCC G GGAGCCCG	CCCCGCCG G GAGCCCGC	CCCCCGG G VCCCCGCG	GCUGCCCA G GCUGGCCG	CCCAGGCU G GCCGCCGC	GAUGUAGC G GCCUCCGG	AUGUAGEG G GEUEEGGA	CGGGCUCC G GAUCCCAG	GGCCUCCG G AUCCCAGC	uccucuec e exucucec	GCUCUGCG G AUCUCCCC	CACAGCCC G GACCCGGG	ACAGCCCG G ACCCGGGG	CCGGACCC G GGGGCUGG	CGGACCCG G GGGCUGGC	GGACCCGG G GGCUGGCC	GACCCGGG G GCUGGCCC	CGGGGGCU G GCCCAGGG	CUGGCCCA G GGCCCUGC	UGGCCCAG G GCCCUGCA	GCCCUGCA G GCCCUGGC	CAGGCCCU G GCGUCCUG	UCUCCUGA G AAGCCACC	ACCACCCA G ACUUGGGG	CCAGACUU G GGGGCAGG	CAGACUUG G GGGCAGGC	AGACUUGG G GGCAGGCG	GACUUGGG G GCAGGCGC	UGGGGGCA G GCGCCAGG	AGGCGCCA G GGACGGAC
130	131	143	175	176	177	197	201	224	225	231	232	265	366	294	295	300	301	302	303	307	313	314	323	329	362	382	387	388	389	390	394	401

403	GCGCCAGG G ACGGACGU	1501	ACGUECGU GGAGGAAACUEC CU UCAAGGACAUCGUCCGGG CCUGGCGC	3698
406	CCAGGGAC G GACGUGGG	1502	CCCACGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUCCCUGG	3699
403	CAGGGACG G ACGUGGGC	1503	GCCCACGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGUCCCUG	3700
412	ACCOACCU G GGCCAGUG	1504	CACUGGCC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG ACGUCCGU	3701
413	CGGACGUG G GCCAGUGC	1505	GCACUGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACGUCCG	3702
429	CGAGCCCA G AGGGCCCG	1506	CGGGCCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGGCUCG	3703
431	AGCCCAGA G GGCCCGAA	1507	UDCGGGCC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UCUGGGCU	3704
432	GCCCAGAG G GCCCGAAG	1508	CUUCGGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUCUGGGC	3705
440	GOCCCGAA G GCCGGGGC	1509	GCCCCGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UUCGGGCC	3706
444	CGAAGGCC G GGGCCCAC	1510	GUGGGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCCUUCG	3707
445	GAAGGCCG G GGCCCACC	1511	GGUGGGCC GGAGGAAACUCC CU UCNAGGACAUCGUCCGGG CGGCCUUC	3708
446	AAGGCCGG G GCCCACCA	1512	UGGUGGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGGCCUU	3709
456	CCCACCAU G GCCCAAGC	1513	GCUUGGGC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AUGGUGGG	3710
473	coneccon e ecoconec	1514	GCAGGAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGCAGG	3711
485	ccuecueu e GAUGGGCG	1515	CGCCCAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAGCAGG	3712
486	CUGCUGUG G AUGGGCGC	1516	GCGCCCAU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CACAGCAG	3713
489	CUGUGGAU G GGCGCGGG	1517	CCCGCGCC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AUCCACAG	3714
490	UGUGGAUG G GCGCGGGA	1518	UCCCGCGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CAUCCACA	3715
495	AUGGGCGC G GGAGUGCU	1519	AGCACUCC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG GCGCCCAU	3716
961	UGGGCGCG G GAGUGCUG	1520	CAGCACUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGCGCCCA	3717
497	GGGCGCG G AGUGCUGC	1521	GCAGCACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGCGCCC	3718
514	CUGCCCAC G GCACCCAG	1522	CUGGGUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUGGGCAG	3719
526	CCCAGCAC G GCAUCCGG	1523	CCGGAUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUGCUGGG	3720
533	CGGCAUCC G GCUGCCCC	1524	GOGGCAGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GGAUGCCG	3721
550	UGCGCAGC G GCCUGGGG	1525	CCCCAGGC GCAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCUGCGCA	3722
555	AGCGGCCU G GGGGGCGC	1526	GCGCCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGCCGCU	3723
955	22909999 9 9A239929	1527	GGCGCCCC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CAGGCCGC	3724
557	CGGCCUGG G GGGCGCCC	1528	GGGCGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAGGCCG	3725
558	32222222 6 86CCCCC	1529	GGGGCGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCAAGGCC	3726
559	32332506 6 65500335	1530	GOGGECGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCCAGGC	3727
570	SCCCCCC G GGCDGCG	1531	CGCAGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGGGCC	3728
571	coccoone e econecee	1532	CCGCAGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGGGGGG	3729
572	CCCCCNGG G GCNGCGGC	1533	GCCGCAGC GGAGGAAACUCC CU UCAAGGACAUÇGUCCGGG CCAGGGGG	3730
578	GGGGCUGC G GCUGCCCC	1534	GGGGCAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCAGCCCC	3731

3732	3733	3734	3735	3736	3737	3738	3739	3740	3741	3742	3743	3744	3745	3746	3747	3748	3749	3750	3751	3752	3753	3754	3755	3756	3757	3758	3759	3760	3761	3762	3763	3764	3765
CGGUCUCC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GGGGCAGC	UCGGUCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGGCAG	GUCGGUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGGGGCA	UCGUCGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCCGGGG	CUCGGGCU GGAGGAACUCC CU UCAAGGACAUCGUCGGG UUCGUCGG	CCGGGCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCGGGCUC	GCCGGCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUCGGGCU	CCUCCGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCUCCU	UGCCCCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCCGGGC	CUGCCCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGCCGGG	AGCUGOCO GGAGGAAACUCO CU UCAAGGACAUCGUCCGGG UCCGGCCG	AAGCUGCC GGAGGMACUCC CU UCAAGGACAUCGUCCGGG CUCCGGCC	MANGCUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUCCGGC	ACCAUCUC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG ACAAAGCU	CACCAUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACAAAGC	UCCACCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCACAAA	UNGUCCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCUCCAC	AGGUUGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCAUCUC	CAGGUUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACCAUCU	ACUTIGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCAGGUUG	GACUUGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUCAGGUU	CSACUUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUCAGGU	CCCUGCCC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GACUUGCC	GCCCUGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGACUUGC	AGCCCUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGACUUG	UAGUAGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCCCCGA	GUAGUAGO GGAGGAAACUCO OU UCAAGGACAUCGUCOGGG CUGCCCCG	GUCAUCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGUAGUA	GGUCAUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACGUAGU	ACGGUCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCACGUA	GGGCUGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGGUCAU	GGGGCUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACGGUCA	UNGAGOGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCGGGG	GUAUCCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGAUGUU
1535	1536	1537	1538	1539	1540	1541	1542	1543	1544	1545	1546	1547	1548	1549	1550	1551	1552	1553	1554	1555	1556	1557	1558	1559	1560	1561	1562	1563	1564	1565	1566	1567	1568
GCUGCCCC G GGAGACCG	CUGCCCCG G GAGACCGA	UGCCCCGG G AGACCGAC	CCCCGGGA G ACCGACGA	CCGACGAA G AGCCCGAG	GAGCCCGA G GAGCCCGG	AGCCCGAG G AGCCCGGC	AGGAGCCC G GCCGGAGG	GCCCGGCC G GAGGGGCA	CCCGGCCG G AGGGGCAG	CGCCCGGA G GGCCAGCU	GGCCGGNG G GGCAGCUU	GCCGGAGG G GCAGCUUU	AGCUUUGU G GAGAUGGU	GCUUUGUG G AGAUGGUG	UUUGUGGA G AUGGUGGA	GUGGAGAU G GUGGACAA	GAGAUGGU G GACAACCU	AGAUGGUG G ACAACCUG	CAACCUGA G GGGCAAGU	AACCUGAG G GGCAAGUC	ACCUGAGG G GCAAGUCG	GGCAAGUC G GGGCAGGG	GCAAGUCG G GGCAGGGC	CAAGUCGG G GCAGGGCU	UCGGGGCA G GGCUACUA	CGGGGCAG G GCUACUAC	UACUACGU G GAGAUGAC	ACUACGUG G AGAUGACC	UACGUGGA G AUGACCGU	AUGACCGU G GGCAGCCC	UGACCGUG G GCAGCCCC	CCCCCGCA G ACGCUCAA	AACAUCCU G GUGGAUAC
587	588	589	591	109	609	610	616	620	621	623	624	625	989	637	639	642	645	949	999	657	859	999	299	899	672	673	684	685	687	969	697	711	726

1570. 1571. 1570. 1571. 1571. 1574. 1578. 1578. 1580.			3550	CHIGHING AGAGGAAMING ON UCAAGGACAUCGUCGGG ACCAGGAU	3766
UGENINGA G GARCHOST 1371 ANDEGREGO GRAGARANCHOC OR UNIVARIONA DE UNI	729	ع e	1570.	GCCUGUAU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CACCAGGA	3767
	736) e	1571	ACUGCUGO GGAGGAAACUCO CU UCAAGGACAUCGUCCGGG UGUAUCCA	3768
UNICACIONE O BURGURGO: 18.73 GOOGGOOG CORRONANCE O UTO-MACRACHICOCORRO USUARA CONTROLLA UNICACIONE O REGISTRO 1374 ACCIOCOCO GRAGADARCE O UTO-MACRACHICOCORRO USUARA CONTROLLA UNICACIONE O REGISTRO 1374 ACCIOCOCO GRAGADARCE O UTO-MACRACHICOCORRO USUARA CONTROLLA UNICACIONE O RACIONE 1377 ACCIOCOCO GRAGADARCE O UTO-MACRACHICOCORRO GRAGADARCE O UTO-MACRACHICOCORRO GRAGADARCE CALLANCOR O RACIONE 1378 CORRORA GRAGADARCE O UTO-MACRACHICOCORRO GRAGADARCE CALLANCOR O RACIONE 1379 CORRORA GRAGADARCE O UTO-MACRACHICOCORRO GRAGADARCE CALLANCOR O RACIONE 1378 CORRORA GRAGADARCE CORRORA GRAGADARCE CALCOLOR GRAGADARCE 1378 CORRORA GRAGADARCE CALCOLOR GRAGADARCE	130	THIS C CONTROL OF THE CONTROL	1572	GCAGCACC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUGCAAA	3769
UNICACIONE O AGRICULOR 15.74 AGRICURED GRAGAMARTICE OLI UDARGIARULUCIUCORD GRAGAMARTICE OLI UDARGIARULUCIUCORD GRAGAMARTICE COLI GRAGAMARTICE COLI UDARGIARULUCIUCORD GRAGAMARTICE COLI UDARGIARULUCIUCORD GRAGAMARTICE COLI UDARGIARULUCIUCORD GRAGAMARTI	000	Company o discount	1573	GGAGGAAACUCC	3770
CONCIDAD G. GO-JGG3301 15-55 ADDITIONE CONGRAMMENT CE OF UNANGARAD LUCKUROUS GOUNDING ACRILLANDE G. GO-JGG3301 15-76 CORRESPONDENCE OF UNANGARAD LUCKUROUS GOUNDING ACRILLANDE G. BACKLOGG 15-77 CORRESPONDENCE OF UNANGARAD LUCKUROUS GOUNDING COLOCIOGO 15-77 CORRESPONDENCE OF UNANGARAD CORRESPONDENCE OR CORRIVIUS COLOCIOGO 15-77 CORRESPONDENCE OF UNANGARAD CORRESPONDENCE OR CORRIVIUS COLOCIOGO 15-77 CORRESPONDENCE OF UNANGARAD CORRESPONDENCE OR CORRIVIUS COLOCIOGO 15-77 COLOCIOGO GONDANA CORRESPONDENCE OR CORRIVIUS COLOCIOGO 15-78 COLOCIOGO GONDANA CORRESPONDENCE OR CORRESPONDE	100	TIPOTING & AGGORGOU	1574		3771
CACAMACE O GRACITOR 15.76 GRAGIARAMACINE CO IU USANGARAMUCICORO COROLLARIO CALAMACE O GRACITOR 15.77 COROAGUE GRAGIARAMACINE CU UNANGARAMUCICOROGO COROLLARIO CALAMACE O RACCORO 15.77 COROAGUE GRAGIARAMACINE CU UNANGARAMUCICOROGO GRAGIARAMACINE CU UNANGARAMUCICOROGO GRAGIARAM CALAMACE O RACCORO 15.79 COROCORO CALAMACE O RACCORO 15.70 CALAMACINE CO UNANGARAMUCICOROGO GRAGIARAMACINE CU UNANGARAMUCICOROGO GRAGIARAMACINE CO UNANGARAMACINE DE ROCCOROLLARIO CALAMACINE A RACCOROLLO GRAGIARAMACINE CU UNANGARAMUCICOROGO GRAGIARAMACINE CO UNANGARAMACINE DE ROCCOROLLO GRAGIARAMACINE CU UNANGARAMACINE COROLLO GRAGIARAMACINE CU UNANGARAMACINE CU UNANGARAMACIN	707	0	1575	ACAGCUGE GGAGGAAACUCE CU UCAAGGACAUCGUCCGGG UCUGGUAG	3772
ACRIMICCIO G MACTICICO 1577 COGNOGIO GIAGNAMANICO CE ULICAMORA INCUSTOCIONE DI CONTRATA CALACCOLO 1578 COCREDADO GIAGNAMANICO CE ULICAMORA INCUSTOCIONE DI CONTRATA CALACCOLO 1578 CALACCOLO CALACCALO 1578 CALACCALO CALACCALO 1578 CALACCALO CALACCALO 1578 CALACCALO CALACCALO 1578 CALACCALO CALACCALO	818	0	1576	GGAGGUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGUAUGUG	3773
CIVILACIDE O GANGEROR 15.78 COCREDADE GRADAMANICE CU ULANGARALMUSCUCCORRA GRADAMANICE CORRADOR TORRADOR TORRADOR CORRADOR CORRADOR TORRADOR TORRADOR TORRADOR CORRADOR CORRADOR CORRADOR CORRADOR CORRADOR TORRADOR CORRADOR CORRADOR CORRADOR TORRADOR CORRADOR CORRADOR CORRADOR CORRADOR CORRADOR CORRADOR CORRADOR CORRADOR TORRADOR CORRADOR SERVICIOS CORRADOR CORRADOR CORRADOR CORRADOR CORRADOR CORRADOR CORRADOR SERVICIO CORRADOR COR	0 10	C	1577	COGAGGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGUAUGU	3774
GIACCTOTIC G GARAGRADIO 15.99 CALCOCTUD GRAGADANICCE OF USANGARDHOUGHOUGHOUGHOUGHOUGHOUGHOUGHOUGHOUGHOUG	820	Chilacres a Accuedes	1578	CCGGAGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGGUAUG	3775
фистото 6 даждаяти 1580 АССРОИНИ БУДИВНИЕ В В В В В В В В В В В В В В В В В В В	837	GRACHICE G GAAGGGUG	1579	CACCCUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGAGGUCC	3776
CHICCOSTA G GRADIERA 1511 UNACONC GRADIANACIC CU UCANGACHUCURONA UCCOSTA G GRADIERA 1582 UNACONC GRADIANACIC CU UCANGACHUCURORE UCANGACHUCURORE UCCOSTA G GRADIERA 1582 CARTICO CONTRACTOR ULCOSTAGO GUARRANIA 1583 ALACCIDA GARANIA 1584 CARTICO CONTRACTOR CONTRACTOR GRADIANO 1584 CARTICO CONTRACTOR CONTRACTOR GRADIANO 1584 CARTICO CONTRACTOR CONTRACTOR GRADIANO 1586 CARTICO CONTRACTOR CONTRACTOR GRADIANO 1586 CARTICO CONTRACTOR GARANIA CONTRACTOR GRADIANO 1581 CARTICO CONTRACTOR GARANIA CONTRACTOR GRADIANO 1581 CARTICOR GARANIA CONTRACTOR	828	GACCUCCO G AAGGGUGU	1580	ACACCCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGAGGUC	3777
UNICODADA G GRUGURIAN 1582 AUNICACIONE GRADARACICE CU ULANAGA-AULGUECCORDA NACIONARIO G GRADARA 1581 AUNICACE GRADARACICE CU ULANAGA-AULGUECCORA NACIONARIO G GRADARA 1581 CACTUDE GRADARACICE CU ULANAGA-AULGUECCORA ACACTAGO G GRADARA 1581 CACTUDE GRADARA CORRESCO CONTRACTORA 1581 CACTUDE GRADARA CORRESCO CONTRACTORA 1581 CACTUDE GRADARACICE CU ULANAGA-AUTGUECCORA GRADARA 1581 CACTUDE GRADARACICE CU ULANAGA-AUTGUECORA GRADARA 1581 CACCUCUC GRADARACICE CU ULANAGA-AUTGUECCORA GRADARA 1581 CACCUCUC GRADARACICE CU ULANAGA-AUTGUECCORA GRADARA 1582 CACCUCUC GRADARACICE CU ULANAGA-AUTGUECCORA GRADARA 1582 CACCUCUC GRADARACICE CU ULANAGA-AUTGUECCORA GRADARA 1583 CACCUCUC GRADARACICE CU ULANAGA-AUTGUECCORA GRADARA 1583 CACCUCUC GRADARACICE CU ULANAGA-AUTGUECCORA GRADARA 1584 CACCUCUC GRADARACICE CU ULANAGA-AUTGUECCORA GRADARA 1585 CACCUCUC GRADARACICE CU ULANAGA-AUTGUECCORA GRADARA 1584 GRADARACICE CU ULANAGA-AUTGUECCORA	831	CUCCGGAA G GGUGUGUA	1581	UACACACE GGAGGAAACUCE CU UCAAGGACAUCGUECGGG UUCCGGAG	3778
UNICACION G GORDAGIGO 15513 CANTIDIDE GRADABANCIUC CU UNABACHANCHUCUCORRO BURGARUAN GRADABANCIUC CU UNABACHANCHUCUCORRO BURGARUAN GRACABANCIUC CU UNABACHANCHUCUCORRO BURGARUAN GRADABANCIUC CU UNABACHANCHUCUCORRO GRADABANCIUC CU UNABACHANCHUC CU UNABACHANCHUCUCORRO GRADABANCIUC CU UNABACHANCHUC CU UNABACHANCHUCUCORRO GRADABANCHUC CU UNABACHANCHUC CU UNABACHANCH	832	HCCGGAAG G GUGUGUAU	1582	AUACACAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUUCCGGA	3779
ACHICAGOSTO GORAGIOS 1584 CONCIUTO GORAGIANCO CU UCHARGARALUCICOSOS CHARGARALUCICOSOS CHARGARALUCICOSOS CONCIUNOS GRACAMAGO GORAGIAS 1584 CONCUENTO GORGARALUCE CU UCHARGARALUCICOSOS CHARGARALUCICOSOS CHARGARAL	2 2	HACACCCA G GGCAAGUG	1583	CACUUGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGGUGUA	3780
GOGGOADHUY G GRAACOGG 1556 COCCOUNTIC GRAACAGACCUC CU UCAAGACAUNCOCOGG DAUGACCA GOGGOADHUY G GRAACAGACA 1557 CUCCOUNTIC GRAACACACCACU UCAAGACAUNCOCOGG CUAAGACAUNCOCOGG CUAACACACACACACACACACACACACACACACACACAC	856		1584	CCACUUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGGGUGU	3781
0407A001G G GAAGGGGA 15566 UTCCCCCUUE GORGARANCEC CU UU-AAGACAUUGUCOSOB CANUUGC 0407A001G G AAAGGGAA 15566 UTCCCCCUUE GORGARANCEC CU UU-AAGACAUUGUCOSOB UU-CCAUUC 040400GAAA 0 608A0CGG 15569 CAACUCCC GAAGGAAAACCC CU UU-AAGACAUUGUCOSOB UU-CCAUC 040600GAAA 0 608A0CGG 15569 CACCACCUU GAAGGAAAACCC CU UU-AAGACAUUGUCOSOB UU-CCACC 040600GAAA 0 608A0CGG 15599 CACCACCUU GAAGGAAAACCC CU UU-AAGACAUUGUCOSOB UU-CCCACC 040600AAA 0 608A0CGG 15599 CACCACCUU GAAGGAAAACCC CU UU-AAGACAUUGUCOGG CAACCACC 040600AAA 0 60ACCGGAC 15599 CACCACCUU GAAGGAAAACCC CU UU-AAGACAUUGUCOGG CAACCACCACC 040600ACG 15590 CACCACCUU GAAGGAAAACCC CU UU-AAGACAAUUCCCCACCACCACCACCACCACCACCACCACCACC	863	GGGCAAGU G GGAAGGGG	1585	CCCCUUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUUGCCC	3782
GONADIGO E A ARAGGARA 1587 CUIDOCCO GRADARANCE O U UNAMAGINALUCIDODAS CUANDO AGURANDO E O ARAGGARA 1589 COMPONCE GRADARANCE O U UNAMAGINALUCIDODAS U UNCONTO UNITARIO DE CONTOCO CONTO CONTO UNITARIO DE CONTOCO CONTO CONTO CONTO UNITARIO DE CONTOCO CONTO CONTO CONTO UNITARIO DE CONTOCO CONTO CONTO CONTO CONTO UNITARIO DE CONTOCO CONTO CONTO CONTO UNITARIO DE CONTOCO CONTO C	864	GGCAAGUG G GAAGGGGA	1586	UCCCCUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACUUGCC	3783
ARTICIDADA O GRADACIDO 1588 CAMPONTO GRADACIDO 1588 CAMPONTO GRADACIDO CONTRO CONTRO GRADACIDO CONTRO CO	865	GCAAGUGG G AAGGGGAG	1587	CUCCCCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCACUUGC	3784
	868	AGUGGGAA G GGGAGCUG	1588	CAGCUCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCCCACU	3785
19950ANGG G GRECURGE 1559 CCCOLACTOR GRAGARANCHUC CU UUCANGERULUUGUUGUUGU 0803ANGG G ARCUGGG 1591 CCCOLACTU GRAGARANCHUC CU UUCANGERULUUGUUGU 0803ANGG G ARCUGGG 1592 GCCCOLACTU GRAGARANCHUC CU UUCANGERULUUGUCGGG 0803ANGG G GARCUGGA 1593 GUCCOLACTU GRAGARANCHUC CU UUCANGERULUUGUCGGG 0803ANGG G GARCUGGA 1593 GUCCOLACTU GRAGARANCHUC CU UUCANGERULUUGUCGGG 0803ANGG G GARCUGAA 1593 GUCCOLACTU GRAGARANCHUC CU UUCANGERULUUGUCGGG 0803ANGGA 1594 GUCCOLACTU GRAGARANCHUC CU UUCANGERULUUGUCGGG 0803ANGGA 1595 GUCCOLACTU GRAGARANCHUC CU UUCANGERULUUGUCGGG 0803ANGGA 1596 GUCCOLACTU G GARCARANCHUC CU UUCANGERULUGUCGGG 0803ANGAA 1596 GUCCOLACTU G GARCARANCHUC CU UUCANGERUCGGGG 0803ANGAA 1596 GUCCOLACTU G GARCARANCHUC CU UUCANGERUCGGGG 0803ANGAA 1596 GUCCOLACTU G GARCARANCHUC CU UUCANGERUCGGGGG 0803ANGAA 1596 GUCCOLACTU G GARCARANCHUC CU UUCANGERUCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	9,69	GIIGGGAAG G GGAGCUGG	1589	CCAGCUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUUCCCAC	3786
GEORAGOGO G ANCHOGOS 1591 GEORAGOGO CONTROLLO GORAGOGO G ANCHOGOS 1592 GEORAGOGO CONTROLLO GORAGOGO G GARCIOGO 1593 GORGOGO CONTROLLO GORAGOGO G GARCIOGO 1594 GORGOGO CONTROLLO GORGOGO G GARCIOGO 1594 GORGOGO CONTROLLO	870	UGGGAAGG G GAGCUGGG	1590	CCCAGCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUUCCCA	3787
6.08GBAGCU G GROCICCRA 1593 UCORRIDOR GRAGAMACIUC CU UCAMBRICALUCROSCOBA MACUCCC 6.08GAGCU G GROCICARA 1593 GUICAGRA GRAGAMACIUC CU UCAMBRICALUCROSCOBA MACUCCC ACCIDALA 1594 GUICAGRA GRAGAMACIUC CU UCAMBRICALUCROSCOBA MACUCCC ACCIDALA 1595 GUICAGRA GRAGAMACIUC CU UCAMBRICALUCROSCOBA MAGUCCC UCAMACIA 6 GUICAGRA 1599 GUARGIA GUICAGRA GRAGAMACIUC CU UCAMBRICALUCROSCOBA GUARGIA UCAMACIA 6 GUICAGRA 1599 GUARGIA GUARGIA <td>27</td> <td>GRADAGG G AGCUGGGC</td> <td>1591</td> <td>GCCCAGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCUUCCC</td> <td>3788</td>	27	GRADAGG G AGCUGGGC	1591	GCCCAGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCUUCCC	3788
64/36/ACTUS G GENECORE 1553 GITCGRIDE GRADADANICO CU ULUNAGRACHUCOROUCOBO PARIOCOCO 74/36/ACTUS G GENECORE 1554 AURICUNE GRADADANICO CU ULUNAGRACHUCOROUCOBO PARIOCOCO 74/36/ACTUS 1554 AURICUNE GRADADANICO CU ULUNAGRACHUCOCOBO PARIOCOCO 74/36/ACTUS 1556 GRADADANICO CO ULUNAGRACHUCOCOBO PARIOCOCO 74/36/ACTUS 1556 GRADADANICO CO ULUNAGRACHUCOCOO 74/36/ACTUS 1556 GRADADANICO CO ULUNAGRACHUCOCOO 74/36/ACTUS 1559 AURICUNE GRADADANICO CO ULUNAGRACHUCOCOCOO 74/36/ACTUS 1560 AURICUNE GRADADANICO CO ULUNAGRACHUCOCOCOO 74/36/ACTUS 1561 AURICUNE GRADADANICO CO ULUNAGRACHUCOCOCOO 74/36/ACTUS 1561 AURICUNE GRADADANICO CO ULUNAGRACHUCOCOCOO 74/36/ACTUS 1561	876	GGGGAGCU G GGCACCGA	1592	UCGGUGCE GGAGGAAACUCE CU UCAAGGACAUCGUCCGGG AGCUCCCC	3789
ACCREDICE GERDAGICA 1554 AUDICINE GERGEARANCE CE ULPARACHUCHOGOGO ACCUEDO UNICOCOMO CONTROL	877	GOGAGOUG G GCACCGAC	1593	GUCGGUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGCUCCC	3790
UCCOCCOUN G GEOCOLAGE 15555 GUIDRESCRO GRAGARACHUC GU UNAMAGALAUCHUCHUCAGA BAUGAGAA UCAUCALG A GOAGUAC 1556 GARACHUC GRAGARACHUC GU UCAAGACAHUCACCGGG UBAULOA UCAUCALG G GOUCACAC 1559 GARACHUC GRAGARACHUC CU UCAAGACAHUCACCCGGG UBAULOA UCAACUG G RANGARACH 1559 VARCAUCCGGGGAAAACHUC CU UCAAGACAHUCACCCGGG GUBAUCA CUCAACUG G RANGARACH 1559 VARCAUCGGGGAAAACHUC CU UCAAGACAHUCACCCGGG CAGUUGA CUCAACUG G RANGARACH 1550 VARCAUCGGGGAAAACHUC CU UCAAGACAHUCACCCGGG CAGUUGA CUCAACUG G RANGACCH 1560 AAUCACUG GARACHUC CU UCAAGACAHUCACCGGG CAGUUGAA CUCAACUG G RANGACCH 1560 AAUCACUG GARACHUC CU UCAAGACAHUCACCGGGGAAAACHUCACCGGGGAAAAAACHUCACCGGGGAAAAAAAAAA	888	ACCGACCU G GUAAGCAU	1594	AUGCUUNC GGAGGNANCUCC CU UCAAGGACAUCGUCCGGG AGGUCGGU	3791
CUBANIDA G ACABEIRE 1556 GAAAGURU G AGAGURU 1556 GAAAGURU GAAAGURU CUBANADA AGAGURU CUBANADA AGAGURU </td <td>406</td> <td>UCCCCAU G GCCCCAAC</td> <td>1595</td> <td>GUUGGGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGGGGGA</td> <td>3792</td>	406	UCCCCAU G GCCCCAAC	1595	GUUGGGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGGGGGA	3792
UCANCIANE G GCUCCAAC 1597 QUURGAGE GRACAAACUCC CU UCAAGACAACUCCOSG GUUGAUGA CUCCAACU G GGAGGEA 1599 UGCUCCOC GRACAAACUCC CU UCAAGACAACUCCOGG AAACUCC CUCAACUG G GAAGGCAU 1599 AUGCUUC GRACAAACUCC CU UCAAGACAACUCGCOGG CAAGUGG CCAACUG G GAAGGCAU 1599 AUGCCUUC GRACAAACUCC CU UCAAGACAACUCGCOGG CAAGUGG CCAACUGG G AAAGCCAUC 1600 QAUGCCUU GRACAAACUCC CU UCAAGACAACUCCOGG CAAGUGG AACUGCAG G GCAACCC GAAGAAACUCC CU UCAAGACAACUCCGGG CAAGUGG AACUGCAG GAAGACCC GAAGAAAACUCC CU UCAAGACAACUCCGGGG AAAACCG AACUCCAG GAAGACCC GAAGAAAACUCC CU UCAAGACAACACCGGGGGGGGGG	640	CHRANICA G ACAAGUUC	1596	GAACUUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAUUCAG	3793
CUCNACIO G GRAGOZO. 15599 USCUDIC GRACIALACIC CU UCHARAGINUCUSCORDA DAUDIORA UCCANCIGO G GRAGOZU. 15599 USCUDIC GRACIALACIC CU UCHARAGINUCUSCORD CANGINGA CONTROL STORMANICOUNIC GRACIALACIC GO GRAGOZUCO GARAGINUCA GARAGINICA GARAGIN	970	UCAUCAAC G GCUCCAAC	1597	GUUGGAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUUGAUGA	3794
UCCDACUE G GARGECUU 1599 AUGCUUT GRACIAAACUCC CU UCAAGACAUCUCGGG CAGUUGGA CCDACUEG G AAGGCUU 1600 GAUGCUU GAAGGAAACUCC CU UCAAGACAUCUCGGG CAGUUGG ACUGGBAA 1601 CAGGAUC GAAGAAACUCC CU UCAAGACAUCUCGGG CAGGAUCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	086	b	1598	UGCCUUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUUGGAG	3795
CONACUGE 6 AAGRICHUC 1600 GAUGCCUU GRAGANACUC CU UCANGACAUCGUCGOS CUAUDOS ACUGGOS 6 CENTRO 1601 CANGACAUCGUCGOS UCCANGU ACUGGOS 6 CENTRO 1601 CANGACAC GAUGAGANACUC CU UCANGACAUCGUCGOS NUCCANGU ACUGGOS 6 CENTRO 1601 CANGACA CUAUCGUC GAUGAGANACUC CU UCANGACAUCAGCOS AGAUGCC GAUGAGANACUC CU UCANGACAUCAGCOS AGAUGCC GAUGAGANACUC CU UCANGACAUCAGCOS AGAUGCC GAUGAGANACUC CU UCANGACACACACA AGAICA AGAICA CANGACA AGAICA AGA	180	UCCAACUG G GAAGGCAU	1599	AUGCCUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGUUGGA	3796
ACUGGGAA G GCAUCCUG 1.601 CAGGAUGC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG UUCCCAGU CACAILICCU G GGGCUGGC 1.602 GCCAGCC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AGGAUGCC	982	CCAACUGG G AAGGCAUC	1600		3797
AGENIFICA G GGCUGGC 1602 GCCAGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AGGAUGCC	982	ACUGGGAA G GCAUCCUG	1601	CAGGAUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCCCAGU	3798
	000	GGCAUCCU G GGGCUGGC	1602	GCCAGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGAUGCC	3799

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700	GCAUCCUS G GGCUGGCC	1603	GGCCAGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGGAUGC	3800
995	CAUCCUGG G GCUGGCCU	1604	AGGCCAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAGGAUG	3801
666	CUGGGGCU G GCCUAUGC	1605	GCAUAGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCCCCAG	3802
101	UAUGCUGA G AUUGCCAG	1606	CUGGCAAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCAGCAUA	3803
1019	GAUUGCCA G GCCUGACG	1607	CGUCAGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGCAAUC	3804
1035	GACUCCCU G GAGCCUUU	1608	AAAGGCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGAGUC	3805
1036	ACUCCCUG G AGCCUUUC	1609	GAAAGGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGGGAGU	3806
1056	GACUCUCU G GUAAAGCA	1610	UGCUTURE GGRGGRARCUCE CU UCRAGGRCAUCGUECGGG AGRGRGUE	3807
1065	GUANAGCA G ACCCACGU	1611	ACGUGGGU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UGCUUUAC	3808
1102	AGCUUUGU G GUGCUGGC	1612	GCCAGCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAAAGCU	3809
1108	gugguacu a acunococ	1613	GGGGAAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCACCAC	3810
1137	GAAGUGCU G GCCUCUGU	1614	ACAGAGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCACUUC	3811
1147	CCUCUGUC G GAGGGAGC	1615	GCUCCCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GACAGAGG	3812
1148	CUCUGUCG G AGGGAGCA	1616	UGCUCCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGACAGAG	3813
1150	CUGUCGGA G GGAGCAUG	1617	CAUGCUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCGACAG	3814
1151	UGUCGGAG G GAGCAUGA	1618	UCAUGCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUCCGACA	3815
1152	GUCGCAGG G AGCAUGAU	1619	AUCAUGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUCCGAC	3816
1165	UGAUCAUU G GAGGUAUC	1620	GAUACCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUGAUCA	3817
1166	GAUCAUUG G AGGUAUCG	1621	CGAUACCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAUGAUC	3818
1168	UCAUUGGA G GUAUCGAC	1622	GUCGAUAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCAAUGA	3819
1192	UGUAÇAÇA G GCAGUCUC	1623	GAGACUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUGUACA	3820
1202	CAGUCUCU G GUAUACAC	1624	GUGUAUAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAGACUG	3821
1217	ACCCAUCE G GEGGGAGU	1625	ACUCCOGO GGAGGAAACUCO OU UCAAGGACAUCGUCOGGG GGAUGGGU	3822
1220	CAUCCGGC G GGAGUGGU	1626	ACCACUCE GGAGGAAACUCE CU UCAAGGACAUCGUCCGGG GCCGGAUG	3823
1221	AUCCGGCG G GAGUGGUA	1627	UACCACUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGCCGGAU	3824
1222	UCCGGCGG G AGUGGUAU	1628	AUACCACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGCCGGA	3825
1226	GCGGGAGU G GUAUUAUG	1629	CAUAAUAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUCCCGC	3826
1236	UAUUAUGA G GUGAUCAU	1630	AUGAUCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCAUAAUA	3827
1250	CAUUGUGC G GGUGGAGA	1631	UCUCCACC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCACAAUG	3828
1251	AUUGUGCG G GUGGAGAU	1632	AUCUCCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGCACAAU	3829
1254	GUGCGGGU G GAGAUCAA	1633	UNGAUCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCCGCAC	3830
1255	UGCGGGUG G AGAUCAAU	1634	AUUGAUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACCCGCA	3831
1257	CGGGUGGA G AUCAAUGG	1635	CCAUUGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCACCCG	3832
1264	AGAUCAAU G GACAGGAU	1636	AUCCUGUC GGAGGAACUCC CU UCAAGGACAUCGUCOGGG AUUGAUCU	3833

1156 MADRIAGNO G GAUCIDAN 1519 UTUCARANI GARGANACIUC CO UTUCAGARCANICUSCOSIO SUDICICADO 1281 UTUCAGARCANICO CO UTUCAGARCANICUSCOSIO SUDICICADO 1281 UTUCAGARCANICO CO UTUCAGARCANICUSCOSIO GUANDO 1381 UTUCAGARCANICO CO UTUCAGARCANICUSCOSIO GUANDO 1381 UTUCAGARCANICO 1381 UTUCAGARCANICO UTUCAGARCANICUSCOSIO GUANDO 1381 UTUCAGARCANICO 1461 UTUCAGARCANICUSCOSIO GUANDO 1381 UTUCAGARCANICUSCOSIO GUANDO 1381 UTUCAGARCANICUSCOSIO GUANDO 1381 UTUCAGARCANICUSCOSIO GUANDO 1381 UTUCAGARCANICO 1461 UTUCAGARCANICUSCOSIO GUANDO 1381 UTUCAGARCANICO 1461 UTUCAGARCANICO UTUCAGARCANICUSCOSIO GUANDO 1381 UTUCAGARCANICO 1461 UTUCAGARCANICO UTUCA	1265	GAUCAAUG G ACAGGAUC	1637	GAUCCUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUUGAUC	3834
MURIADRIA G ANCURAND 1619 PUNDARIO CRASSIANANCO CO ULUANGRIANUSCOCCORD AUDULON DIGORDIA G ANCURAND 1619 PUNDARIO CRASSIANANCO CO ULUANGRIANUSCOCCORD AUDULON DIADARDIA G ANCURAND 1611 CUTCOGRI CRASSIANANCO CO ULUANGRIANUSCOCCORDO CRASSIANUSCO MURIADRIA G ANCURAND 1614 CUTCOGRI CRASSIANANCO CO ULUANGRIANUSCOCCORDO CRASSIANONO MURIADRIA G ANGUNANO 1614 ACADAMICO CRASSIANANCO CO ULUANGRIANUSCOCCORDO CRASSIANONO MURIADRIA G ANGUNANO 1614 ACADAMICO CRASSIANANCO CO ULUANGRIANUSCOCCORDO CRASSIANONO MURIADRIA G ANGUNANO 1614 ACADAMICO CRASSIANANCO CO ULUANGRIANUSCOCCORDO CRASSIANANCO UNIDERADO CRASSIANANCO CO ULUANGRIANUSCOCCORDO CRASSIANANCO CO ULUANGRIANUSCOCCORDO CRASSIANANCO 1614 ACADAMICO CRASSIANANCO CO ULUANGRIANUSCOCCORDO CRASSIANANCO UNIDERADO CRASSIANANCO CO ULUANGRIANUSCOCCORDO CRASSIANANCO 1614 ACADAMICO CRASSIANANCO 1614 ACADAMICO CRASSIANANCO 1614 ACADAMICO UNCOCIONO G RARGARANO 1614 ACADAMICO CRASSIANANCO 1614 ACADAMICO 1614 ACADAMICO 1614 ACADAMICO UNCOCIONO G RARGARANO 1614 ACADAMICO 1614 ACADAMICO 1614 ACADAMICO 1614 ACADAMICO UNCOCIONO G RARGARANO 1614 ACADAMICO 1614 ACADAMICO 1614 ACADAMICO 1614 ACADAMICO UNCOCIONO G RARGARANO 1614 ACADAMICO	1269	L	1638	UNCAGAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUCCAUU	3835
TORANANI O ANUTACA 1640 UTIONOSTI CARANANICO CU UDAMISALAUCICOGOS ULUDIUDA DISTANCANI O ANUTACA CONCOLO CARANANICO CU UDAMISALAUCICOGOS ULUDIUDA CONCOLO CONCONO CONCOLO CONCOLO CONCOLO CONCOLO CONCOLO CONCOLO CONCOLO CONCO	1270	0	1639	UUUCAGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGUCCAU	3836
HORACOLOGO G ADMINISTRA 11641 CUTOCAMOU BASAGNAMACCE OF UDAMAGNA MURCOCOGO MURCONO DECIDIO DE CONTROLOGO CONTR	1281	O	1640	UNGCAGUE GGAGGAAACUCE CU UCAAGGACAUCGUCCGGG AUUUUCAG	3837
PACINGEM 0 AGUNDAN 1642 UNIVERSITY CHARGE-AND PROCESS UNCADAD CHARGES OF AGUNDAN 1641	1282		1641		3838
MORDANDA 1641 GUILLADAR 1641 GUILLADAR 1641 GUILLADAR 1641 GUILLADAR CARANDA CARANDA 1641 GUILLADAR CARANDA CARANDA 1641 GUILLADAR CARANDA CARANDA 1641 CONCUENTO CARANDA CARANDA CARANDA 1641 CARANDA CARANDA 1641 CARANDA CARANDA 1641	1290		1642	UNGUAÇUE GGAGGAAACUCE EU UEMAGGACAUCGUECGGG UUGCAGUE	3839
UNDIAGONA O RECAURDIU 1664 ACADURURO DIAGNAMARUCE O UNDAMAGNARIORICOCORO UNDUARDA NORDINIORO O RACIANTOR 1664 ACADURURO GRAGARANCE O UNDAMAGNARIORICOCORO O RACIANGE OCARRORO E O RACIANGE 1664 OCCARGINI GRAGARANCE O UNDAMAGNARIORICOGO O RACIANGE UNGACCARI O RACIANGE 1664 OCCARGINI GRAGARANCE O UNDAMAGNARIORICOGO O RACIANGE UNGACCARI O RACIANGE 1664 ACADURU GRAGARANCE O UNDAMAGNARIORICOGO O RACIANGE UNGACCARI O RACIANGE 1664 ACADURU GRAGARANCE O UNDAMAGNARIORICOGO O RACIANGE UNGACCARI O RACIANGE 1664 ACADURU GRAGARANCE O UNDAMAGNARIORICOGO O RACIANGE UNCACCARI O RACIANGE 1664 ACADURU GRAGARANCE O UNDAMAGNARIORICOGO O RACIANGE UNCACCARI O RACIANGE 1664 ACADURU GRAGARANCE O UNDAMAGNARIORICOGO O RACIANGE UNCACCARI O RACIANGE 1664 ACADURU GRAGARANCE O UNDAMAGNARIORICOGO O RACIANGE UNCACCARI O RACIANGE 1665 GUARANCE GRAGARANCE O UNDAMAGNARIORICOGO O RACIANGE UNCACCARI O RACIANGE 1665 GUARANCE GRAGARANCE O UNDAMAGNARIORICOGO O RACIANGE CHICAGARI 1665 GUARANCE GRAGARANCE O UNDAMAGNARIORICOGO O RACIANGE CHICAGARI 1665 GUARANCE GRAGARANCE CO UNDAMAGNARIORICOGO O RACIANGE	1291	ACUGCAAG G AGUACAAC	1643	GUUGUACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUUGCAGU	3840
ACCIVIDIG G ALACADIC 1645 CONCADID CARGADANCIC CU UNAMAGNA UNCENCIOUS DIADANCE DIAGRAM A CONCADE A CANADOC CONCADO CONCA	1308		1644	ACAAUGCU GGAGGAAACUCC CU UCAAGGACAUCGUCGGG UUGUCAUA	3841
CALINDER CALACADEC 1641 CALCADADE CALCADADE CO CURACADA COLORIZOR CO CALCADADE	1317	AGCAUUGU G GACAGUGG	1645	CCACUGUC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG ACAAUGCU	3842
UNIDADORIO G CONCIOCOC. 1647 GUESTIONE CANCERANCE CU UNACARACHUCHCOCOS ACUADOCA. UNIDADORIO CONCIONA O AAACTEMI 1648 AGENCINO GUESTAACCC CU UNACARACHUCHCOCOS UNDERGOA UNDERGOA CONCIONA O C	1318	SCAUUGUS G	1646	GCCACUGU GGAGGAAACUCC CU UCAAGGACAUCGUCGGG CACAAUGC	3843
UDIOCOCOA G AMAGERRU 1648 AAAACHUU DAGGARAACUC CU UUAAGAACHUCHCOCCOG UUGAACH UUGCOCOA G CARAACHU 1649 AAACHUCH GAGGAAACUCC CU UUAAGAACHUCHCOCCOG UUAAGAA UCCUCACA G CARAACHU 1651 AAACHUCH CARGAAACUCC CU UUAAGAACHUCHCOCCOG UUCAAGAACHUCHCOCCOG UCAAGAACHUCHCOCCOG UUCAAGAACHUCHCOCCOG UCAAGAACHUCHCOCCOG UCAAGAACHUC	1324		1647	GGUGGUGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG ACUGUCCA	3844
INCRUINDA O CONDECCIO. 1669 GARCINECE CRARGARANCE O UNDARGARANCHOCCOS ULGARDARA INCRUINDA O CONDECCIO. 1650 GARCINECE CRARGARANCE O UNDARGARANCHOCCOS ULGARDARA CUCCOCOCO ARADINECE CRARGARANCE CONTRACARANCHOCCOS CONTRACARANCHOCCOS CONTRACARANCE CONTRACARANCHOCCOS CONTRACARANCHOCCOS CUCCACARA O RANGUECE CARGARANCE CONTRACARANCHOCCOS CONTRACARANCHOCCOS CONTRACARANCE CONTRACARANCHOCCOS CONTRACARANCHOCCOS CUCCACARA CARGARANCE CONTRACARANCHOCCOS CONTR	1350		1648	AACACUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGGGCAA	3845
DECUCIOCO GAMONICO 1659 AACULUCU CRAGRAMACO U UDAMISAD ULUGUEZO DECUCIOCO GAMONICO 1651 GAMONICO GAMONICO 1010AMACHA ULUGUEZO DECUCIOCO GAMONICO 1652 GERANDIO GAMONICO 1010AMACHA ULUGUEZO DECUCIOCO GAMONICO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO DECUCIOCO GAMONICO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO DECUCIONO GAMONICO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO DECUCIONO GAMONICO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO GUERRADO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO GUERRADO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO GUERRADO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO GUERRADO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO 1010AMACHA ULUGUEZO <t< td=""><td>1383</td><td>L</td><td>1649</td><td>GAGGCUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGAUGGA</td><td>3846</td></t<>	1383	L	1649	GAGGCUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGAUGGA	3846
COUCOCO O AGRADURO 1651 GAMOLIURO GRADAMACO CU UDAMAGANULURICOCOCO CURDORA	1398		1650	AACUUCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUGGAGGA	3847
UCENCIONA DI GUIDUNO 1652 GORDANDO DI GRADAMACO CO ULONAGRIANDIUGICOGGI MUNDARIA UCENCIONA DI GUIDUNO 1653 GORDANO DI GRADAMACO CO ULONAGRIANDIUGICOGGI MUNDARIA UCRIGATIONI DI GRADAMACO CO ULONAGRIANDIUGICOGGI MUNDARIA ULONAGRIANDI CO GUIDAGO DI GUIDAGO CO ULONAGRIANDICOGGI MUNDARIA UCRIGATIONI DI RESPONDATO CO ULONAGRIANDICOGGI MUNDARIA ULONAGRIANDI CO GUIDAGO CO ULONAGRIANDICOGGI MUNDARIA UCRIGATIO RIGINARIA 1653 CUDOCUCU GRAGAMACOC CO ULONAGRIANDICOGGI MUNDARIA GUIDAGO RIGINARIA 1653 CUDOCUCU GRAGAMACOC CO ULONAGRIANDICOGGI DI CONTRACO GUIDAGO RIGINARIA 1653 CUDOCUCU GRAGAMACOC CO ULONAGRIANDICOGGI DI CONTRACO GUIDAGO RIGINARIA 1653 CUDOCUCU GRAGAMACOC CO ULONAGRIANDICOGGI CONTRACO GUIDAGO RIGINARIA 1653 CUDOCUCU GRAGAMACOC CO ULONAGRIANDICOGGI CONTRACO GUIDAGO RIGINARIA 1654 ANACOUCC GIARAMACOC CO ULONAGRIANDICOGGI DIAGNOC GUIDAGO RIGINARIA 1654 ANACOUCC GIARAMACOC CO ULONAGRIANDICOGGI DIAGNOC GUIDAGO RIGINARIA 1664 ANACOUCC GIARAMACOC CO ULONAGRIANDICOGGI DIAGNOCO GUIDAGO RIGINARIA 1664 ANACOUCC GIARAMACOC CO ULONAGRIANDICOCGI DIAGNOCO GUIDAGO RIGINARIA 1664 ANACOUCC GIARAMACOC CO ULONAGRIAN	1399	CCUCCACG	1651	GAACUUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGUGGAGG	3848
DECCRIBATO ESTRUCTORS 1653 CORDANG CORROGANICO U UPANGRACHAUCHOCOCOR INCLUDATO	1401	UCCACGGA G AAGUUCCC	1652	GOGDANCUU GGAGGADACUCC CU UCDAGGACAUCGUCCGGG UCCGUGGA	3849
	1414	L	1653	CCAGAAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCAGGGA	3850
UDIOGOGNE G GADARGEA 11655 CHOCKUNG CARGARACHOC U UDAMOGRACHUCHOCODO UNCOCON CONCONTROL OF CONCONTROL CARGARACHOC UNCOCONTROL CONCONTROL CARGARACHOC UNCOCONTROL CARGARACHOC UNCOCONTROL CARGARACHOC CONCONTROL CARGARACHOC CONTROL CARGA	1421		1654	CUCCUAGO GGAGGAAACUCO CU UCAAGGACAUCGUCOGGG AGAAACCA	3851
CUERCIONA O AGRACIACO 1556 GUEDIOUE GRASIARANCE CU UNAMICANA UNDUCACE UNAMICA O AGRACIACO 1559 GUEDIOUE GRASIARANCE CU UNAMICANA UNDUCACE UNAMICA O AGRACIACO 1559 GUEDIOUE GRASIARANCE CU UNAMICANA UNDUCACE AGRACIACO 1550 A	1426	Ĺ	1655	CUGCUCUC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UAGCCAGA	3852
GECURIORE O RECORCUS 1657 CANCOLOR GRAGAMACO C U UDANGRADUCCOSO ELCUNACO DAGOZZOU O GUIDUCCO 1659 CONCOLOR GRAGAMACO C U UDANGRADUCCOSO ELCUNACO GERURIAGO E GOLAGICO 1659 CUCCOLOR GRAGAMACO C U UDANGRADUCCOCOSO BACACOC GERURIAGO E GOLAGICO 1650 CUCCOLOR GRAGAMACOC C U UDANGRADUCCOCOCO BACACOC CANCADOR O RACADOR 1661 ADANGRADO CO COLORAGAMACOC COU UDANGRADUCCOCOCOCOCOCO CANCADOR 1662 ADANGRADO CO COLORAGAMACOC COU UDANGRADUCCOCOCOCOCOCOCOCO DAGOZDAO 1663 ADANGRADO CO COLORAGAMACOC COU UDANGRADUCCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOC	1427	CUGGCUNG G	1656	GCUGCUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUAGCCAG	3853
	1429	GGCUAGGA G	1657	CAGCUGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCUAGCC	3854
GENDRIGO GENDRIGOS 1659 CHUCKUNE CRASCARACHEC CF UNANCARACHUCHCORD AND ACCOUNT	1437	L	1658	CAGCACAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCUGCUC	3855
GEORGACO 1660 GRUBBIEGO GARGARANCHO CU UDAMGARANUSUUGUCGU USUUGUGUCGGG CHOCCUTU O GAACAUTU 1661 AAANDEUU GAGGARAAACHO CU UUDAMGARANUGUCGUCGGG AACCUCCUT AAANDEUU GAGGARAAACHO CU UUDAMGARANUGUCGGGG AAANDEUU GAGGARAAACHO CU UUDAMGARANUGUCGGGG AACCUCCUT AAACUCCU CGAGGARAAACHO CU UUDAMGARANUGUCCGGG AAANDEUU GAGGARAAACHO CU UUDAMGARANUGUCCGGG AAANDEUU GAGGARAAACHO CU UUDAMGARANUGUCCGGG AAANDEUU GAGGARAAACHO CU UUDAMGARANUGUCCGGG AAANDEUU GAGGARAAACHO CU UUDAMGARANUGUCCGGG AAANDEUU GAGGARAAACHO CU UUDAMGARANUGUCCGGG AAANDEUU GAGGARAAACHO CU UUDAMGARANUGUCCGGG AAANDEUU GAGGARAAAACHO CU UUDAMGARAAACHOCGGG AAANDEUU GAGGARAAAACHO CU UUDAMGARAAACHOCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1445	GGUGUGCU G GCAAGCAG	1659	CUGCUUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCACACC	3856
CHCCCCUT O CARACHUT 1651	1453	Ĺ	1660	GGUGGUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCUUGCC	3857
ACCICIDIO GIAGNATUR 1662 AAANUTUR GIAGNAANCO CU UUNAGRANUOUGUGGG AAAGGGU UACCIAND GIAGNAGUI 1661 AACUTUR CC GIAGNAANCO CU UUNAGRANUOUGUGGG AAANGGUA ACCIDIO TI 1664 AACUTUR CC GIAGNAANCO CU UUNAGRANUGUCGGG TU UNAGRANUGUCGGG TU AAANGGA AAANGGA CU UUNAGRANUGUCGGG TU AAANGA AAANGGA CU UUNAGRANUGUCGGG TU AAANGA AAANGGA CO AAANGA TI 1667 AACUTUR C GIAGNAANCO CU UUNAGRANUGUCGGG TU AAAAGA AAANGA TI 1667 AAAACUTUR G GACAGATU 1667 ACANUTUR GAGAAANACUC CU UUNAGRANUGUCGGG TO AAAAGA AAAAAAAAAAAAAAAAAAAAAAAAAA	1466	L	1991	AAAUGUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGGGGUG	3858
HUCONAN G GREBARRE 1667 ACCUPACIO EGARRAMACIC CU UCANAGRACIACICEGRES AUMORITA AGGERCANI G GREGARIA 1667 ACCUPAC GARGRAMACIC CU UCANAGRACIACICEGRES AUMORITA AGGERCANI G GREGARIA 1666 CACAGRES GARGRAMACIC CU UCANAGRACIACICEGRES GARGRAMACIC GI AGAGRACIACICEGRES GARGRAMACIC GI UCANAGRACIACICEGRES GARGRAMACIC GI UCANAGRACIACICEGRES GARGRAMACIC GI UCANAGRACIACICEGRES GARGRAMACIC GI AGAGRAMACIC CO AGAGRAMACIC GI AGAGRAMACIC CO AG	1467	ACCCCUUG G	1662	AAAAUGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAGGGGU	3859
ACCUMATO GENERALO GENERACIO CE UL UDARASALAUGUECCOS DELLA CARCONA ARCONAGO UNICADA LE SER AACUNECOR CONTROLA	1500	UACCUAAU G	1663	ACCUCACO GGAGGAAACUCO CU UCAAGGACAUCGUCCGGG AUUAGGUA	3860
AIRCRGIURA G GUILLACCAA 1665 UURSCABARA CORRESAMANCHO CUI UURAGRANUUGUUCGGG DOGGGUAL AIRCRGIURA G GUCARGUEG GRASTARANCHOC CUI UURAGRANUUGUUCGGG DOGGGUAL COCRUGUA CUI ACAA CORRESAMANCHOC CUI UURAGRANUUGUUCGGG AUGUSCCC GUI CORRESAMANCHOC CUI UURAGRANUUGUUCGGG AUGUSCCC GUI CORRESAMANCHOC CUI UURAGRANUUGUUCGGG AUGUSCCC GUI GUCARGUA AUGUSCCCC GUI GUCARGUA GUCARGUC GUI CORRESAMANCHOC CUI UURAGRANUUGUUCGGG AUGUSCCC GUI GUCARGUA GUCARGUC GUI GUCARGUA GUI GUCARGUC GUI GUARGUA GUI	1501	ACCURAUG G	1664	AACCUCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUUAGGU	3861
MANCHORE O ECCARGES 1666 CONCLUDE ORGANISACIONE ORGANISACIONE OL UNIVARISACIONECCIONE DAMBACIONE ORGANISACIONECCIONE ORGANISACIONE ORGANISACI	1506	AUGGGUGA G	1665	UUGGUAAC GGAGGAAACUCC CU UCAAGGACAUGGUCCGGG UCACCCAU	3862
COCCUENT G GARGANUM 1667 APAUCIUC COSAGRAMACIUC CU UDALGRANIUGUICOGGA ANDIGOCOS GACUNATO A MANUECCO 1669 GACUNUM GARGAMACIUC CU UDALGRANIUGUICOGGA CALCUGOCO GACUNATO A MANUECCO 1669 GACUNUM GARGAMACIUC CU UDALGRANIUGUICOGGA BUCANOS GACUNATO A GARGAGO 1669 GACUNUM GARGAMACIUC CU UDALGRANIUGUICOGGA BUCANOS GACUNATO GACUNUM GARGAMACIUC CU UDALGRANIUGUICOGGA ACAUCUUC GACUNATOR GACUNUM GACUNUM GARGAMACIUC CU UDALGRANIUGUICOGGA ACAUCUUC GACUNATOR GACUNUM GA	1556	AUACCUGC G GCCAGUGG	1666	CCACUGGC GGAGGAAACUCC CU UCNAGGACAUCGUCCGGG GCAGGUAU	3863
GECCHADO A MARAKERS 1668 CANANCIU CRAGRAMACUC CU UNAGRAMUCIOSSE CAUGGOC CAGUZARA O AUTUGIOCC 1669 GECCHANU GRAGRAMACUC CU UNAGRAMACUCOCOGO INCONO SARANDU G GCCACIOC 1679 GACUBOCC GRASRAMACUC CU UNAGRAMACUCOGOS INCONOTO	1563	CGGCCAGU G	1667	ACAUCUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUGGCCG	3864
CAGUGGAA G AUGUGGCC 1669 GGCCACAU GGAGGAAACUCC CU UCAAGGACAUCGUCCAGG UUCCACUG GAAGANGU G GCCACGUC 1670 GACGUGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCAGG ACAUCUUC	1564	GGCCAGUG	1668	CACAUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACUGGCC	3865
GARGANGU G GCCACGUC 1670 GACGUGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAUCUUC	1567	CAGUGGAA G	1669	GGCCACAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG : UUCCACUG	3866
	1572	L	1670	GACGUGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAUCUUC	3867

0000	2808	3869	3870	3871	3872	3873	3874	3875	3876	3877	3878	3879	3880	3881	3882	3883	3884	3885	3886	3887	3888	3889	3890	3891	3892	3893	3894	3895	3896	3897	3898	3839	3900	3901
CO TO STATE OF THE	ACAGUCGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGGGACG	ACAGUGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUGGAUGA	AACAGUGO GGAGGAAACUCO CU UCAAGGACAUCGUCCGGG CGUGGAUG	ACAGCUCC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AUAACAGU	AACAGCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUAACAG	UNACAGEU GGAGGAAACUCE CU UCAAGGACAUCGUCOGGG CCAUAACA	AAGCCCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGAUAAC	GAAGCCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUGAUAA	UNGANGES GGNGGNANCUCC CU UCNAGGNCAUCGUCCGGG UCCNUGNU	GUAGAAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUCCAUGA	UUCGGGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAUCAAAG	UNUCEGEC GCAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGAUCAAA	AGCAAAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUUCGUU	CUGCCGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAACUCA	GCUGCCGU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CUGAACUC	ACCECUEC GEAGGAAACUCC CU UCAAGGACAUCGUCGGGG GUCCUGAA	CCUUCCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCUGCCGU	GGGCCUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCGCUGC	AGGGCCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACCGCUG	AAAAGGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCCACCG	UCCAUGUE GGAGGAAACUCE CU UCAAGGACAUCGUCCGGG AAGGUGAC	UNCCAUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAGGUGA	CAGUCUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGUCCAA	ACAGUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUGUCCA	GCCACAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCCAUGU	GUIGUAGO GGAGGAAACUCO OU UCAAGGACAUCGUCOGGG ACAGUCUU	UCAUCUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUGGAAU	UGACUCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUCUGUG	AUGGCAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGACAUA	UGACACAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGAGGCA	GGCAGCGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG ACUGACAC	UGGGCCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCACUUCA	AUGGGCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUCACUUC	CCAUGGGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UCCUCACU
	1671	1672	1673	1674	1675	1676	1677	1678	1679	1680	1681	1682	1683	1684	1685	1686	1687	1688	1689	1690	1691	1692	1693	1694	1695	1696	1691	1698	1699	1700	1701	1702	1703	1704
	CGUCCCAA G ACGACUGU	UCAUCCAC G GGCACUGU	CAUCCACG G GCACUGUU	ACTIGINIALI G GGAGCUGU	CHOILING G GAGCHGIN	HEITHIGG G AGCUGUUA	GUAUCAU G GAGGGCUU	UNAUCAUG G AGGGCUUC	AUCAUGGA G GGCUUCUA	UCAUGGAG G GCUUCUAC	CUUUGAUC G GGCCCGAA	UNUGAUCG G GCCCGAAA	AACGAAUU G GCUUUGCU	UGAGUUCA G GACGGCAG	GAGUUCAG G ACGGCAGC	UUCAGGAC G GCAGCGGU	ACGGCAGC G GUGGAAGG	GCAGCGGU G GAAGGCCC	CAGCGGUG G AAGGCCCU	CGGUGGAA G GCCCUUUU	GUCACCUU G GACAUGGA	UCACCUUG G ACAUGGAA	UNGGACAU G GAAGACUG	UGGACAUG G AAGACUGU	ACAUGGAA G ACUGUGGC	AAGACUGU G GCUACAAC	AUUCCACA G ACAGAUGA	CACAGACA G AUGAGUCA	UAUGUCAU G GCUGCCAU	UGCCUCAU G GUGUGUCA	GUGUCAGU G GCGCUGCC	UGAAGUGA G GAGGCCCA	GAAGUGAG G AGGCCCAU	AGUGAGGA G GCCCAUGG
	1585	1623	1624	1635	1636	1637	1650	1651	1653	1654	1676	1677	1693	1733	1734	1737	1743	1746	1747	1750	1767	1768	1773	1774	1777	1783	1800	1804	1839	1881	1892	1960	1961	1963

3902	3903	3904	3905	3906	3907	3908	3909	3910	3911	3912	3913	3914	3915	3916	3917	3918	3919	3920	3921	3922	3923	3924	3925	3926	3927	3928	3929	3930	3931	3932	3933	3934	3935
9	2	3	3	3	_		m	6	Ľ	_		E1	1"	۱۰۱	e1			*1	1-3		Ľ	_				_	_	Ľ			Ľ	Ľ	Ľ
CUICUGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGGGCCU	UCUUCUBC GGAGGAACUCC CU UCAAGGACAUCGUCGGG CAUGGGCC	UCUAUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCCCAUG	AUCUCUAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCUGCCC	GGGAAUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAUCUUCU	AGGGGAAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCUAUCUU	GUGUGGUC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AGGGGAAU	GGUGUGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGGGGAA	AAGUGAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGGAGGU	CUUGUGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAGUGAA	UGUGUCUC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG UACUUGUG	CUGUGUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUACUUGU	AUCUGUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCUACUU	GGUGCCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUGUCUC	ACAGGUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCUGUGU	GCUCUGGC GGAGGNAACUCC CU UCAAGGACAUCGUCCGGG ACAGGUGC	GAGGUGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGCCACA	GGAGGGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAGGUGC	GGGAGGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGAGGUG	UCCUUCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCAAGGC	UNCCUUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUCAAGG	UUUUCCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCAUCAA	GCCUUIUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCUCCAU	AGCCUUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUUCUCCA	UNGCCAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUUCCUU	CACCUUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCCUUUU	GAACCCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGCCAGC	CUGGNACC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCUUGCC	CCUGGAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACCUUGC	UACAGUCE GGAGGAAACUCE CU UCAAGGACAUCGUCEGGG UGGAACCE	GUACAGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGGAACC	GGUACAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUGGAAC	UCUGUOUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UACAGGUA	UNCUGUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUACAGGU
1705	1706	1707	1708	1709	1710	1711	1712	1713	1714	1715	1716	1717	1718	1719	1720	1721	1722	1723	1724	1725	1726	1727	1728	1729	1730	1731	1732	1733	1734	1735	1736	1737	1738
AGGCCCAU G GGCAGAAG	GGCCCAUG G GCAGAAGA	CAUGGGCA G AAGAUAGA	GGGCAGAA G AUAGAGAU	AGAAGAUA G AGAUUCCC	AAGAUAGA G AUUCCCCU	AUUCCCCU G GACCACAC	UUCCCCUG G ACCACACC	ACCUCCGU G GUUCACUU	UUCACUUU G GUCACAAG	CACAAGUA G GAGACACA	ACANGUAG G AGACACAG	AAGUAGGA G ACACAGAU	GAGACACA G AUGGCACC	ACACAGAU G GCACCUGU	GCACCUGU G GCCAGAGC	UGUGGCCA G AGCACCUC	GCACCUCA G GACCCUCC	CACCUCAG G ACCCUCCC	GCCUUGAU G GAGAAGGA	CCUUGAUG G AGAAGGAA	UUGAUGGA G AAGGAAAA	AUGGAGAA G GAAAAGGC	UGGAGAAG G AAAAGGCU	AAGGAAAA G GCUGGCAA	AAAAGGCU G GCAAGGUG	GCUGGCAA G GUGGGUUC	GGCAAGGU G GGUUCCAG	GCAAGGUG G GUUCCAGG	GGGUUCCA G GGACUGUA	GGUUCCAG G GACUGUAC	GUUCCAGG G ACUGUACC	UACCUGUA G GAAACAGA	ACCUGUAG G AAACAGAA
1970	1971	1975	1978	1982	1984	1993	1994	2008	2018	2029	2030	2032	2038	2041	2050	2055	2065	2066	2101	2102	2104	2107	2108	2113	2117	2122	2125	2126	2133	2134	2135	2148	2149

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	1	0.00	TOTAL SCACCAMACTICS OF FICAAGGACAUGGUCGGG UGUUUCCU	3936
2155	AGGAAACA G	1739	UCOCCOGO GENERALIZACION CITTORAGGACATICCICCEGE UUUUCUGU	3937
2160	ACAGAAAA G AGAAGAAA	1740	UNUCUUCU GGAGGAAACUCO CU CONTOCAGO CONTOCAGO ICOUUCO	3938
2162	_	1741	UCCOCCO GOAGGAAACCCC CO COCCOCCO ACCOCCO DO COCCOCCO ACCOCCO DO COCCOCCO ACCOCCO ACCOCCOCCO ACCOCCO AC	3939
2165	AAAGAGAA G NAAGAAGC	1742	GCUUCUUU GGAGGAAACUCC CU UCAAGAACAOCAGGCCGGG GGCGGGGGGGGGGGGGGGGGG	3940
2169	AGAAGAAA G AAGCACUC	1743	GAGUGCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUCCGCG	2041
2182	ACUCUGCO G GCGGGAAU	1744	AUTOCCOGO GGAGGAAACUCO CU UCAAGGACAUCGUCCGGG AGCAGAGU	1566
21.85	L	1745	AGUAUUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCCAGCAG	3942
20 10	D BOSDINGI	1746	GAGUAUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGCCAGCA	3943
2 2	0 55000000	1747	AGAGUAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGCCAGC	3944
7017	1	1748	GAGGUGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGAGUAU	3945
617	1	1749	GAAUUUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GACUUAAA	3946
177	1	1750	AGAAUTUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGACUUAA	3947
2218		1751	CAGAAITIII GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGACUUA	3948
2219	1	1252	CAGIACITI GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAAACUA	3949
2311	UAGUUUCA G	70,7	CASSILLES CONCERNATION OF THE PARTICUITORISC AGUACIUC	3950
2319	_	1/53	OGOGANGE GOAGGAAAGIO EL TICARGOAGA DIGOGUEGO	3951
2332	CACACGCA G GUDACCUU	1754	AAGGUAAC GCACGAAACUCC CO UCANAGACCCCCCCC CCCCC	2952
2341	GUUACCUU G GCGUGUGU	1755	ACACACGC GGAGGAAACUCC CU UCAAGGACAUCGGCCGGG AAGGGAAC	2000
2356	GUCCCUGU G GUACCCUG	1756	CAGGGUAC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG ACAGGAAC	2222
2364	GGUACCCU G GCAGAGAA	1757	UNCUCUGE GGAGGAAACUCE EU UCAAGGACAUCGUCEGGG AGGUACE	1060
2368	L	1758	UCUCUUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCCAGGG	3955
2220	L	1759	GGUCUCUU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UCUGCCAG	3320
22.00	1	1760	CUUGGUCU GCAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCUCUGC	3957
23/3	1	1761	AGCUUGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCUUCUCU	3958
757	1	1762	ACTITIOGIC GGAGGNAACUCC CU UCAAGGACAUCGUCCGGG AGCAGGGA	3959
2336	l	1763	AUCCUCUC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG UACUGACU	3960
71.7	1	1764	CALICCICI GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUACUGAC	3961
77.52	1	1765	UGCAUCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCUACUG	3962
2473	o woowood	1766	INSTRUMENT GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCUCCUAC	3963
2415		2014	CHICAGAIL GOAGGAAACHCC CH HCAAGGACAUCGUCCGGG CUCUCCUA	3964
2416		10/1	CONTROLL CONCORDENIES CIT HODAGGACAUCGUCGGG UNAAGCAA	3965
2441		7,00	CCCCCCC CONCONANCIOC OIL HONANGRACAINGRICGUCCGGG UCUAAAGC	3966
2443		1/69	GOCCOGO GORGONANCICO OI ICANOGADAICONOCIONOS IIGUCUCUA	3967
2447	UAGAGACA	1770	UACAGUC GGAGGAAACOCC CO CCASCOLLISTOCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCO	3968
2448		1771	AUACAGUC GGAGGAAACUCC CO OCAAGGACACCCCCCCC CCCCCCCCCCCCCCCC	3969
2449	9 GAGACAGG G ACUGUAUA	1772	UAUACAGU GGAGGAAACUCC CU UCAAGAACAOCCCOO CCCCCC	

Table 23

- 6			
	3970	146E	3972
	3G AAUGUUAG	se unuscacc	cese uacumum
	UCAAGGACAUCGUCCGG	UCAAGGACAUCGUCCG	CAAGGACAUCGUC
	c co	D O	C CO
	CUIUGCAC GGAGGAAACUCC CI	GGAGGAAACUCC C	GGAGGAAACUCC CU U
	CUUUGCAC	GAGGCAAU GC	DODDODO C
	1773	1774	1775
	CUAACAUU G GUGCAAAG	GGUGCAAA G AUUGCCUC	AAAAACUA G AAAAAAA
	2473	2481	2511

Input Sequence a A799725. Cut Site a (g), Stem Length a C October Sequence a GARGAAACUCC CU UCAAGGACAUCGUCGGG Stem Length a (g) C Cote Sequence a GARGAAACUCC CU UCAAGGACAUCGUCGGG P (g) (g)

Table 24: Human Phospholamban (PLN) Hammerhead Ribozyme and Target Sequence

Pos	Substrate	Seq ID	Ribozyme	Rz Seq
16	AGAAAACU C CCCAGCUA	1	UAGCUGGG CUGAUGAG X CGAA AGUUUUCU	1137
24	CCCCAGCU A AACACCCG	2	CGGGUGUU CUGAUGAG X CGAA AGCUGGGG	1138
34	ACACCCGU A AGACUUCA	3	UGAAGUCU CUGAUGAG X CGAA ACGGGUGU	1139
40	GUAAGACU U CAUACAAC	4	GUUGUAUG CUGAUGAG X CGAA AGUCUUAC	1140
41	UAAGACUU C AUACAACA	5	UGUUGUAU CUGAUGAG X CGAA AAGUCUUA	1141
44	GACUUCAU A CAACACAA	6	UUGUGUUG CUGAUGAG X CGAA AUGAAGUC	1142
54	AACACAAU A CUCUAUAC	7	GUAUAGAG CUGAUGAG X CGAA AUUGUGUU	1143
57	ACAAUACU C UAUACUGU	8	ACAGUAUA CUGAUGAG X CGAA AGUAUUGU	1144
59	AAUACUCU A UACUGUGA	9	UCACAGUA CUGAUGAG X CGAA AGAGUAUU	1145
61	UACUCUAU A CUGUGAUG	10	CAUCACAG CUGAUGAG X CGAA AUAGAGUA	1146
72	GUGAUGAU C ACAGCUGC	11	GCAGCUGU CUGAUGAG X CGAA AUCAUCAC	1147
88	CCAAGGCU A CCUAAAAG	12	CUUUUAGG CUGAUGAG X CGAA AGCCUUGG	1148
92	GGCUACCU A AAAGAAGA	13	UCUUCUJU CUGAUGAG X CGAA AGGUAGCC	1149
105	AAGACAGU U AUCUCAUA	14	UAUGAGAU CUGAUGAG X CGAA ACUGUCUU	1150
106	AGACAGUU A UCUCAUAU	15	AUAUGAGA CUGAUGAG X CGAA AACUGUCU	1151
108	ACAGUUAU C UCAUAUUU	16	AAAUAUGA CUGAUGAG X CGAA AUAACUGU	1152
110	AGUUAUCU C AUAUUUGG	17	CCAAAUAU CUGAUGAG X CGAA AGAUAACU	1153
113	UAUCUCAU A UUUGGCUG	18	CAGCCAAA CUGAUGAG X CGAA AUGAGAUA	1154
115	UCUCADAU U UGGCUGCC	19	GGCAGCCA CUGAUGAG X CGAA AUAUGAGA	1155
116	CUCAUAUU U GGCUGCCA	20	UGGCAGCC CUGAUGAG X CGAA AAUAUGAG	1156
128	UGCCAGCU U UUUAUCUU	21	AAGAUAAA CUGAUGAG X CGAA AGCUGGCA	1157
129	GCCAGCUU U UUAUCUUU	22	AAAGAUAA CUGAUGAG X CGAA AAGCUGGC	1158
130	CCAGCUUU U UAUCUUUC	23	GAAAGAUA CUGAUGAG X CGAA AAAGCUGG	1159
131	CAGCUUUU U AUCUUUCU	24	AGAAAGAU CUGAUGAG X CGAA AAAAGCUG	1160
132	AGCUJUUU A UCUJUCUC	25	GAGAAAGA CUGAUGAG X CGAA AAAAAGCU	1161
134	CUUUUUAU C UUUCUCUC	26	GAGAGAAA CUGAUGAG X CGAA AUAAAAAG	1162
136	UUUUAUCU U UCUCUCGA	27	UCGAGAGA CUGAUGAG X CGAA AGAUAAAA	1163
137	UUUAUCUU U CUCUCGAC	28	GUCGAGAG CUGAUGAG X CGAA AAGAUAAA	1164
138	UUAUCUUU C UCUCGACC	29	GGUCGAGA CUGAUGAG X CGAA AAAGAUAA	1165
140	AUCUUUCU C UCGACCAC	30	GUGGUCGA CUGAUGAG X CGAA AGAAAGAU	1166
142	CUUUCUCU C GACCACUU	31	AAGUGGUC CUGAUGAG X CGAA AGAGAAAG	1167
150	CGACCACU U AAAACUUC	32	GAAGUUUU CUGAUGAG X CGAA AGUGGUCG	1168
151	GACCACUU A AAACUUCA	33	UGAAGUUU CUGAUGAG X CGAA AAGUGGUC	1169
157	UUAAAACU U CAGACUUC	34	GAAGUCUG CUGAUGAG X CGAA AGUUUUAA	1170
158	UAAAACUU C AGACUUCC	35	GGAAGUCU CUGAUGAG X CGAA AAGUUUUA	1171
164	UUCAGACU U CCUGUCCU	36	AGGACAGG CUGAUGAG X CGAA AGUCUGAA	1172
165	UCAGACUU C CUGUCCUG	37	CAGGACAG CUGAUGAG X CGAA AAGUCUGA	1173
170	CUUCCUGU C CUGCUGGU	38	ACCAGCAG CUGAUGAG X CGAA ACAGGAAG	1174
179	CUGCUGGU A UCAUGGAG	39	CUCCAUGA CUGAUGAG X CGAA ACCAGCAG	1175
181	GCUGGUAU C AUGGAGAA	40	UUCUCCAU CUGAUGAG X CGAA AUACCAGC	1176
193	GAGAAAGU C CAAUACCU	41	AGGUAUUG CUGAUGAG X CGAA ACUUUCUC	1177
198	AGUCCAAU A CCUCACUC	42	GAGUGAGG CUGAUGAG X CGAA AUUGGACU	1178

Table 24

202	CAAUACCU C ACUCGCUC	43	GAGCGAGU CUGAUGAG X CGAA AGGUAUUG	1179
206	ACCUCACU C GCUCAGCU	44	AGCUGAGC CUGAUGAG X CGAA AGUGAGGU	1180
210	CACUCGCU C AGCUAUAA	45	UUAUAGCU CUGAUGAG X CGAA AGCGAGUG	1181
215	GCUCAGCU A UAAGAAGA	46	UCUUCUUA CUGAUGAG X CGAA AGCUGAGC	1182
217	UCAGCUAU A AGAAGAGC	47	GCUCUUCU CUGAUGAG X CGAA AUAGCUGA	1183
228	AAGAGCCU C AACCAUUG	48	CAAUGGUU CUGAUGAG X CGAA AGGCUCUU	1184
235	UCAACCAU U GAAAUGCC	49	GGCAUUUC CUGAUGAG X CGAA AUGGUUGA	1185
245	AAAUGCCU C AACAAGCA	50	UGCUUGUU CUGAUGAG X CGAA AGGCAUUU	1186
257	AAGCACGU C AAAAGCUA	51	UAGCUUUU CUGAUGAG X CGAA ACGUGCUU	1187
265	CAAAAGCU A CAGAAUCU	52	AGAUUCUG CUGAUGAG X CGAA AGCUUUUG	1188
272	UACAGAAU C UAUUUAUC	53	GAUAAAUA CUGAUGAG X CGAA AUUCUGUA	1189
274	CAGAAUCU A UUUAUCAA	54	UUGAUAAA CUGAUGAG X CGAA AGAUUCUG	1190
276	GAAUCUAU U UAUCAAUU	55	AAUUGAUA CUGAUGAG X CGAA AUAGAUUC	1191
277	AAUCUAUU U AUCAAUUU	56	AAAUUGAU CUGAUGAG X CGAA AAUAGAUU	1192
278	AUCUAUUU A UCAAUUUC	57	GAAAUUGA CUGAUGAG X CGAA AAAUAGAU	1193
280	CUAUUUAU C AAUUUCUG	58	CAGAAAUU CUGAUGAG X CGAA AUAAAUAG	1194
284	UUAUCAAU U UCUGUCUC	59	GAGACAGA CUGAUGAG X CGAA AUUGAUAA	1195
285	UAUCAAUU U CUGUCUCA	60	UGAGACAG CUGAUGAG X CGAA AAUUGAUA	1196
286	AUCAAUUU C UGUCUCAU	61	AUGAGACA CUGAUGAG X CGAA AAAUUGAU	1197
290	AUUUCUGU C UCAUCUUA	62	UAAGAUGA CUGAUGAG X CGAA ACAGAAAU	1198
292	UUCUGUCU C AUCUUAAU	63	AUUAAGAU CUGAUGAG X CGAA AGACAGAA	1199
295	UGUCUCAU C UUAAUAUG	64	CAUAUUAA CUGAUGAG X CGAA AUGAGACA	1200
297	UCUCAUCU U AAUAUGUC	65	GACAUAUU CUGAUGAG X CGAA AGAUGAGA	1201
298	CUCAUCUU A AUAUGUCU	66	AGACAUAU CUGAUGAG X CGAA AAGAUGAG	1202
301	AUCUUAAU A UGUCUCUU	67	AAGAGACA CUGAUGAG X CGAA AUUAAGAU	1203
305	UAAUAUGU C UCUUGCUG	68	CAGCAAGA CUGAUGAG X CGAA ACAUAUUA	1204
307	AUAUGUCU C UUGCUGAU	69	AUCAGCAA CUGAUGAG X CGAA AGACAUAU	1205
309	AUGUCUCU U GCUGAUCU	70	AGAUCAGC CUGAUGAG X CGAA AGAGACAU	1206
316	UUGCUGAU C UGUAUCAU	71	AUGAUACA CUGAUGAG X CGAA AUCAGCAA	1207
320	UGAUCUGU A UCAUCGUG	72	CACGAUGA CUGAUGAG X CGAA ACAGAUCA	1208
322	AUCUGUAU C AUCGUGAU	73	AUCACGAU CUGAUGAG X CGAA AUACAGAU	1209
325	UGUAUCAU C GUGAUGCU	74	AGCAUCAC CUGAUGAG X CGAA AUGAUACA	1210
334	GUGAUGCU U CUCUGAAG	75	CUUCAGAG CUGAUGAG X CGAA AGCAUCAC	1211
335	UGAUGCUU C UCUGAAGU	76	ACUUCAGA CUGAUGAG X CGAA AAGCAUCA	1212
337	AUGCUUCU C UGAAGUUC	77	GAACUUCA CUGAUGAG X CGAA AGAAGCAU	1213
344	UCUGAAGU U CUGCUACA	78	UGUAGCAG CUGAUGAG X CGAA ACUUCAGA	1214
345	CUGAAGUU C UGCUACAA	79	UUGUAGCA CUGAUGAG X CGAA AACUUCAG	1215
350	GUUCUGCU A CAACCUCU	80	AGAGGUUG CUGAUGAG X CGAA AGCAGAAC	1216
357	UACAACCU C UAGAUCUG	81	CAGAUCUA CUGAUGAG X CGAA AGGUUGUA	1217
359	CAACCUCU A GAUCUGCA	82	UGCAGAUC CUGAUGAG X CGAA AGAGGUUG	1218
363	CUCUAGAU C UGCAGCUU	83	AAGCUGCA CUGAUGAG X CGAA AUCUAGAG	1219
371	CUGCAGCU U GCCACAUC	84	GAUGUGGC CUGAUGAG X CGAA AGCUGCAG	1220
379	UGCCACAU C AGCUUAAA	85	UUUAAGCU CUGAUGAG X CGAA AUGUGGCA	1221
384	CAUCAGCU U AAAAUCUG	86	CAGAUUUU CUGAUGAG X CGAA AGCUGAUG	1222
385	AUCAGCUU A AAAUCUGU	87	ACAGAUUU CUGAUGAG X CGAA AAGCUGAU	1223
390	CUUAAAAU C UGUCAUCC	88	GGAUGACA CUGAUGAG X CGAA AUUUUAAG	1224
394	AAAUCUGU C AUCCCAUG	89	CAUGGGAU CUGAUGAG X CGAA ACAGAUUU	1225
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Table 24

397	UCUGUCAU C CCAUGCAG	90	CUGCAUGG CUGAUGAG X CGAA AUGACAGA	1226
419	AAAACAAU A UUGUAUAA	91	UUAUACAA CUGAUGAG X CGAA AUUGUUUU	1227
421	AACAAUAU U GUAUAACA	92	UGUUAUAC CUGAUGAG X CGAA AUAUUGUU	1228
424	AAUAUUGU A UAACAGAC	93	GUCUGUUA CUGAUGAG X CGAA ACAAUAUU	1229
426	UAUUGUAU A ACAGACCA	94	UGGUCUGU CUGAUGAG X CGAA AUACAAUA	1230
437	AGACCACU U CCUGAGUA	95	UACUCAGG CUGAUGAG X CGAA AGUGGUCU	1231
438	GACCACUU C CUGAGUAG	96	CUACUCAG CUGAUGAG X CGAA AAGUGGUC	1232
445	UCCUGAGU A GAAGAGUU	97	AACUCUUC CUGAUGAG X CGAA ACUCAGGA	1233
453	AGAAGAGU U UCUUUGUG	98	CACAAAGA CUGAUGAG X CGAA ACUCUUCU	1234
454	GAAGAGUU U CUUUGUGA	99	UCACAAAG CUGAUGAG X CGAA AACUCUUC	1235
455	AAGAGUUU C UUUGUGAA	100	UUCACAAA CUGAUGAG X CGAA AAACUCUU	1236
457	GAGUUUCU U UGUGAAAA	101	UUUUCACA CUGAUGAG X CGAA AGAAACUC	1237
458	AGUUUCUU U GUGAAAAG	102	CUUUUCAC CUGAUGAG X CGAA AAGAAACU	1238
469	GAAAAGGU C AAGAUUAA	103	UUAAUCUU CUGAUGAG X CGAA ACCUUUUC	1239
475	GUCAAGAU U AAGACUAA	104	UUAGUCUU CUGAUGAG X CGAA AUCUUGAC	1240
476	UCAAGAUU A AGACUAAA	105	UUUAGUCU CUGAUGAG X CGAA AAUCUUGA	1241
482	UUAAGACU A AAACUUAU	106	AUAAGUUU CUGAUGAG X CGAA AGUCUUAA	1242
488	CUAAAACU U AUUGUUAC	107	GUAACAAU CUGAUGAG X CGAA AGUUUUAG	1243
489	UAAAACUU A UUGUUACC	108	GGUAACAA CUGAUGAG X CGAA AAGUUUUA	1244
491	AAACUUAU U GUUACCAU	109	AUGGUAAC CUGAUGAG X CGAA AUAAGUUU	1245
494	CUUAUUGU U ACCAUAUG	110	CAUAUGGU CUGAUGAG X CGAA ACAAUAAG	1246
495	UUAUUGUU A CCAUAUGU	111	ACAUAUGG CUGAUGAG X CGAA AACAAUAA	1247
500	GUUACCAU A UGUAUUCA	112 .	UGAAUACA CUGAUGAG X CGAA AUGGUAAC	1248
504	CCAUAUGU A UUCAUCUG	113	CAGAUGAA CUGAUGAG X CGAA ACAUAUGG	1249
506	AUAUGUAU U CAUCUGUU	114	AACAGAUG CUGAUGAG X CGAA AUACAUAU	1250
507	UAUGUAUU C AUCUGUUG	115	CAACAGAU CUGAUGAG X CGAA AAUACAUA	1251
510	GUAUUCAU C UGUUGGAU	116	AUCCAACA CUGAUGAG X CGAA AUGAAUAC	1252
514	UCAUCUGU U GGAUCUUG	117	CAAGAUCC CUGAUGAG X CGAA ACAGAUGA	1253
519	UGUUGGAU C UUGUAAAC	118	GUUUACAA CUGAUGAG X CGAA AUCCAACA	1254
521	UUGGAUCU U GUAAACAU	119	AUGUUUAC CUGAUGAG X CGAA AGAUCCAA	1255
524	GAUCUUGU A AACAUGAA	120	UUCAUGUU CUGAUGAG X CGAA ACAAGAUC	1256
540	AAAGGCU U UAUUUUCA	121	UGAAAAUA CUGAUGAG X CGAA AGCCCUUU	1257
541	AAGGGCUU U AUUUUCAA	122	UUGAAAAU CUGAUGAG X CGAA AAGCCCUU	1258
542	AGGGCUUU A UUUUCAAA	123	UUUGAAAA CUGAUGAG X CGAA AAAGCCCU	1259
544	GGCUUUAU U UUCAAAAA	124	UUUUUGAA CUGAUGAG X CGAA AUAAAGCC	1260
545	GCUUUAUU U UCAAAAAU	125	AUUUUUGA CUGAUGAG X CGAA AAUAAAGC	1261
546	CUUUAUUU U CAAAAAUU	126	AAUUUUUG CUGAUGAG X CGAA AAAUAAAG	1262
547	UUUAUUUU C AAAAAUUA	127	UAAUUUUU CUGAUGAG X CGAA AAAAUAAA	1263
554	UCAAAAAU U AACUUCAA	128	UUGAAGUU CUGAUGAG X CGAA AUUUUUGA	1264
555	CAAAAAUU A ACUUCAAA	129	UUUGAAGU CUGAUGAG X CGAA AAUUUUUG	1265
559	AAUUAACU U CAAAAUAA	130	UUAUUUUG CUGAUGAG X CGAA AGUUAAUU	1266
560	AUUAACUU C AAAAUAAG	131	CUUAUUUU CUGAUGAG X CGAA AAGUUAAU	1267
566	UUCAAAAU A AGUGUAUA	132	UAUACACU CUGAUGAG X CGAA AUUUUGAA	1268
572	AUAAGUGU A UAAAAUGC	133	GCAUUUUA CUGAUGAG X CGAA ACACUUAU	1269
574	AAGUGUAU A AAAUGCAA	134	UUGCAUUU CUGAUGAG X CGAA AUACACUU	1270
587	GCAACUGU U GAUUUCCU	135	AGGAAAUC CUGAUGAG X CGAA ACAGUUGC	1271
591	CUGUUGAU U UCCUCAAC	136	GUUGAGGA CUGAUGAG X CGAA AUCAACAG	1272

592	UGUUGAUU U CCUCAACA	137	UGUUGAGG CUGAUGAG X CGAA AAUCAACA	1273
593	GUUGAUUU C CUCAACAU	138	AUGUUGAG CUGAUGAG X CGAA AAAUCAAC	1274
596	GAUUUCCU C AACAUGGC	139	GCCAUGUU CUGAUGAG X CGAA AGGAAAUC	1275
606	ACAUGGCU C ACAAAUUU	140	AAAUUUGU CUGAUGAG X CGAA AGCCAUGU	1276
613	UCACAAAU U UCUAUCCC	141	GGGAUAGA CUGAUGAG X CGAA AUUUGUGA	1277
614	CACAAAUU U CUAUCCCA	142	UGGGAUAG CUGAUGAG X CGAA AAUUUGUG	1278
615	ACAAAUUU C UAUCCCAA	143	UUGGGAUA CUGAUGAG X CGAA AAAUUUGU	1279
617	AAAUUUCU A UCCCAAAU	144	AUUUGGGA CUGAUGAG X CGAA AGAAAUUU	1280
619	AUUUCUAU C CCAAAUCU	145	AGAUUUGG CUGAUGAG X CGAA AUAGAAAU	1281
626	UCCCAAAU C UUUUCUGA	146	UCAGAAAA CUGAUGAG X CGAA AUUUGGGA	1282
628	CCAAAUCU U UUCUGAAG	147	CUUCAGAA CUGAUGAG X CGAA AGAUUUGG	1283
629	CAAAUCUU U UCUGAAGA	148	UCUUCAGA CUGAUGAG X CGAA AAGAUUUG	1284
630	AAAUCUUU U CUGAAGAU	149	AUCUUCAG CUGAUGAG X CGAA AAAGAUUU	1285
631	AAUCUUUU C UGAAGAUG	150	CAUCUUCA CUGAUGAG X CGAA AAAAGAUU	1286
646	UGAAGAGU U UAGUUUUA	151	UAAAACUA CUGAUGAG X CGAA ACUCUUCA	1287
647	GAAGAGUU U AGUUUUAA	152	UUAAAACU CUGAUGAG X CGAA AACUCUUC	1288
648	AAGAGUUU A GUUUUAAA	153	UUUAAAAC CUGAUGAG X CGAA AAACUCUU	1289
651	AGUUUAGU U UUAAAACU	154	AGUUUUAA CUGAUGAG X CGAA ACUAAACU	1290
652	GUUUAGUU U UAAAACUG	155	CAGUUUUA CUGAUGAG X CGAA AACUAAAC	1291
653	UUUAGUUU U AAAACUGC	156	GCAGUUUU CUGAUGAG X CGAA AAACUAAA	1292
654	UUAGUUUU A AAACUGCA	157	UGCAGUUU CUGAUGAG X CGAA AAAACUAA	1293
675	CAACAAGU U CACUUCAU	158	AUGAAGUG CUGAUGAG X CGAA ACUUGUUG	1294
676	AACAAGUU C ACUUCAUA	159	UAUGAAGU CUGAUGAG X CGAA AACUUGUU	1295
680	AGUUCACU U CAUAUAUA	160	UAUAUAUG CUGAUGAG X CGAA AGUGAACU	1296
681	GUUCACUU C AUAUAUAA	161	UUAUAUAU CUGAUGAG X CGAA AAGUGAAC	1297
684	CACUUCAU A UAUAAAGC	162	GCUUUAUA CUGAUGAG X CGAA AUGAAGUG	1298
686	CUUCAUAU A UAAAGCAU	163	AUGCUUUA CUGAUGAG X CGAA AUAUGAAG	1299
688	UCAUAUAU A AAGCAUUA	164	UAAUGCUU CUGAUGAG X CGAA AUAUAUGA	1300
695	UAAAGCAU U AUUUUUAC	165	GUAAAAAU CUGAUGAG X CGAA AUGCUUUA	1301
696	AAAGCAUU A UUUUUACU	166	AGUAAAAA CUGAUGAG X CGAA AAUGCUUU	1302
698	AGCAUUAU U UUUACUCU	167	AGAGUAAA CUGAUGAG X CGAA AUAAUGCU	1303
699	GCAUUAUU U UUACUCUU	168	AAGAGUAA CUGAUGAG X CGAA AAUAAUGC	1304
700	CAUUAUUU U UACUCUUU	169	AAAGAGUA CUGAUGAG X CGAA AAAUAAUG	1305
701	AUUAUUUU U ACUCUUUU	170	AAAAGAGU CUGAUGAG X CGAA AAAAUAAU	1306
702	UUAUUUUU A CUCUUUUG	171	CAAAAGAG CUGAUGAG X CGAA AAAAAUAA	1307
705	UUUUUACU C UUUUGAGG	172	CCUCAAAA CUGAUGAG X CGAA AGUAAAAA	1308
707	UUUACUCU U UUGAGGUG	173	CACCUCAA CUGAUGAG X CGAA AGAGUAAA	1309
708	UUACUCUU U UGAGGUGA	174	UCACCUCA CUGAUGAG X CGAA AAGAGUAA	1310
709	UACUCUUU U GAGGUGAA	175	UUCACCUC CUGAUGAG X CGAA AAAGAGUA	1311
719	AGGUGAAU A UAAUUUAU	176	AUAAAUUA CUGAUGAG X CGAA AUUCACCU	1312
721	GUGAAUAU A AUUUAUAU	177	AUAUAAAU CUGAUGAG X CGAA AUAUUCAC	1313
724	AAUAUAAU U UAUAUUAC	178	GUAAUAUA CUGAUGAG X CGAA AUUAUAUU	1314
725	AUAUAAUU U AUAUUACA	179	UGUAAUAU CUGAUGAG X CGAA AAUUAUAU	1315
726	UAUAAUUU A UAUUACAA	180	UUGUAAUA CUGAUGAG X CGAA AAAUUAUA	1316
728	UAAUUUAU A UUACAAUG	181	CAUUGUAA CUGAUGAG X CGAA AUAAAUUA	1317
730	AUUUAUAU U ACAAUGUA	182	UACAUUGU CUGAUGAG X CGAA AUAUAAAU	1318
731	UUUAUAUU A CAAUGUAA	183	UUACAUUG CUGAUGAG X CGAA AAUAUAAA	1319

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738	UACAAUGU A AAAGCUUC	184	GAAGCUUU CUGAUGAG X CGAA ACAUUGUA	1320
745	UAAAAGCU U CUUUAAUA	185	UAUUAAAG CUGAUGAG X CGAA AGCUUUUA	1321
746	AAAAGCUU C UUUAAUAC	186	GUAUUAAA CUGAUGAG X CGAA AAGCUUUU	1322
748	AAGCUUCU U UAAUACUA	187	UAGUAUUA CUGAUGAG X CGAA AGAAGCUU	1323
749	AGCUUCUU U AAUACUAA	188	UUAGUAUU CUGAUGAG X CGAA AAGAAGCU	1324
750	GCUUCUUU A AUACUAAG	189	CUUAGUAU CUGAUGAG X CGAA AAAGAAGC	1325
753	UCUUUAAU A CUAAGUAU	190	AUACUUAG CUGAUGAG X CGAA AUUAAAGA	1326
756	UUAAUACU A AGUAUUUU	191	AAAAUACU CUGAUGAG X CGAA AGUAUUAA	1327
760	UACUAAGU A UUUUUCAG	192	CUGAAAAA CUGAUGAG X CGAA ACUUAGUA	1328
762	CUAAGUAU U UUUCAGGU	193	ACCUGAAA CUGAUGAG X CGAA AUACUUAG	1329
763	UAAGUAUU U UUCAGGUC	194	GACCUGAA CUGAUGAG X CGAA AAUACUUA	1330
764	AAGUAUUU U UCAGGUCU	195	AGACCUGA CUGAUGAG X CGAA AAAUACUU	1331
765	AGUAUUUU U CAGGUCUU	196	AAGACCUG CUGAUGAG X CGAA AAAAUACU	1332
766	GUAUUUUU C AGGUCUUC	197	GAAGACCU CUGAUGAG X CGAA AAAAAUAC	1333
771	UUUCAGGU C UUCACCAA	198	UUGGUGAA CUGAUGAG X CGAA ACCUGAAA	1334
773	UCAGGUCU U CACCAAGU	199	ACUUGGUG CUGAUGAG X CGAA AGACCUGA	1335
774	CAGGUCUU C ACCAAGUA	200	UACUUGGU CUGAUGAG X CGAA AAGACCUG	1336
782	CACCAAGU A UCAAAGUA	201	UACUUUGA CUGAUGAG X CGAA ACUUGGUG	1337
784	CCAAGUAU C AAAGUAAU	202	AUTIACUTU CUGAUGAG X CGAA AUACUUGG	1338
790	AUCAAAGU A AUAACACA	203	UGUGUUAU CUGAUGAG X CGAA ACUUUGAU	1339
793	AAAGUAAU A ACACAAAU	204	AUUUGUGU CUGAUGAG X CGAA AUUACUUU	1340
809	UGAAGUGU C AUUAUUCA	205	UGAAUAAU CUGAUGAG X CGAA ACACUUCA	1341
812	AGUGUCAU U AUUCAAAA	206	UUUUGAAU CUGAUGAG X CGAA AUGACACU	1342
813	GUGUCAUU A UUCAAAAU	207	AUUUUGAA CUGAUGAG X CGAA AAUGACAC	1343
815	GUCAUUAU U CAAAAUAG	208	CUAUUUUG CUGAUGAG X CGAA AUAAUGAC	1344
816	UCAUUAUU C AAAAUAGU	209	ACUAUUUU CUGAUGAG X CGAA AAUAAUGA	1345
822	UUCAAAAU A GUCCACUG	210	CAGUGGAC CUGAUGAG X CGAA AUUUUGAA	1346
825	AAAAUAGU C CACUGACU	211	AGUCAGUG CUGAUGAG X CGAA ACUAUUUU	1347
834	CACUGACU C CUCACAUC	212	GAUGUGAG CUGAUGAG X CGAA AGUCAGUG	1348
837	UGACUCCU C ACAUCUGU	213	ACAGAUGU CUGAUGAG X CGAA AGGAGUCA	1349
842	CCUCACAU C UGUUAUCU	214	AGAUAACA CUGAUGAG X CGAA AUGUGAGG	1350
846	ACAUCUGU U AUCUUAUU	215	AAUAAGAU CUGAUGAG X CGAA ACAGAUGU	1351
847	CAUCUGUU A UCUUAUUA	216	UAAUAAGA CUGAUGAG X CGAA AACAGAUG	1352
849	UCUGUUAU C UUAUUAUA	217	UAUAAUAA CUGAUGAG X CGAA AUAACAGA	1353
851	UGUUAUCU U AUUAUAAA	218	UUUAUAAU CUGAUGAG X CGAA AGAUAACA	1354
852	GUUAUCUU A UUAUAAAG	219	CUUUAUAA CUGAUGAG X CGAA AAGAUAAC	1355
854	UAUCUUAU U AUAAAGAA	220	UUCUUUAU CUGAUGAG X CGAA AUAAGAUA	1356
855	AUCUUAUU A UAAAGAAC	221	GUUCUUUA CUGAUGAG X CGAA AAUAAGAU	1357
857	CUUAUUAU A AAGAACUA	222	UAGUUCUU CUGAUGAG X CGAA AUAAUAAG	1358
865	AAAGAACU A UUUGUAGU	223	ACUACAAA CUGAUGAG X CGAA AGUUCUUU	1359
867	AGAACUAU U UGUAGUAA	224	ITUACUACA CUGAUGAG X CGAA AUAGUUCU	1360
868	GAACUAUU U GUAGUAAC	225	GUIACUAC CUGAUGAG X CGAA AAUAGUUC	1361
871	CUAUUUGU A GUAACUAU	225	AUAGUUAC CUGAUGAG X CGAA ACAAAUAG	1362
874	UUUGUAGU A ACUAUCAG	227	CUGAUAGU CUGAUGAG X CGAA ACUACAAA	1363
878	UAGUAACU A UCAGAAUC	228	GAUUCUGA CUGAUGAG X CGAA AGUUACUA	1364
880	GUAACUAU C AGAAUCUA	229	UAGAUUCU CUGAUGAG X CGAA AUAGUUAC	1365
886	AUCAGAAU C UACAUUCU	230	AGAAUGUA CUGAUGAG X CGAA AUUCUGAU	1366
880	AUCAGRAD C DACADUCU	230	ANADOUN COMOUND A COMA MODEOGRO	1300

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898 CAGANICU A CAUTICURA 231	1367 1368 1369 1370 1371 1372 1373
893	1369 1370 1371 1372 1373 1374
Sep.	1370 1371 1372 1373 1374
905 ACAGAAAU U GUAUUUUU 235 AAAAAUAC CUGAUGAG X CGAA AUUUCUGU 236 AAAAAUAC CUGAUGAG X CGAA AUUUCUGU 236 AGAAAAAA CUGAUGAG X CGAA CACAUUUC 236 AGAAAAAA CUGAUGAG X CGAA ACAUUUC 236 AGAAAAAA CUGAUGAG X CGAA ACAUUUC 237 AUAGAAAA CUGAUGAG X CGAA ACAUUUC 237 AUAGAAAA CUGAUGAG X CGAA ACAUUC 238 CAUAGAA CUGAUGAG X CGAA ACAUCAAU 331 UUGUAUUU U UUCUAUGC 239 GCAUAGAA CUGAUGAG X CGAA AAAAACAA 331 UUGUAUUU U UCUAUGCC 239 GCAUAGAA CUGAUGAG X CGAA AAAAACAA 331 UUGUAUUUU U UCUAUGCC 240 GCCAUGAG CUGAUGAG X CGAA AAAAACAA 331 UUUUUUUU C UUGAUGAC 241 UGGCAUGA CUGAUGAG X CGAA AAAAAACA 331 UUUUUUUU C UUGAGCCA 241 UGGCAUGA CUGAUGAG X CGAA AAAAAAAA 331 UUGUUUUU A UGCCACAU 243 AUGUGGCA CUGAUGAG X CGAA AAAAAAAA 332 UUGACCAU A AACAUCUU 244 AAGAUGUU CUGAUGAG X CGAA AAAAAAAA 332 UGCCACAU A AACAUCUU 244 AAGAUGUU CUGAUGAG X CGAA AAGAUGGC 333 AUUAACAU C UUUUAAAG 246 CUUUAAAA CUGAUGAG X CGAA AUGUGGCA 333 AUUAACAU C UUUUAAAG 246 CUUUAAAA CUGAUGAG X CGAA AUGUGGCA 343 AACAUCUU UCAAGAG X CGAA AUGUGGC 343 AACAUCUU CUGAUGAG X CGAA AUGUGGC AAAAAAAAAA 344 AACAUCUU UAAAAAAAA CUGAUGAG X CGAA AUGUGGC AAAAAAAAAAAAAAAAAAAAAAAAAA	1371 1372 1373 1374
909	1372 1373 1374
911 AAUUGUAU U UUUUCUAU 237 AUAGAAAA CUGAUGAG X CGAA AUACAAUU 912 AUUGUAUU U UUUCUAU 238 CAUAGAA CUGAUGAG X CGAA AUACCAAU 913 UUUUUUUU U UUUCUAUGC 239 CAUAGAA CUGAUGAG X CGAA AAAUACAA 914 UGUAUUUU U UCUAUGCC 240 GCCAUGAA CUGAUGAG X CGAA AAAUACAA 915 GUAUUUUUU C UUUCUACC 240 GCCAUGAA CUGAUGAG X CGAA AAAAUACA 916 UUUUUUUU C UUUCCCAC 242 GUGGCAUA CUGAUGAG X CGAA AAAAUACA 918 UUUUUUUU C UUUCCCAC 242 GUGGCAUA CUGAUGAG X CGAA AAAAAUA 918 UUUUUUUU C UUCCCAC 243 AUGUGGCA CUGAUGAG X CGAA AAAAAUA 918 GUCACAAU A ACAUCUUU 244 AAGAUGUU CUGAUGAG X CGAA AUGUGGCA 928 GCCACAAU A ACAUCUUU 244 AAGAUGUU CUGAUGAG X CGAA AUGUGGCA 933 AUUACACU CUUUAAAAU 245 AAAAAUGA CUGAUGAG X CGAA AUGUGGA 935 UAACAUCU U UAAAGUU 247 AACUUUAA CUGAUGAG X CGAA AAGAUGUUA 935 AUCACUUU U UAAAGUU 247 AACUUUAA CUGAUGAG X CGAA AAAAAUGU 936 AACAUCUU U UAAAGUUA 247 AACUUUA CUGAUGAG X CGAA AAAAAUGU	1373 1374
912 AUUGUAUU U UUUCUAUG 238 CAUAGAAA CUGAUGAA X CGAA AAUACAAU 913 UUGUAUUU U UUUCUAUGC 239 GOXIMARA CUGAUGAA X CGAA AAUACAA 914 UUGUAUUU U UUCUAUGCC 240 GOXIMARA CUGAUGAA X CGAA AAAUACAA 915 GUAUUUUU U UCUAUGCCA 241 UGGCAUAG CUGAUGAAA X CGAA AAAAAUACA 916 UUUUUUUU U A UGCCACA 242 GUGGCAUA CUGAUGAGA X CGAA AAAAAAUA 927 UUCCCACAU U AACAUCUU 244 AAGAUGUU CUGAUGAGA X CGAA AGAAAAAUA 927 UGCCACAU U AACAUCUU 244 AAGAUGUU CUGAUGAG X CGAA AGAAAAAUA 928 GCCACAUU A AACAUCUU 244 AAGAUGUU CUGAUGAGA X CGAA AGAUGUGAC 933 AUUAACAUU U UAAAGUU 245 AAAGAUGU CUGAUGAGA X CGAA AUGUUAAU 935 BAACAUUU U UAAAGUU 247 AACCUUUAAA CUGAUGAG X CGAA AUGUUAAU 936 CACACUUU U UAAAGUU 247 AACCUUUU CUGAUGAG X CGAA AAAGAUGU 937 AACCUUUU U AAAGUUGA 249 UCAACUU CUGAUGAG X CGAA AAAAAUGU 938 CAUCUUU A AAGUUGA 249 UCAACUU CUGAUGAG X CGAA AAAAAUGU 938 CAUCUUAU A AAGUUGAA 250 <t< td=""><td>1374</td></t<>	1374
913 UUGUAUUU U UUCUAUGC 239 GCAUAGAA CUGAUGAG X CGAA AAAUACAA 1914 UUGUAUUU U UUCUAUGCC 240 GCCAUAGA CUGAUGAG X CGAA AAAUACAA 1915 GUAUUUUU U CUGAUGCC 241 UGGCAUAG CUGAUGAG X CGAA AAAAUACAA 1915 GUAUUUUUUUUU C UUGUCCCA 241 UGGCAUAG CUGAUGAG X CGAA AAAAUACAA 1916 UAUUUUUUUU U CUGAUGCAA 242 GUGGCAUA CUGAUGAG X CGAA AAAAAUACA 1918 UUUUUUUUUU A UGCCACAU 241 AUGUGGCA CUGAUGAG X CGAA AAGAAAAAAA 1918 UUGCCACAU U AACAUCUU 244 AAGAUGUU CUGAUGAG X CGAA AAGAAGAAA 1918 GCCACAUU A ACAUCUUU 244 AAGAUGUU CUGAUGAG X CGAA AAGUGGCA 1918 AAGAACAU CUUUAAAAA 246 CUUUAAAA CUGAUGAG X CGAA AAGUGGCA 1918 AAGAACAU U UUAAAGUU 247 AACAUCUU CUGAUGAG X CGAA AAGUGGCA 1916 AACAUCUU U UAAAGUUG 248 CAACUUUA CUGAUGAG X CGAA AAGUGUU 1916 AACAUCUU U AAAGUGG 249 UCAACUUU CUGAUGAG X CGAA AAGUGUU 1918 AACAUCUU U AAAGUGG 249 UCAACUUU CUGAUGAG X CGAA AAGAUGUU 1918 UGAAGUGG 250 AUCAACUU CUGAUGAG X CGAA AAGAUGUU 1918 UGAAGUGG 250 AUCAACUU CUGAUGAG X CGAA AAGAUGUU 1918 UGAAGUGGA 251 UUCCCAUCU CUGAUGAG X CGAA AAGAUGUU 1918 UUCCCAUCU CUGAUGAG X CGAA ACUUUUAACA 255 UUCCCAUCUU CUGAUGAG X CGAA ACUUUUAACA 255 UUCCCAUCUU CUGAUGAG X CGAA ACUUGAUCU 1919 AAGACCAU X ACCACCAUCU CUGAUGAG X CGAA ACUUGAUCU 1919 GCCACCACCU CUGAUGAG X CGAA ACUUGAUCA 255 UUAAGAGA CUCGAUGAG X CGAA ACUUGAUCA X CGAA ACUUGAUCA 255 UUAAGAGA CUCGAUGAG X CGAA ACUUGAUCA X CGAA ACUUGACA X CGAA ACUUGAUCA X CGAA ACUUGAUCA X CGAA ACUUGACA X CCACCACCA ACUCACACCA ACUCAC	
914 UGUADUUU U UCUAUGCC 240 GGCAUAGA CUGAUGAG X CGAA AAAAUACA 915 GUAURUUU U UCUAUGCCA 241 UGGCAUAG CUGAUGAG X CGAA AAAAAUACA 916 UAUUUUUU C UAUGCCAC 242 GUGACGAUG CUGAUGAG X CGAA AAAAAUA 918 UUUUUUUU A UGCCACAU 243 AUGUGGCA CUGAUGAG X CGAA AAAAAUA 927 UGCCACAU U AACAUCUU 244 AAGAUGU CUGAUGAG X CGAA AAUGUGGC 928 GCCACAUU A ACAUCUU 245 AAAGAUGU CUGAUGAG X CGAA AAUGUGGC 933 AUUAACAU U UUAAAGUU 245 AAAGAUGU CUGAUGAG X CGAA AAUGUGGC 935 UAACAUCU U UUAAAGUU 247 AACUUUAA CUGAUGAG X CGAA AAGAUGUUA 936 AACAUCUU U UAAAGUU 247 AACUUUAA CUGAUGAG X CGAA AAGAUGUUA 937 ACAUCUUU AAAGUUGA 249 CAACUUU CUGAUGAG X CGAA AAGAUGUUA 938 CAUCUUU AAAGUUGA 249 UAACAUCUU CUGAUGAG X CGAA AAGAUGU 938 CAUCUUU AAAGUUA 249 DACACUU CUGAUGAG X CGAA AACAUGUU 943 UUUAAAGUU A GAGUAAA 251 UUCUCAUC CUGAUGAG X CGAA ACUUUAAA 953 AUGAACAU CUUCAAGAA CEGAA CUCUCUCUCUCUCUCUCUCUCUCUCUCUCUCUCUCUC	
915 GUAUUUUU U CUAUGCCA 241 UGGCAUAG CUGAUGAG X COAA AAAAAUAC 916 UAUUUUUU U CUAUGCCA 242 GUGGCAUA CUGAUGAG X CGAA AAAAAAUA 918 UUUUUUUU A UGCCACAU 243 AUGUGGCA CUGAUGAGA X CGAA AGAAAAAA 927 UGCCACAU U AACAUCUU 244 AAGAUGU CUGAUGAGA X CGAA AGUGGC 928 GCCACAUU A ACAUCUU 245 AAAGAUGU CUGAUGAGA X CGAA AAUGUGCC 933 AUUAACAU CUUUAAAAG 246 CUUUAAAA CUGAUGAGA X CGAA AAUGUGCC 935 UAACAUCU U UUAAAGUU 247 AACUUUAA CUGAUGAG X CGAA AUGUUUAA 936 AACAUCUU U UAAAGUUGA 247 AACUUUAA CUGAUGAG X CGAA AAUGUUUAA 937 ACAUCUUU U AAAGUUGA 249 UCAACUUU CUGAUGAG X CGAA AAAUGUU 938 CAUCUUUU U AAAGUUGA 249 UCAACUUU CUGAUGAG X CGAA AAAUGUU 939 JUUCAAGUU U GAAGAGA 251 UUCCACUC CUGAUGAG X CGAA AACUUUAA 943 JUULAAGAG U GAUGAGA 251 UUCCACU CUGAUGAG X CGAA ACUUUUAA 953 AUGAGAAAGU A GAGAAAACU CUGAUGAG X CGAA ACUUUUAA 954 AUGAGAGA AAUGUU ACAACUC CUGAUGAG X CGAA ACUUUUAA 955 AUGAGAGA CUCUCCACA 254	1375
1916 UNUUUUUU C UNUGCCAC 242 GUGGCAUA CUGAUGAG X CGAA AAAAANA	1376
918 UUUUUUUCU A UGCCACAU 243 AUGUGGCA CUGAUGAG X CGAA AGRAAAAA 927 UGCCACCAU U AACAUCUU 244 AAGAUGUU CUGAUGAG X CGAA AGRAAAAA 928 GCCACAUU A ACAUCUU 245 AAGAUGUU CUGAUGAG X CGAA AUGUGGC 933 AUDACAU C UUUUAAAGU 246 CUUUAAAA CUGAUGAG X CGAA AGAUGUUA 915 UAACAUCUU U UUAAAGUU 247 AACAUUUA CUGAUGAG X CGAA AAGAUGUU 916 AACAUCUU U AAAGUUGA 249 CAACUUU CUGAUGAG X CGAA AAGAUGUU 937 ACAUCUU A AAGUUGA 249 UCAACUUU CUGAUGAG X CGAA AAAGAUGU 943 UUUAAAGU A GAGAGAA 251 AUCACUU CUGAUGAG X CGAA AAGAUGU 943 UUAAAGUU A AAGUUGAA 251 AUCACUU CUGAUGAG X CGAA AACUUUAAA 953 AUGAAGUU A AAGUUGAA 251 UUCUCAUC CUGAUGAG X CGAA ACUUUAAAA 953 AUGAAGUU A KAGAAAAA 252 CCAUACUU CUGAUGAG X CGAA ACUUUAAA 958 AAUGAAGUU A KAGAAAAAAAA 253 CUUUCCAU CUGAUGAG X CGAA ACUUUCC 958 AAGGCCAU A KOGAAAAAAAAAAA 254 UUAUGAGAG CUGAUGAG X CGAA ACUUUCC 976 AAGGCCAU A CUCUAAAA 255 UU	1377
927 UGCCACAU U AACAUCUU 244 AAGANEUU CUGAUGAG X CGAA AUGUGGCA 928 GCCACAUU A ACAUCUUU 245 AAAGANGU CUUUAGAG X CGAA AUGUGGCA 938 AUUAAACAU CUUUAAAAAO 246 CUUUAAA CUCAUGAGA X CGAA AUGUGAA 935 UAACAUCU U UUAAAGUU 247 AACUUUAA CUGAUGAG X CGAA AGAUGUUA 936 AACAUCUU U UAAAGUUGA 247 AACUUUAA CUGAUGAG X CGAA AAAGUGUU 937 ACRUCUUU U AAAGUUGA 249 UCAACUU CUGAUGAG X CGAA AAAGUGU 938 CALCULUU U AAAGUUGA 250 AUCAACUU CUGAUGAG X CGAA AAAGAUGU 939 CUUUUCAC CUCANUGAG X CGAA AAAGAUGU 1000000000000000000000000000000000000	1378
	1379
933 AUJAACAU C UUJUAAAG 246 CUUJUAAAA CUGAUGAG X CGAA AUGUJUAAU 935 UAACAUCU U UJAAAGUJU 247 AACUJUAA CUGAUGAG X CGAA AUGUJUAAU 936 AACAUCUU U UAAAGUJU 248 CAACUJUA CUGAUGAG X CGAA AGAUGUJUA 937 ACAUCUJU U AAAGUJUGA 249 UCAACUJUI CUGAUGAG X CGAA AAGAUGUJ 938 CAUCUJUU A AAGUJUGA 250 AUCAACUJU CUGAUGAG X CGAA AAAGAUGU 938 CAUCUJUU A AAGUJUGAU 250 AUCAACUJ CUGAUGAG X CGAA AAGAUGU 939 JUJUAAAGU U GAUGAGAA 251 UUCUCAUC CUGAUGAG X CGAA ACUJUTAA 953 AUGAGAU A AGGACAA 252 CCAUACUJU CUGAUGAG X CGAA ACUJUTAA 954 AAGGACAU A CUCUJACA 254 UAUGGAC CUGAUGAG X CGAA ACUJUTICC 956 GGAAAAGU A UGGAAAAA 253 UGGAC CUGAUGAG X CGAA ACUJUTICC 976 AAGGACCAU A CUCUJACA 255 UGGAGA CUCAUJAG X CGAA AGUJUTICC 979 GCCAUACU C UUGACAUAA 256 UAUAUGAG CUGAUGAG X CGAA AGUJUTICC 981 CAUACUCU C UUGACUJA 256 UAUAUGAG X CUGAAGAG CUGAAGAG X CGAA AGUJUTICC 982 AUGACUCU A CAUAAUAA 257 UAUAUGAG X CGAAGA AGUJUTICC 983 AUGACUCU A AUJAAAAAU 257 UAUAUGAG X CGAAGA AGUJAGAGAG X CGAA AGUJAGAGA X CGAA	1380
1935 UAACAUCU U UUAAAGUU 247 AACUUUAA CUGAUGAG X CGAA AGAUGUUA	1381
936	1382
937 ACRUCUUU U AAAGUUGA 249 UCAACUUU CUGAUGAG X CGAA AAAGAUGU 938 CAUCUUUU A AAGUUGAU 250 AUCAACUU CUGAUGAG X CGAA AAAGAUGU 943 UUULAAAGU U GAUGAGAA 251 UUCUCAU CUGAUGAG X CGAA AAAGAUGA 953 AUSAGAAU C AAGUAUGA 252 CCAUACUU CUGAUGAG X CGAA ACUUUUAA 958 ANICAAGU A UGGAAAAG 252 CCAUACUU CUGAUGAG X CGAA ACUUUUCC 958 GGAAAAGU A UGGAAAAG 254 UAUUGAC CUGAUGAG X CGAA ACUUUUCC 976 AAGGCCAU A CUCUUACA 255 UGAAGAG CUGAUGAG X CGAA ACUUUUCC 979 GCCAUACU C UUCACUAA 256 UUAUUGAC CUGAUGAG X CGAA AGUAUGAG 981 CAUACUCU U ACAUAAUAA 257 UAUUGAG CUGAUGAG X CGAA AGUAUGAG 982 AUACUCUU A CAUAAUAA 258 UUAUUGAG X CGAAGA AGUAUGAG 984 CUCUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAUGAG 986 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAUGAG 986 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAUGAG 986 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAUGAGA 986 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAUGAGA 986 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAUGAGA 986 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAUGAGA 986 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAGAGAGA 986 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAGAGAU 986 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAGAGAGA 986 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAGAGAGA 986 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAGAGAGA 987 AAGUUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAGAGAGA 988 UCUUCACAU A AUGAAAATAU 259 AAGUUUUUC CUGAUGAG X CGAA AAAGAGAGAGA 988 UCUUCACAU A AUGAAAATAU 259 AAGUUUUC CUGAUGAG X CGAA AUGUGAG X CGAA AUGUGAGA X CGAA	1383
938 CAUCUUUU A AAGUUGAU 250 AUCAACUU CUGAUGAG X CGAA AAAAGAUG 943 UUULAAAGU U GAUGAGAA 251 UUCUCAUC CUGAUGAG X CGAA AACUUUNAA 955 AUSAABAU C AAGUUNIAG 252 CCAUACUU CUGAUGAG X CGAA AUCUUCAU 958 AAUCAAGU A UGGAAAAG 253 CUUUUCCA CUGAUGAG X CGAA ACUUGAUU 958 GGAAAGU A AUGCCAUA 254 UAUGGCCU CUGAUGAG X CGAA ACUUGUCU 959 CAAGCCCU A CUCCIUACA 255 UGUAUGAG X CGAA AGUUUUCC 979 GCCAUACU C UUACAUAA 256 UUAUGUAA CUGAUGAG X CGAA AGUAUGG C 981 CAUACUCU U ACAUAAUA 257 UAUUAUGU CUGAUGAG X CGAA AGGUAUG 982 AUACUCUU A CAUAAUAA 258 UUAUGUG CUGAUGAG X CGAA AAGGUAUG 986 UCUUGACA A AUGAAAATU 259 AAUGUUUG CUGAUGAG X CGAA AAGGUAU	1384
943 UUUNAAGU U GAUGAGAA 251 UUCUCAUC CUGAUGAG X CGAA ACUUUAAA 953 AUGAGAAU C AAGUAUGG 252 COXUACUU CUGAUGAG X CGAA ACUUCUCAU 956 AUGAGAU A UGGAAAAAQ 253 CUUUUCCA CUGAUGAG X CGAA ACUUCUCC 958 GGAAAGU A AOGCCAUA 254 UAUGGCCU CUGAUGAG X CGAA ACUUUUCC 976 AAGGCCAU A CUCUUACA 255 UGUAAGGA CUGAUGAG X CGAA AGUUUUCC 979 GCAUACU C UUCACAUAA 256 UUAUGUAA CUGAUGAG X CGAA AGUAUGGC 981 CAUACUCU U A CAUAAUAA 257 UAUAUGUAG CUGAUGAG X CGAA AGUAUGG 982 AUACUCUU A CAUAAUAA 258 UUUAUUUG CUGAUGAG X CGAA AAGAGUAU 986 UCUUACAU A AUAAAAATU 259 AAGUUUUG CUGAUGAG X CGAA AAGAGUAU	1385
955 AUGAGAAU C ANGUAU90 252 COLUNCUU CUGAUGAG X CGAA AUGUCAU 958 AUGAAGU A UGGAAAAO 253 CUUJUCCA CUGAUGAG X CGAA ACUUCAUU 958 GGAAAGU A DAGCCAUA 254 UAUGGCCU CUGAUGAG X CGAA ACUUCHUCA 976 AAGGCCAU A CUCUJACA 255 UGUAAGAG CUGAUGAG X CGAA AGUGCU 979 GCCAUCACU C UUCACHIAA 256 UUAUGHAA CUGAUGAG X CGAA AGUAUGGC 981 CRUACUCU U A CAUAAUAA 257 UAUGUAUG CUGAUGAG X CGAA AGAGUAUG 982 AUGUCUCU A CAUAAUAA 258 UUAUGUAG CAUGAUGA X CGAA AAGGAGA 961 UCUJACAU A AUGAAAATU 259 AAIJUHUG CUGAUGAG X CGAA AAAGGAGA	1386
958 AAUCAAGU A UGGAAAAG 253 CUUUUCCA CUGAUGAG X CGAA ACUUGAUU 958 GGAAAAGU A AOGCCAUA 254 UAUGGCCU CUGAUGAG X CGAA ACUUUUCC 9796 AAGGCCAU A CUCULUACA 255 UGUAAGAG CUGAUGAG X CGAA AUGUCCUU 979 GCCAUACU C UUACAUAA 256 UUAUGUAA CUGAUGAG X CGAA AGGAUGAG 981 CAUACUCU U ACAUAAUA 257 UAUTAUGU CUGAUGAG X CGAA AAGGAUAUG 982 AUACUCUU A CAUAAAAA 258 UUAUGUUG CUGAUGAG X CGAA AAGGAUAU 986 UUCUUACAU A AUAAAAATU 259 AAUGUUTUG CUGAUGAG X CGAA AAGGAUAU	1387
958 GGAAAAGU A AGGCCAUA 254 UAUGGCCU CUGAUGAG X CGAA ACUUUUCC 976 AAGGCCAU A CUCUUACA 255 UGUAAGAG CUGAUGAG X CGAA AGGCCAU 979 GCCAUACU C UUACAUAA 256 UUAUGUAA CUGAUGAG X CGAA AGGUAUGAG 981 CAUACUCU I ACAUAAUA 257 UAUAUGA CUGAUGAG X CGAA AGAUAUGG 982 AUACUCUU A CAUAAUAA 258 UUAUUAUG CUGAUGAG X CGAA AAGAUAUG 986 UCUUACAU A AUAAAAATU 259 AAIDUIUAU CUGAUGAG X CGAA AAGAUA	1388
976 AAGSCCAU A CUCUUACA 255 UGUAAGAG CUGAUGAG X CGAA AUGGCCUU 979 GCCAUACU C UTACAUAAA 256 UGUAUGUAA CUGAUGAG X CGAA AGUAUGGCC 981 CAUACUCU U ACAUAAUA 257 UAUUAUGU CUGAUGAG X CGAA AGAGUAUG 982 AUACUCUU A CAUAAUAA 258 UUAUUAUG CUGAUGAG X CGAA AMGAGUAU 986 UCUUACAU A AUAAAAUU 259 AAUUUUAU CUGAUGAG X CGAA AUGAGAUA	1389
979 GCCAUACU C UUACAUAA 256 UUAUGUAA CUGAUGAG X CGAA AGUAUGGC 981 CAUACUCU U A CAUAAUAA 257 UAUTUAUGU CUGAUGAG X CGAA AGGUAUG 982 AUACUCUU A CAUAAUAA 258 UUAUUAUG CUGAUGAG X CGAA AAGGUAU 986 UCUTACAU A AUAAAATU 259 AAIDUIUG CUGAUGAG X CGAA AUGUAGAG	1390
991 CAUACUCU U ACAUAAUA 257 UAJUAUGU CUGAUGAG X CGAA AGAGUAUG 982 AUACUCUU A CAUAAUAA 258 UUAUUAUG CUGAUGAG X CGAA AAGAGUAU 986 UCUJACAU A AUAAAAUU 259 AAJUJUAU CUGAUGAG X CGAA AUGUAAGA	1391
982 AUACUCUU A CAUAAUAA 258 UUAUUAUG CUGAUGAG X CGAA AAGAGUAU 986 UCUUACAU A AUAAAAUU 259 AAUUUUAU CUGAUGAG X CGAA AUGUAAGA	1392
986 UCUUACAU A AUAAAAUU 259 AAUUUUAU CUGAUGAG X CGAA AUGUAAGA	1393
	1394
	1395
989 UACAUAAU A AAAUUCCU 260 AGGAAUUU CUGAUGAG X CGAA AUUAUGUA	1396
994 AAUAAAAU U CCUUUUAA 261 UUAAAAGG CUGAUGAG X CGAA AUUUUAUU	1397
995 AUAAAAUU C CUUUUAAG 262 CUUAAAAG CUGAUGAG X CGAA AAUUUUAU	1398
998 AAAUUCCU U UUAAGUAA 263 UUACUUAA CUGAUGAG X CGAA AGGAAUUU	1399
999 AAUUCCUU U UAAGUAAU 264 AUUACUUA CUGAUGAG X CGAA AAGGAAUU	1400
1000 AUUCCUUU U AAGUAAUU 265 AAUUACUU CUGAUGAG X CGAA AAAGGAAU	1401
1001 UUCCUUUU A AGUAAUUU 266 AAAUUACU CUGAUGAG X CGAA AAAAGGAA	1402
1005 UUUUAAGU A AUUUUUUC 267 GAAAAAAU CUGAUGAG X CGAA ACUUAAAA	1403
1008 UAAGUAAU U UUUUCAAA 268 UUUGAAAA CUGAUGAG X CGAA AUUACUUA	1404
1009 AAGUAAUU U UUUCAAAG 269 CUUUGAAA CUGAUGAG X CGAA AAUUACUU	1405
1010 AGUAAUUU U UUCAAAGA 270 UCUUUGAA CUGAUGAG X CGAA AAAUUACU	1406
1011 GUAAUUUU U UCAAAGAA 271 UUCUUUGA CUGAUGAG X CGAA AAAAUUAC	1407
1012 UAAUUUUU U CAAAGAAU 272 AUUCUUUG CUGAUGAG X CGAA AAAAAUUA	1408
1013 AAUUUUUU C AAAGAAUC 273 GAUUCUUU CUGAUGAG X CGAA AAAAAAUU	1409
1021 CAAAGAAU C ACAGAAUU 274 AAUUCUGU CUGAUGAG X CGAA AUUCUUUG	1410
1029 CACAGAAU U CUAGUACA 275 UGUACUAG CUGAUGAG X CGAA AUUCUGUG	1411
1030 ACAGAAUU C UAGUACAU 276 AUGUACUA CUGAUGAG X CGAA AAUUCUGU	1412
1032 AGAAUUCU A GUACAUGU 277 ACAUGUAC CUGAUGAG X CGAA AGAAUUCU	1413

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1035	AUUCUAGU A CAUGUAGG	278	CCUACAUG CUGAUGAG X CGAA ACUAGAAU	1414
1041	GUACAUGU A GGUAAAUC	279	GAUUUACC CUGAUGAG X CGAA ACAUGUAC	1415
1045	AUGUAGGU A AAUCAUAA	280	UUAUGAUU CUGAUGAG X CGAA ACCUACAU	1416
1049	AGGUAAAU C AUAAAUCU	281	AGAUUUAU CUGAUGAG X CGAA AUUUACCU	1417
1052	UAAAUCAU A AAUCUGUU	282	AACAGAUU CUGAUGAG X CGAA AUGAUUUA	1418
1056	UCAUAAAU C UGUUCUAA	283	UUAGAACA CUGAUGAG X CGAA AUUUAUGA	1419
1060	AAAUCUGU U CUAAGACA	284	UGUCUUAG CUGAUGAG X CGAA ACAGAUUU	1420
1061	AAUCUGUU C UAAGACAU	285	AUGUCUUA CUGAUGAG X CGAA AACAGAUU	1421
1063	UCUGUUCU A AGACAUAU	286	AUAUGUCU CUGAUGAG X CGAA AGAACAGA	1422
1070	UAAGACAU A UGAUCAAC	287	GUUGAUCA CUGAUGAG X CGAA AUGUCUUA	1423
1075	CAUAUGAU C AACAGAUG	288	CAUCUGUU CUGAUGAG X CGAA AUCAUAUG	1424
1096	CUGGUGGU U AAUAUGUG	289	CACAUAUU CUGAUGAG X CGAA ACCACCAG	1425
1097	UGGUGGUU A AUAUGUGA	290	UCACAUAU CUGAUGAG X CGAA AACCACCA	1426
1100	UGGUUAAU A UGUGACAG	291	CUGUCACA CUGAUGAG X CGAA AUUAACCA	1427
1115	AGUGAGAU U AGUCAUAU	292	AUAUGACU CUGAUGAG X CGAA AUCUCACU	1428
1116	GUGAGAUU A GUCAUAUC	293	GAUAUGAC CUGAUGAG X CGAA AAUCUCAC	1429
1119	AGAUUAGU C AUAUCACU	294	AGUGAUAU CUGAUGAG X CGAA ACUAAUCU	1430
1122	UUAGUCAU A UCACUAAU	295	AUUAGUGA CUGAUGAG X CGAA AUGACUAA	1,431
1124	AGUCAUAU C ACUAAUAU	296	AUAUUAGU CUGAUGAG X CGAA AUAUGACU	1432
1128	AUAUCACU A AUAUACUA	297	UAGUAUAU CUGAUGAG X CGAA AGUGAUAU	1433
1131	UCACUAAU A UACUAACA	298	UGUUAGUA CUGAUGAG X CGAA AUUAGUGA	1434
1133	ACUAAUAU A CUAACAAC	299	GUUGUUAG CUGAUGAG X CGAA AUAUUAGU	1435
1136	AAUAUACU A ACAACAGA	300	UCUGUUGU CUGAUGAG X CGAA AGUAUAUU	1436
1147	AACAGAAU C UAAUCUUC	301	GAAGAUUA CUGAUGAG X CGAA AUUCUGUU	1437
1149	CAGAAUCU A AUCUUCAU	302	AUGAAGAU CUGAUGAG X CGAA AGAUUCUG	1438
1152	AAUCUAAU C UUCAUUUA	303	UAAAUGAA CUGAUGAG X CGAA AUUAGAUU	1439
1154	UCUAAUCU U CAUUUAAG	304	CUUAAAUG CUGAUGAG X CGAA AGAUUAGA	1440
1155	CUAAUCUU C AUUUAAGG	305	CCUUAAAU CUGAUGAG X CGAA AAGAUUAG	1441
1158	AUCUUCAU U UAAGGCAC	306	GUGCCUUA CUGAUGAG X CGAA AUGAAGAU	1442
1159	UCUUCAUU U AAGGCACU	307	AGUGCCUU CUGAUGAG X CGAA AAUGAAGA	1443
1160	CUUCAUUU A AGGCACUG	308	CAGUGCCU CUGAUGAG X CGAA AAAUGAAG	1444
1170	GGCACUGU A GUGAAUUA	309	UAAUUCAC CUGAUGAG X CGAA ACAGUGCC	1445
1177	UAGUGAAU U AUCUGAGC AGUGAAUU A UCUGAGCU	310	GCUCAGAU CUGAUGAG X CGAA AUUCACUA	1446
1180	UGAAUUAU C UGAGCUAG	311	AGCUCAGA CUGAUGAG X CGAA AAUUCACU CUAGCUCA CUGAUGAG X CGAA AHAAHIICA	1447
1187	UCUGAGUI A GAGUIACC	312		
1197	GCUAGAGU U ACCUAGCU	313	GGUAACUC CUGAUGAG X CGAA AGCUCAGA	1449
1192	CUAGAGUU A CCUAGCUU	314	AGCUAGGU CUGAUGAG X CGAA ACUCUAGC	1450
1193	AGUUACCU A GCUUACCA	316	AAGCUAGG CUGAUGAG X CGAA AACUCUAG UGGUAAGC CUGAUGAG X CGAA AGGUAACU	1451
1201	ACCUAGCU U ACCAUACU	316	AGUAUGGU CUGAUGAG X CGAA AGCUAGGU	1452
1201	CCUAGCUU A CCAUACUA	317	UAGUAUGG CUGAUGAG X CGAA AGCUAGG	1453
1202	CUUACCAU A CUAUAUCU	319	AGAUAUAG CUGAUGAG X CGAA AUGGUAAG	1455
1210	ACCAUACU A UAUCUUUG	320	CAAAGAUA CUGAUGAG X CGAA AGUAUGGU	1456
1210	CAUACUAU A UCUUUGGA	320	UCCAAAGA CUGAUGAG X CGAA AUAGUAUGU	1456
1212	UACUAUAII C UUUGGAAII	322	AUUCCAAA CUGAUGAG X CGAA AUAUAGUA	1457
1214	CUAUAUCH U HGGAAUCA	323	UGAUUCCA CUGAUGAG X CGAA AGAUAUAG	1458
1217	UAUAUCUU U GGAAUCAU	324	AUGAUUCC CUGAUGAG X CGAA AGAUAUA	1460
	C.I.S. IOCOD O GGARDCAU			1400

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1223	UUUGGAAU C AUGAAACC	325	GGUUUCAU CUGAUGAG X CGAA AUUCCAAA	1461
1233	UGAAACCU U AAGACUUC	326	GAAGUCUU CUGAUGAG X CGAA AGGUUUCA	1462
1234	GAAACCUU A AGACUUCA	327	UGAAGUCU CUGAUGAG X CGAA AAGGUUUC	1463
1240	UUAAGACU U CAGAAUGA	328	UCAUUCUG CUGAUGAG X CGAA AGUCUUAA	1464
1241	UAAGACUU C AGAAUGAU	329	AUCAUUCU CUGAUGAG X CGAA AAGUCUUA	1465
1250	AGAAUGAU U UUGCAGGU	330	ACCUGCAA CUGAUGAG X CGAA AUCAUUCU	1466
1251	GAAUGAUU U UGCAGGUU	331	AACCUGCA CUGAUGAG X CGAA AAUCAUUC	1467
1252	AAUGAUUU U GCAGGUUG	332 ,	CAACCUGC CUGAUGAG X CGAA AAAUCAUU	1468
1259	UUGCAGGU U GUCUUCCA	333	UGGAAGAC CUGAUGAG X CGAA ACCUGCAA	1469
1262	CAGGUUGU C UUCCAUUC	334	GAAUGGAA CUGAUGAG X CGAA ACAACCUG	1470
1264	GGUUGUCU U CCAUUCCA	335	UGGAAUGG CUGAUGAG X CGAA AGACAACC	1471
1265	GUUGUCUU C CAUUCCAG	336	CUGGAAUG CUGAUGAG X CGAA AAGACAAC	1472
1269	UCUUCCAU U. CCAGCCUA	337	UAGGCUGG CUGAUGAG X CGAA AUGGAAGA	1473
1270	CUUCCAUU C CAGCCUAA	338	UUAGGCUG CUGAUGAG X CGAA AAUGGAAG	1474
1277	UCCAGCCU A ACAUCCAA	339	UUGGAUGU CUGAUGAG X CGAA AGGCUGGA	1475
1282	CCUAACAU C CAAUGCAG	340	CUGCAUUG CUGAUGAG X CGAA AUGUUAGG	1476
1302	AGGAAAAU A AAAGAUUU	341	AAAUCUUU CUGAUGAG X CGAA AUUUUCCU	1477
1309	UAAAAGAU U UCCAGUGA	342	UCACUGGA CUGAUGAG X CGAA AUCUUUUA	1478
1310	AAAAGAUU U CCAGUGAC	343	GUCACUGG CUGAUGAG X CGAA AAUCUUUU	1479
1311	AAAGAUUU C CAGUGACA	344	UGUCACUG CUGAUGAG X CGAA AAAUCUUU	1480
1327	AGAAAAU A UAUUAUCU	345	AGAUAAUA CUGAUGAG X CGAA AUUUUUCU	1481
1329	AAAAAUAU A UUAUCUCA	346	UGAGAUAA CUGAUGAG X CGAA AUAUUUUU	1482
1331	AAAUAUAU U AUCUCAAG	347	CUUGAGAU CUGAUGAG X CGAA AUAUAUUU	1483
1332	AAUAUAUU A UCUCAAGU	348	ACUUGAGA CUGAUGAG X CGAA AAUAUAUU	1484
1334	UAUAUUAU C UCAAGUAU	349	AUACUUGA CUGAUGAG X CGAA AUAAUAUA	1485
1336	UAUUAUCU C AAGUAUUU	350	AAAUACUU CUGAUGAG X CGAA AGAUAAUA	1486
1341	UCUCAAGU A UUUUUUAA	351	UUAAAAAA CUGAUGAG X CGAA ACUUGAGA	1487
1343	UCAAGUAU U UUUUAAAA	352	UUUUAAAA CUGAUGAG X CGAA AUACUUGA	1488
1344	CAAGUAUU U UUUAAAAA	353	UUUUUAAA CUGAUGAG X CGAA AAUACUUG	1489
1345	AAGUAUUU U UUAAAAAU	354	AUUUUUAA CUGAUGAG X CGAA AAAUACUU	1490
1346	AGUAUUUU U UAAAAAUA	355	UAUUUUUA CUGAUGAG X CGAA AAAAUACU	1491
1347	GUAUUUUU U AAAAAUAU	356	AUAUUUUU CUGAUGAG X CGAA AAAAAUAC	1492
1348	AUAUUUUUA A AUAUAUAU	357	UAUAUUUU CUGAUGAG X CGAA AAAAAAUA	1493
1354	UUAAAAAU A UAUGAAUU	358	AAUUCAUA CUGAUGAG X CGAA AUUUUUAA	1494
1356	AAAAAUAU A UGAAUUCU	359	AGAAUUCA CUGAUGAG X CGAA AUAUUUUU	1495
1362	AUAUGAAU U CUCUCUCC	360	GGAGAGAG CUGAUGAG X CGAA AUUCAUAU	1496
1363	UAUGAAUU C UCUCUCCA	361	UGGAGAGA CUGAUGAG X CGAA AAUUCAUA	1497
1365	UGAAUUCU C UCUCCAAA	362	UUUGGAGA CUGAUGAG X CGAA AGAAUUCA	1498
1367	AAUUCUCU C UCCAAAUA	363	UAUUUGGA CUGAUGAG X CGAA AGAGAAUU	1499
1369	UUCUCUCU C CAAAUAUU	364	AAUAUUUG CUGAUGAG X CGAA AGAGAGAA	1500
1375	CUCCAAAU A UUAACUAA	365	UUAGUUAA CUGAUGAG X CGAA AUUUGGAG	1501
1377	CCAAAUAU U AACUAAUU	366	AAUUAGUU CUGAUGAG X CGAA AUAUUUGG	1502
1378	CAAAUAUU A ACUAAUUA	367	UAAUUAGU CUGAUGAG X CGAA AAUAUUUG	1503
1382	UAUUAACU A AUUAUUAG	368	CUAAUAAU CUGAUGAG X CGAA AGUUAAUA	1504
1385	UAACUAAU U AUUAGAUU	369	AAUCUAAU CUGAUGAG X CGAA AUUAGUUA	1505
1386	AACUAAUU A UUAGAUUA	370	UAAUCUAA CUGAUGAG X CGAA AAUUAGUU	1506
1388	CUAAUUAU U AGAUUAUA	371	UAUAAUCU CUGAUGAG X CGAA AUAAUUAG	1507

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1389	UAAUUAUU A GAUUAUAU	372	AUAUAAUC CUGAUGAG X CGAA AAUAAUUA	1508
1393	UAUUAGAU U AUAUUUUG	373	CAAAAUAU CUGAUGAG X CGAA AUCUAAUA	1509
1394	AUUAGAUU A UAUUUUGA	374	UCAAAAUA CUGAUGAG X CGAA AAUCUAAU	1510
1396	UAGAUUAU A UUUUGAAA	375	UUUCAAAA CUGAUGAG X CGAA AUAAUCUA	1511
1398	GAUUAUAU U UUGAAAUG	376	CAUUUCAA CUGAUGAG X CGAA AUAUAAUC	1512
1399	AUUAUAUU U UGAAAUGA	377	UCAUUUCA CUGAUGAG X CGAA AAUAUAAU	1513
1400	UUAUAUUU U GAAAUGAA	378	UUCAUUUC CUGAUGAG X CGAA AAAUAUAA	1514
1411	AAUGAACU U GUUGGCCC	379	GGGCCAAC CUGAUGAG X CGAA AGUUCAUU	1515
1414	GAACUUGU U GGCCCAUC	380	GAUGGGCC CUGAUGAG X CGAA ACAAGUUC	1516
1422	UGGCCCAU C VAUUACAU	381	AUGUAAUA CUGAUGAG X CGAA AUGGGCCA	1517
1424	GCCCAUCU A UUACAUCU	382	AGAUGUAA CUGAUGAG X CGAA AGAUGGGC	1518
1426	CCAUCUAU U ACAUCUAC	383	GUAGAUGU CUGAUGAG X CGAA AVAGAUGG	1519
1427	CAUCUAUU A CAUCUACA	384	UGUAGAUG CUGAUGAG X CGAA AAUAGAUG	1520
1431	UAUUACAU C UACAGCUG	385	CAGCUGUA CUGAUGAG X CGAA AUGUAAUA	1521
1433	UUACAUCU A CAGCUGAC	386	GUCAGCUG CUGAUGAG X CGAA AGAUGUAA	1522
1445	CUGACCCU U GAACAUGG	387	CCAUGUUC CUGAUGAG X CGAA AGGGUCAG	1523
1458	AUGGGGU U AGGGGAGC	388	GCUCCCCU CUGAUGAG X CGAA ACCCCCAU	1524
1459	UGGGGGUU A GGGGAGCU	389	AGCUCCCC CUGAUGAG X CGAA AACCCCCA	1525
1474	CUGACAAU U CGUGGGUC	390	GACCCACG CUGAUGAG X CGAA AUUGUCAG	1526
1475	UGACAAUU C GUGGGUCC	391	GGACCCAC CUGAUGAG X CGAA AAUUGUCA	1527
1482	UCGUGGGU C CGCAAAAU	392	AUUUUGCG CUGAUGAG X CGAA ACCCACGA	1528
1491	CGCAAAAU C UUAACUAC	393	GUAGUUAA CUGAUGAG X CGAA AUUUUGCG	1529
1493	CAAAAUCU U AACUACCU	394	AGGUAGUU CUGAUGAG X CGAA AGAUUUUG	1530
1494	AAAAUCUU A ACUACCUA	395	UAGGUAGU CUGAUGAG X CGAA AAGAUUUU	1531
1498	UCUUAACU A CCUAAUAG	396	CUAUUAGG CUGAUGAG X CGAA AGUUAAGA	1532
1502	AACUACCU A AUAGCCUA	397	UAGGCUAU CUGAUGAG X CGAA AGGUAGUU	1533
1505	UACCUAAU A GCCUACUA	398	UAGUAGGC CUGAUGAG X CGAA AUUAGGUA	1534
1510	AAUAGCCU A CUAUUGAC	399	GUCAAUAG CUGAUGAG X CGAA AGGCUAUU	1535
1513	AGCCUACU A UUGACCAU	400	AUGGUCAA CUGAUGAG X CGAA AGUAGGCU	1536
1515	CCUACUAU U GACCAUAA	401	UUAUGGUC CUGAUGAG X CGAA AUAGUAGG	1537
1522	UUGACCAU A AACCUUAC	402	GUAAGGUU CUGAUGAG X CGAA AUGGUCAA	1538
1528	AUAAACCU U ACUGAUAA	403	UUAUCAGU CUGAUGAG X CGAA AGGUUUAU	1539
1529	UAAACCUU A CUGAUAAC	404	GUUAUCAG CUGAUGAG X CGAA AAGGUUUA	1540
1535	UUACUGAU A ACAUAAAC	405	GUUUAUGU CUGAUGAG X CGAA AUCAGUAA	1541
1540	GAUAACAU A AACAGUAA	406	UUACUGUU CUGAUGAG X CGAA AUGUUAUC	1542
1547	UAAACAGU A AAUUAACA	407	UGUUAAUU CUGAUGAG X CGAA ACUGUUUA	1543
1551	CAGUAAAU U AACACAUA	408	UAUGUGUU CUGAUGAG X CGAA AUUUACUG	1544
1552	AGUAAAUU A ACACAUAU	409	AUAUGUGU CUGAUGAG X CGAA AAUUUACU	1545
1559	UAACACAU A UUUUGCGU	410	ACGCAAAA CUGAUGAG X CGAA AUGUGUUA	1546
1561	ACACAUAU U UUGCGUGU	411	ACACGCAA CUGAUGAG X CGAA AUAUGUGU	1547
1562	CACAUAUU U UGCGUGUU	412	AACACGCA CUGAUGAG X CGAA AAUAUGUG	1548
1563	ACAUAUUU U GCGUGUUA	413	UAACACGC CUGAUGAG X CGAA AAAUAUGU	1549
1570	UUGCGUGU U AUAUGUAU	414	AUACAUAU CUGAUGAG X CGAA ACACGCAA	1550
1571	UGCGUGUU A UAUGUAUU	415	AAUACAUA CUGAUGAG X CGAA AACACGCA	1551
1573	CGUGUUAU A UGUAUUAU	416	AUAAUACA CUGAUGAG X CGAA AUAACACG	1552
1577	UUAUAUGU A UUAUACAC	417	GUGUAUAA CUGAUGAG X CGAA ACAUAUAA	1553
1579	AUAUGUAU U AUACACUA	418	UAGUGUAU CUGAUGAG X CGAA AUACAUAU	1554

Table 24

1580	UAUGUAUU A UACACUAU	419	AUAGUGUA CUGAUGAG X CGAA AAUACAUA	1555
1582	UGUAUUAU A CACUAUAU	420	AUAUAGUG CUGAUGAG X CGAA AUAAUACA	1556
1587	UAUACACU A UAUUCCUA	421	UAGGAAUA CUGAUGAG X CGAA AGUGUAUA	1557
1589	UACACUAU A UUCCUACA	422	UGUAGGAA CUGAUGAG X CGAA AUAGUGUA	1558
1591	CACUAUAU U CCUACAAU	423	AUUGUAGG CUGAUGAG X CGAA AUAUAGUG	1559
1592	ACUAUAUU C CUACAAUA	424	UAUUGUAG CUGAUGAG X CGAA AAUAUAGU	1560
1595	AUAUUCCU A CAAUAAAG	425	CUUUAUUG CUGAUGAG X CGAA AGGAAUAU	1561
1600	CCUACAAU A AAGUAAGC	426	GCUUACUU CUGAUGAG X CGAA AUUGUAGG	1562
1605	AAUAAAGU A AGCUAGAG	427	CUCUAGCU CUGAUGAG X CGAA ACUUUAUU	1563
1610	AGUAAGCU A GAGAAAAU	428	AUUUUCUC CUGAUGAG X CGAA AGCUUACU	1564
1621	GAAAAUGU U AUUUAGAA	429	UUCUAAAU CUGAUGAG X CGAA ACAUUUUC	1565
1622	AAAAUGUU A UUUAGAAA	430	UUUCUAAA CUGAUGAG X CGAA AACAUUUU	1566
1624	AAUGUUAU U UAGAAAAU	431	AUUUUCUA CUGAUGAG X CGAA AUAACAUU	1567
1625	AUGUUAUU U AGAAAAUC	432	GAUUUUCU CUGAUGAG X CGAA AAUAACAU	1568
1626	UGUUAUUU A GAAAAUCA	433	UGAUUUUC CUGAUGAG X CGAA AAAUAACA	1569

Input Sequence = PLN, Cut Site = UH/.

Stem Length = 8 . Core Sequence = CUGAUGAG X CGAA (X = GCCGUUAGGC or other stem II)

PLN (Homo suppliens phospholamban (PLN) mRNA.; 1635 bp)

Table 25: Human Phospholamban (PLN) NCH Ribozyme and Target Sequence

Pos	Substrate	Seq ID	Ribozyme	Rz Seq ID
15	CAGAAAAC U AGCUAAAC	434	GUUUAGCU CUGAUGAG X CGAA IUUUUCUG	1570
17	GAAAACUC C CUAAACAC	435	GUGUUUAG CUGAUGAG X CGAA IAGUUUUC	1571
18	AAAACUCC C UAAACACC	436	GGUGUUUA CUGAUGAG X CGAA IGAGUUUU	1572
19	AAACUCCC C AAACACCC	437	GGGUGUUU CUGAUGAG X CGAA IGGAGUUU	1573
20	AACUCCCC A AACACCCG	438	CGGGUGUU CUGAUGAG X CGAA IGGGAGUU	1574
23	UCCCCAGC U ACCCGUAA	439	UUACGGGU CUGAUGAG X CGAA ICUGGGGA	1575
28	AGCUAAAC A UAAGACUU	440	AAGUCUUA CUGAUGAG X CGAA IUUUAGCU	1576
30	CUAAACAC C AGACUUCA	441	UGAAGUCU CUGAUGAG X CGAA IUGUUUAG	1577
31	UAAACACC C GACUUCAU	442	AUGAAGUC CUGAUGAG X CGAA IGUGUUUA	1578
39	CGUAAGAC U ACAACACA	443	UGUGUUGU CUGAUGAG X CGAA IUCUUACG	1579
42	AAGACUUC A ACACAAUA	444	UAUUGUGU CUGAUGAG X CGAA IAAGUCUU	1580
46	CUUCAUAC A AAUACUCU	445	AGAGUAUU CUGAUGAG X CGAA IUAUGAAG	1581
49	CAUACAAC A ACUCUAUA	446	UAUAGAGU CUGAUGAG X CGAA IUUGUAUG	1582
51	UACAACAC A UCUAUACU	447	AGUAUAGA CUGAUGAG X CGAA IUGUUGUA	1583
56	CACAAUAC U ACUGUGAU	448	AUCACAGU CUGAUGAG X CGAA IUAUUGUG	1584
58	CAAUACUC U UGUGAUGA	449	UCAUCACA CUGAUGAG X CGAA IAGUAUUG	1585
63	CUCUAUAC U UGAUCACA	450	UGUGAUCA CUGAUGAG X CGAA IUAUAGAG	1586
73	UGAUGAUC A UGCCAAGG	451	CCUUGGCA CUGAUGAG X CGAA IAUCAUCA	1587
75	AUGAUCAC A CCAAGGCU	452	AGCCUUGG CUGAUGAG X CGAA IUGAUCAU	1588
78	AUCACAGC U AGGCUACC	453	GGUAGCCU CUGAUGAG X CGAA ICUGUGAU	1589
81	ACAGCUGC C CUACCUAA	454	UUAGGUAG CUGAUGAG X CGAA ICAGCUGU	1590
82	CAGCUGCC A UACCUAAA	455	UUUAGGUA CUGAUGAG X CGAA IGCAGCUG	1591
87	GCCAAGGC U AAAAGAAG	456	CUUCUUUU CUGAUGAG X CGAA ICCUUGGC	1592
90	AAGGCUAC C AGAAGACA	457	UGUCUUCU CUGAUGAG X CGAA IUAGCCUU	1593
91	AGGCUACC U GAAGACAG	458	CUGUCUUC CUGAUGAG X CGAA IGUAGCCU	1594
102	AAGAAGAC A UCUCAUAU	459	AUAUGAGA CUGAUGAG X CGAA IUCUUCUU	1595
109	CAGUUAUC U UUUGGCUG	460	CAGCCAAA CUGAUGAG X CGAA IAUAACUG	1596
111	GUUAUCUC A UGGCUGCC	461	GGCAGCCA CUGAUGAG X CGAA IAGAUAAC	1597
120	UAUUUGGC U GCUUUUUA	462	UAAAAAGC CUGAUGAG X CGAA ICCAAAUA	1598
123	UUGGCUGC C UUUUAUCU	463	AGAUAAAA CUGAUGAG X CGAA ICAGCCAA	1599
124	UGGCUGCC A UUUAUCUU	464	AAGAUAAA CUGAUGAG X CGAA IGCAGCCA	1600
127	CUGCCAGC U AUCUUUCU	465	AGAAAGAU CUGAUGAG X CGAA ICUGGCAG	1601
135	UUUUUAUC U CUCGACCA	466	UGGUCGAG CUGAUGAG X CGAA IAUAAAAA	1602
139	UAUCUUUC U ACCACUUA	467	UAAGUGGU CUGAUGAG X CGAA IAAAGAUA	1603
141	UCUUUCUC U CACUUAAA	468	UUUAAGUG CUGAUGAG X CGAA IAGAAAGA	1604
146	CUCUCGAC C AAAACUUC	469	GAAGUUUU CUGAUGAG X CGAA IUCGAGAG	1605
147	UCUCGACC A AAACUUCA	470	UGAAGUUU CUGAUGAG X CGAA IGUCGAGA	1606
149	UCGACCAC U ACUUCAGA	471	UCUGAAGU CUGAUGAG X CGAA IUGGUCGA	1607
156	CUUAAAAC U ACUUCCUG	472	CAGGAAGU CUGAUGAG X CGAA IUUUUAAG	1608
159	AAAACUUC A UCCUGUCC	473	GGACAGGA CUGAUGAG X CGAA IAAGUUUU	1609
163	CUUCAGAC U GUCCUGCU	474	AGCAGGAC CUGAUGAG X CGAA IUCUGAAG	1610
166	CAGACUUC C CUGCUGGU	475	ACCAGCAG CUGAUGAG X CGAA IAAGUCUG	1611
167	AGACUUCC U UGCUGGUA	476	UACCAGCA CUGAUGAG X CGAA IGAAGUCU	1612
171	UUCCUGUC C GGUAUCAU	477	AUGAUACC CUGAUGAG X CGAA IACAGGAA	1613

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Table 25

172	UCCUGUCC U GUAUCAUG	478	CAUGAUAC CUGAUGAG X CGAA IGACAGGA	1614
175	UGUCCUGC U UCAUGGAG	479	CUCCAUGA CUGAUGAG X CGAA ICAGGACA	1615
182	CUGGUAUC A GAAAGUCC	480	GGACUUUC CUGAUGAG X CGAA IAUACCAG	1515
194	AGAAAGUC C CCUCACUC	481	GAGUGAGG CUGAUGAG X CGAA IACUUUCU	1617
195	GAAAGUCC A CUCACUCG	482	CGAGUGAG CUGAUGAG X CGAA IGACUUUC	1618
200	UCCAAUAC C UCGCUCAG	483	CUGAGCGA CUGAUGAG X CGAA IUAUUGGA	1619
201	CCAAUACC U CGCUCAGC	484	GCUGAGCG CUGAUGAG X CGAA IGUAUUGG	1620
203	AAUACCUC A CUCAGCUA	485	UAGCUGAG CUGAUGAG X CGAA IAGGUAUU	1621
205	UACCUCAC U CAGCUAUA	486	UAUAGCUG CUGAUGAG X CGAA IUGAGGUA	1622
209	UCACUCGC U UAUAAGAA	487	UUCUUAHA CUGAUGAG X CGAA ICGAGUGA	1623
211	ACUCGCUC A UAAGAAGA	488	UCUUCUUA CUGAUGAG X CGAA IAGCGAGU	1624
214	CGCUCAGC U GAAGAGCC	489	GGCUCUUC CUGAUGAG X CGAA ICUGAGCG	1525
226	AGAAGAGC C CCAUUGAA	490	UUCAAUGG CUGAUGAG X CGAA ICUCUUCU	1625
227	GAAGAGCC U CAUUGAAA	491	UUUCAAUG CUGAUGAG X CGAA IGCUCUUC	1527
229	AGAGCCUC A UUGAAAUG	492	CAUUUCAA CUGAUGAG X CGAA IAGGCUCU	1528
232	GCCUCAAC C AAAUGCCU	493	AGGCAUUU CUGAUGAG X CGAA IUUGAGGC	1629
233	CCUCAACC A AAUGCCUC	494	GAGGCAUU CUGAUGAG X CGAA IGUUGAGG	1630
243	UGAAAUGC C CAAGCACG	495	CGUGCUUG CUGAUGAG X CGAA ICAUUUCA	1631
244	GAAAUGCC U AAGCACGU	496	ACGUGCUU CUGAUGAG X CGAA IGCAUUUC	1632
245	AAUGCCUC A GCACGUCA	497	UGACGUGC CUGAUGAG X CGAA IAGGCAUU	1633
249	GCCUCAAC A CGUCAAAA	498	UUUUGACG CUGAUGAG X CGAA IUUGAGGC	1634
253	CAACAAGC A AAAAGCUA	499	UAGCUUUU CUGAUGAG X CGAA ICUUGUUG	1635
258	AGCACGUC A CUACAGAA	500	UUCUGUAG CUGAUGAG X CGAA IACGUGCU	1636
264	UCAAAAGC U AAUCUAUU	501	AAUAGAUU CUGAUGAG X CGAA ICUUUUGA	1637
267	AAAGCUAC A CUAUUUAU	502	AUAAAUAG CUGAUGAG X CGAA IUAGCUUU	1638
273	ACAGAAUC U AUCAAUUU	503	AAAUUGAU CUGAUGAG X CGAA IAUUCUGU	1639
281	UAUUUAUC A CUGUCUCA	504	UGAGACAG CUGAUGAG X CGAA IAUAAAUA	1640
287	UCAAUUUC U CAUCUUAA	505	UUAAGAUG CUGAUGAG X CGAA IAAAUUGA	1641
291	UUUCUGUC U UUAAUAUG	505	CAUAUUAA CUGAUGAG X CGAA IACAGAAA	1642
293	UCUGUCUC A AAUAUGUC	507	GACAUAUU CUGAUGAG X CGAA IAGACAGA	1643
296	GUCUCAUC U AUGUCUCU	508	AGAGACAU CUGAUGAG X CGAA IAUGAGAC	1644
306	AAUAUGUC U CUGAUCUG	509	CAGAUCAG CUGAUGAG X CGAA IACAUAUU	1645
308	UAUGUCUC U GAUCUGUA	510	UACAGAUC CUGAUGAG X CGAA IAGACAUA	1546
312	UCUCUUGC U UGUAUCAU	511	AUGAUACA CUGAUGAG X CGAA ICAAGAGA	1647
317	UGCUGAUC U CAUCGUGA	512 -	UCACGAUG CUGAUGAG X CGAA IAUCAGCA	1648
323	UCUGUAUC A GAUGCUUC	513	GAAGCAUC CUGAUGAG X CGAA IAUACAGA	1649
333	CGUGAUGC U UGAAGUUC	514	GAACUUCA CUGAUGAG X CGAA ICAUCACG	1650
335	GAUGCUUC U AGUUCUGC	515	GCAGAACU CUGAUGAG X CGAA IAAGCAUC	1651
338	UGCUUCUC U UUCUGCUA	516	UAGCAGAA CUGAUGAG X CGAA IAGAAGCA	1652
346	UGAAGUUC U CAACCUCU	517	AGAGGUUG CUGAUGAG X CGAA IAACUUCA	1653
349	AGUUCUGC U CCUCUAGA	518	UCUAGAGG CUGAUGAG X CGAA ICAGAACU	1654
352	UCUGCUAC A CUAGAUCU	519	AGAUCUAG CUGAUGAG X CGAA IUAGCAGA	1655
355	GCUACAAC C GAUCUGCA	520	UGCAGAUC CUGAUGAG X CGAA IUUGUAGC	1656
356	CUACAACC U AUCUGCAG	521	CUGCAGAU CUGAUGAG X CGAA IGUUGUAG	1657
358	ACAACCUC U CUGCAGCU	522	AGCUGCAG CUGAUGAG X CGAA IAGGUUGU	1658
354	UCUAGAUC U CUUGCCAC	523	GUGGCAAG CUGAUGAG X CGAA IAUCUAGA	1659
367	AGAUCUGC A GCCACAUC	524	GAUGUGGC CUGAUGAG X CGAA ICAGAUCU	1660
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	Table 25

370	UCUGCAGC U ACAUCAGC	525	GCUGAUGU CUGAUGAG X CGAA ICUGCAGA	1661
374	CAGCUUGC C CAGCUUAA	526	UUAAGCUG CUGAUGAG X CGAA ICAAGCUG	1662
375	AGCUUGCC A AGCUUAAA	527	UUUAAGCU CUGAUGAG X CGAA IGCAAGCU	1663
377	CUUGCCAC A CUUAAAAU	528	AUUUUAAG CUGAUGAG X CGAA IUGGCAAG	1664
380	GCCACAUC A AAAAUCUG	529	CAGAUUUU CUGAUGAG X CGAA IAUGUGGC	1665
383	ACAUCAGC U AUCUGUCA	530	UGACAGAU CUGAUGAG X CGAA ICUGAUGU	1666
391	UUAAAAUC U UCCCAUGC	531	GCAUGGGA CUGAUGAG X CGAA IAUUUUAA	1667
395	AAUCUGUC A AUGCAGAC	532	GUCUGCAU CUGAUGAG X CGAA IACAGAUU	1668
398	CUGUCAUC C CAGACAGG	533	CCUGUCUG CUGAUGAG X CGAA IAUGACAG	1669
399	UGUCAUCC C AGACAGGA	534	UCCUGUCU CUGAUGAG X CGAA IGAUGACA	16,70
400	GUCAUCCC A GACAGGAA	535	UUCCUGUC CUGAUGAG X CGAA IGGAUGAC	1671
404	UCCCAUGC A GGAAAACA	536	UGUUUUCC CUGAUGAG X CGAA ICAUGGGA	1672
408	AUGCAGAC A AACAAUAU	537	AUAUUGUU CUGAUGAG X CGAA IUCUGCAU	1673
416	AGGAAAAC A UGUAUAAC	538	GUUAUACA CUGAUGAG X CGAA IUUUUCCU	1674
429	UGUAUAAC A ACUUCCUG	539	CAGGAAGU CUGAUGAG X CGAA IUUAUACA	1675
433	UAACAGAC C CCUGAGUA	540	UACUCAGG CUGAUGAG X CGAA IUCUGUUA	1676
434	AACAGACC A CUGAGUAG	541	CUACUCAG CUGAUGAG X CGAA IGUCUGUU	1677
436	CAGACCAC U GAGUAGAA	542	UUCUACUC CUGAUGAG X CGAA IUGGUCUG	1678
439	ACCACUUC C UAGAAGAG	543	CUCUUCUA CUGAUGAG X CGAA IAAGUGGU	1679
440	CCACUUCC U AGAAGAGU	544	ACUCUUCU CUGAUGAG X CGAA IGAAGUGG	1680
456	AGAGUUUC U GAAAAGGU	545	ACCUUUUC CUGAUGAG X CGAA IAAACUCU	1681
470	AAAAGGUC A UAAGACUA	546	UAGUCUUA CUGAUGAG X CGAA IACCUUUU	1682
481	AUUAAGAC U CUUAUUGU	547	ACAAUAAG CUGAUGAG X CGAA IUCUUAAU	1683
487	ACUAAAAC U GUUACCAU	548	AUGGUAAC CUGAUGAG X CGAA IUUUUAGU	1684
497	AUUGUUAC C GUAUUCAU	549	AUGAAUAC CUGAUGAG X CGAA IUAACAAU	1685
498	UUGUUACC A UAUUCAUC	550	GAUGAAUA CUGAUGAG X CGAA IGUAACAA	1686
508	AUGUAUUC A UUGGAUCU	551	AGAUCCAA CUGAUGAG X CGAA IAAUACAU	1687
511	UAUUCAUC U GAUCUUGU	552	ACAAGAUC CUGAUGAG X CGAA IAUGAAUA	1688
520	GUUGGAUC U AACAUGAA	553	UUCAUGUU CUGAUGAG X CGAA IAUCCAAC	1689
528	UUGUAAAC A AAGGGCUU	554	AAGCCCUU CUGAUGAG X CGAA IUUUACAA	1690
539	AAAAGGGC U UUUCAAAA	555	UUUUGAAA CUGAUGAG X CGAA ICCCUUUU	1691
548	UUAUUUUC A UUAACUUC	556	GAAGUÚAA CUGAUGAG X CGAA IAAAAUAA	1692
558	AAAUUAAC U AAUAAGUG	557	CACUUAUU CUGAUGAG X CGAA IUUAAUUU	1693
561	UUAACUUC A AAGUGUAU	558	AUACACUU CUGAUGAG X CGAA IAAGUUAA	1694
581	UAAAAUGC A UUGAUUUC	559	GAAAUCAA CUGAUGAG X CGAA ICAUUUUA	1695
584	AAUGCAAC U AUUUCCUC	560	GAGGAAAU CUGAUGAG X CGAA IUUGCAUU	1696
594	UUGAUUUC C CAUGGCUC	561	GAGCCAUG CUGAUGAG X CGAA IAAAUCAA	1697
595	UGAUUUCC U AUGGCUCA	562	UGAGCCAU CUGAUGAG X CGAA IGAAAUCA	1698
597	AUUUCCUC A GGCUCACA	563	UGUGAGCC CUGAUGAG X CGAA IAGGAAAU	1699
600	UCCUCAAC A UCACAAAU	564	AUJUGUGA CUGAUGAG X CGAA IUUGAGGA	1700
605	AACAUGGC U AAUUUCUA	565	UAGAAAUU CUGAUGAG X CGAA ICCAUGUU	1701
607	CAUGGCUC A UUUCUAUC	566	GAUAGAAA CUGAUGAG X CGAA IAGCCAUG	1702
609	UGGCUCAC A UCUAUCCC	567	GGGAUAGA CUGAUGAG X CGAA IUGAGCCA	1703
616	CAAAUUUC U CAAAUCUU	568	AAGAUUUG CUGAUGAG X CGAA IAAAUUUG	1704
620	UUUCUAUC C UCUUUUCU	569	AGAAAAGA CUGAUGAG X CGAA IAUAGAAA	1705
621	UUCUAUCC C CUUUUCUG	570	CAGAAAAG CUGAUGAG X CGAA IGAUAGAA	1706
622	UCUAUCCC A UUUUCUGA	571	UCAGAAAA CUGAUGAG X CGAA IGGAUAGA	1707

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627 CCCAAAUC U UGAMGAUG 572 CAUCUUCA CUGAUGAG X CGAA IAJUUG 632 AUCUUUCU U AUGAAGAG 573 CUCUUCAU CUGAUGAG X CGAA IAJAWA 659 UUUMAAAC U UGCCAACA 574 UGUUGAG X CGAA IUUUU 662 AAAACUGC A CAACAAGU 575 ACUUGUUG CUGAUGAG X CGAA ICAGU	GAU 1709 AAA 1710 UUU 1711
659 UUUAAAAC U UGCCAACA 574 UGUUGGCA CUGAUGAG X CGAA IUUUU 662 AAAACUGC A CAACAAGU 575 ACUUGUUG CUGAUGAG X CGAA ICAGU	AAA 1710 JUU 1711
662 AAAACUGC A CAACAAGU 575 ACUUGUUG CUGAUGAG X CGAA ICAGU	JUU 1711
664 AACUGCAC U ACAAGUUC 576 GAACUUGU CUGAUGAG X CGAA IUGCAC	3UU 1712
667 UGCACUGC C AGUUCACU 577 AGUGAACU CUGAUGAG X CGAA ICAGUC	3CA 1713
668 GCACUGCC A GUUCACUU 578 AAGUGAAC CUGAUGAG X CGAA IGCAG	JGC 1714
671 CUGCCAAC A CACUUCAU 579 AUGAAGUG CUGAUGAG X CGAA IUUGGG	CAG 1715
677 ACAAGUUC A AUAUAUAA 580 UUAUAUAU CUGAUGAG X CGAA IAACU	JGU 1716
679 AAGUUCAC U AUAUAAAG 581 CUUUAUAU CUGAUGAG X CGAA IUGAA	CUU 1717
682 UUCACUUC A UAAAGCAU 582 AUGCUUUA CUGAUGAG X CGAA IAAGUC	3AA 1718
693 UAUAAAGC A UUUUACUC 583 GAGUAAAA CUGAUGAG X CGAA ICUUUA	AUA 1719
704 AUUUUUAC U UGAGGUGA 584 UCACCUCA CUGAUGAG X CGAA IUAAAA	AAU 1720
706 UUUUACUC U AGGUGAAU 585 AUUCACCU CUGAUGAG X CGAA IAGUAA	AAA 1721
733 UAUAUUAC A AAAAGCUU 586 AAGCUUUU CUGAUGAG X CGAA IUAAU	AUA 1722
744 GUAAAAGC U UAAUACUA 587 UAGUAUUA CUGAUGAG X CGAA ICUUUT	JAC 1723
747 AAAGCUUC U UACUAAGU 588 ACUUAGUA CUGAUGAG X CGAA IAAGCU	JUU 1724
755 UUUAAUAC U AUUUUUCA 589 UGAAAAAU CUGAUGAG X CGAA IUAUU	AAA 1725
767 UAUUUUUC A UUCACCAA 590 UUGGUGAA CUGAUGAG X CGAA IAAAAA	AUA 1726
772 UUCAGGUC U CAAGUAUC 591 GAUACUUG CUGAUGAG X CGAA IACCUC	GAA 1727
775 AGGUCUUC A GUAUCAAA 592 UUUGAUAC CUGAUGAG X CGAA IAAGAC	CCU 1728
777 GUCUUCAC C AUCAAAGU 593 ACUUUGAU CUGAUGAG X CGAA IUGAAC	3AC 1729
778 UCUUCACC A UCAAAGUA 594 UACUUUGA CUGAUGAG X CGAA IGUGAA	AGA 1730
785 CAAGUAUC A AAUAACAC 595 GUGUUAUU CUGAUGAG X CGAA IAUACU	JUG 1731
796 GUAAUAAC A UGAAGUGU 596 ACACUUCA CUGAUGAG X CGAA IUUAUT	JAC 1732
798 AAUAACAC A AAGUGUCA 597 UGACACUU CUGAUGAG X CGAA IUGUUA	AUU 1733
810 GAAGUGUC A UCAAAAUA 598 UAUUUUGA CUGAUGAG X CGAA IACAC	JUC 1734
817 CAUUAUUC A AGUCCACU 599 AGUGGACU CUGAUGAG X CGAA IAAUA	AUG 1735
826 AAAUAGUC C ACUCCUCA 600 UGAGGAGU CUGAUGAG X CGAA IACUA	JUU 1736
827 AAUAGUCC A CUCCUCAC 501 GUGAGGAG CUGAUGAG X CGAA IGACUA	AUU 1737
829 UAGUCCAC U CCUCACAU 602 AUGUGAGG CUGAUGAG X CGAA IUGGAG	CUA 1738
833 CCACUGAC U ACAUCUGU 603 ACAGAUGU CUGAUGAG X CGAA IUCAGU	JGG 1739
835 ACUGACUC C AUCUGUUA 604 UAACAGAU CUGAUGAG X CGAA IAGUCA	AGU 1740
836 CUGACUCC U UCUGUUAU 605 AUAACAGA CUGAUGAG X CGAA IGAGUC	CAG 1741
838 GACUCCUC A UGUUAUCU 606 AGAUAACA CUGAUGAG X CGAA IAGGAC	JUC 1742
840 CUCCUCAC A UUAUCUUA 607 UAAGAUAA CUGAUGAG X CGAA IUGAG	3AG 1743
843 CUCACAUC U UCUUAUUA 608 UAAUAAGA CUGAUGAG X CGAA IAUGUO	GAG 1744
850 CUGUUAUC U AUAAAGAA 609 UUCUUUAU CUGAUGAG X CGAA IAUAAG	CAG 1745
864 UAAAGAAC U GUAGUAAC 610 GUUACUAC CUGAUGAG X CGAA IUUCU	JUA 1746
877 GUAGUAAC U GAAUCUAC 611 GUAGAUUC CUGAUGAG X CGAA IUUACU	JAC 1747
881 UAACUAUC A CUACAUUC 612 GAAUGUAG CUGAUGAG X CGAA IAUAGU	JUA 1748
887 UCAGAAUC U UCUAAAAC 613 GUUUUAGA CUGAUGAG X CGAA IAUUCU	JGA 1749
890 GAAUCUAC A AAAACAGA 614 UCUGUUUU CUGAUGAG X CGAA IUAGAU	ЛUС 1750
894 CUACAUUC U CAGAAAUU 615 AAUUUCUG CUGAUGAG X CGAA IAAUGU	JAG 1751
900 UCUAAAAC A UUGUAUUU 616 AAAUACAA CUGAUGAG X CGAA IUUUUA	AGA 1752
917 AUUUUUUC U CACAUUAA 617 UUAAUGUG CUGAUGAG X CGAA IAAAAA	AAU 1753
922 UUCUAUGC C UAACAUCU 618 AGAUGUUA CUGAUGAG X CGAA ICAUAC	GAA 1754

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Table 25

923 UCUANGEC A AACAUCUU 619 AAGAUGUU CURANGAG X CGAA IGCAUAGA 925 UUBGECCA C ACUCUUUU 620 AABAGANIG CURANGAG X CGAA IGGCAUA 931 ACAUUAAC A UUAAAGUU 621 AACUUUAA CUGAUGAG X CGAA IGUCAAIGG 934 UUBACAUC U AAGUUGAU 622 AUCAACUU CUGAUGAG X CGAA IGUCUAA 954 0936AAUC A UGGAAAAG 623 CUUUUCA CUGAUGAG X CGAA IGUCUAA	1755 1756 1757 1758 1759
931 ACRUUAAC A UUAAAGUU 521 AACUUUAA CUGAUGAG X CGAA IUUAAUGU 934 UUAACAUC U AAGUUGAU 522 AUCAACUU CUGAUGAG X CGAA IAUGUUAA	1757 1758 1759
934 UUAACAUC U AAGUUGAU 622 AUCAACUU CUGAUGAG X CGAA IAUGUUAA	1758 1759
	1759
954 UGAGAAUC A UGGAAAAG 623 CUUUUCCA CUGAUGAG X CGAA IAUUCUCA	
	1000
973 AGUAAGGC C UCUUACAU 624 AUGUAAGA CUGAUGAG X CGAA ICCUUACU	1760
974 GUAAGGCC A CUUACAUA 625 UAUGUAAG CUGAUGAG X CGAA IGCCUUAC	1761
978 GGCCAUAC U CAUAAUAA 626 UUAUUAUG CUGAUGAG X CGAA IUAUGGCC	1762
980 CCAUACUC U UAAUAAAA 627 UUUUAUUA CUGAUGAG X CGAA IAGUAUGG	1763
984 ACUCUUAC A AAAAUUCC 628 GGAAUUUU CUGAUGAG X CGAA IUAAGAGU	1764
996 UAAAAUUC C AAGUAAUU 629 AAUUACUU CUGAUGAG X CGAA IAAUUUUA	1765
997 AAAAUUCC U AGUAAUUU 630 AAAUUACU CUGAUGAG X CGAA IGAAUUUU	1766
1014 AUUUUUUC A AUCACAGA 631 UCUGUGAU CUGAUGAG X CGAA IAAAAAAU	1767
1022 AAAGAAUC A AUUCUAGU 632 ACUAGAAU CUGAUGAG X CGAA IAUUCUUU	1768
1024 AGAAUCAC A UCUAGUAC 633 GUACUAGA CUGAUGAG X CGAA IUGAUUCU	1769
1031 CAGAAUUC U CAUGUAGG 634 CCUACAUG CUGAUGAG X CGAA IAAUUCUG	1770
1037 UCUAGUAC A GGUAAAUC 635 GAUUUACC CUGAUGAG X CGAA IUACUAGA	1771
1050 GGUAAAUC A UCUGUUCU 636 AGAACAGA CUGAUGAG X CGAA IAUUUACC	1772
1057 CAUAAAUC U UAAGACAU 637 AUGUCUUA CUGAUGAG X CGAA IAUUUAUG	1773
1062 AUCUGUUC U CAUAUGAU 638 AUCAUAUG CUGAUGAG X CGAA IAACAGAU	1774
1068 UCUAAGAC A AUCAACAG 639 CUGUUGAU CUGAUGAG X CGAA IUCUUAGA	1775
1076 AUAUGAUC A AUGAGAAC 640 GUUCUCAU CUGAUGAG X CGAA IAUCAUAU	1776
1079 UGAUCAAC A AGAACUGG 641 CCAGUUCU CUGAUGAG X CGAA IUUGAUCA	1777
1089 AUGAGAAC U GUUAAUAU 642 AUAUUAAC CUGAUGAG X CGAA IUUCUCAU	1778
1107 UAUGUGAC A GAUUAGUC 643 GACUAAUC CUGAUGAG X CGAA IUCACAUA	1779
1120 GAUUAGUC A ACUAAUAU 644 AUAUUAGU CUGAUGAG X CGAA IACUAAUC	1780
1125 GUCAUAUC A UAUACUAA 645 UUAGUAUA CUGAUGAG X CGAA IAUAUGAC	1781
1127 CAUAUCAC U UACUAACA 646 UGUUAGUA CUGAUGAG X CGAA IUGAUAUG	1782
1135 UAAUAUAC U ACAGAAUC 647 GAUUCUGU CUGAUGAG X CGAA IUAUAUUA	1783
1139 AUACUAAC A AAUCUAAU 648 AUUAGAUU CUGAUGAG X CGAA IUUAGUAU	1784
1142 CUAACAAC A CUAAUCUU 649 AAGAUUAG CUGAUGAG X CGAA IUUGUUAG	1785
1148 ACAGAAUC U UUCAUUUA 650 UAAAUGAA CUGAUGAG X CGAA IAUUCUGU	1786
1153 AUCUAAUC U UUAAGGCA 651 UGCCUUAA CUGAUGAG X CGAA IAUUAGAU	1787
1156 UAAUCUUC A AGGCACUG 652 CAGUGCCU CUGAUGAG X CGAA IAAGAUUA	1788
1165 UUUAAGGC A AGUGAAUU 653 AAUUCACU CUGAUGAG X CGAA ICCUUAAA	1789
1167 UAAGGCAC U UGAAUUAU 654 AUAAUUCA CUGAUGAG X CGAA IUGCCUUA	1790
1181 GAAUUAUC U UAGAGUUA 655 UAACUCUA CUGAUGAG X CGAA IAUAAUUC	1791
1186 AUCUGAGC U UUACCUAG 656 CUAGGUAA CUGAUGAG X CGAA ICUCAGAU	1792
1195 AGAGUUAC C UUACCAUA 657 UAUGGUAA CUGAUGAG X CGAA IUAACUCU	1793
1196 GAGUUACC U UACCAUAC 658 GUAUGGUA CUGAUGAG X CGAA IGUAACUC	1794
1200 UACCUAGC U AUACUAUA 659 UAUAGUAU CUGAUGAG X CGAA ICUAGGUA	1795
1204 UAGCUUAC C UAUAUCUU 660 AAGAUAUA CUGAUGAG X CGAA IUAAGCUA	1796
1205 AGCUUACC A AUAUCUUU 661 AAAGAUAU CUGAUGAG X CGAA IGUAAGCU	1797
1209 UACCAUAC U CUUUGGAA 662 UUCCAAAG CUGAUGAG X CGAA IUAUGGUA	1798
1215 ACUAUAUC U AAUCAUGA 663 UCAUGAUU CUGAUGAG X CGAA IAUAUAGU	1799
1224 UUGGAAUC A ACCUUAAG 664 CUUAAGGU CUGAUGAG X CGAA IAUUCCAA	1800
1231 CAUGAAAC C GACUUCAG 665 CUGAAGUC CUGAUGAG X CGAA IUUUCAUG	1801

Table 25

1232	AUGAAACC U ACUUCAGA	666	UCUGAAGU CUGAUGAG X CGAA IGUUUCAU	1802
1239	CUUAAGAC U AAUGAUUU	667	AAAUCAUU CUGAUGAG X CGAA IUCUUAAG	1803
1242	AAGACUUC A GAUUUUGC	668	GCAAAAUC CUGAUGAG X CGAA IAAGUCUU	1804
1255	GAUUUUGC A GUCUUCCA	669	UGGAAGAC CUGAUGAG X CGAA ICAAAAUC	1805
1263	AGGUUGUC U UUCCAGCC	670	GGCUGGAA CUGAUGAG X CGAA IACAACCU	1806
1266	UUGUCUUC C CAGCCUAA	671	UUAGGCUG CUGAUGAG X CGAA IAAGACAA	1807
1267	UGUCUUCC A AGCCUAAC	672	GUUAGGCU CUGAUGAG X CGAA IGAAGACA	1808
1271	UUCCAUUC C UAACAUCC	673	GGAUGUUA CUGAUGAG X CGAA IAAUGGAA	1809
1272	UCCAUUCC A AACAUCCA	674	UGGAUGUU CUGAUGAG X CGAA IGAAUGGA	1810
1275	AUUCCAGC C AUCCAAUG	675	CAUUGGAU CUGAUGAG X CGAA ICUGGAAU	1811
1276	UUCCAGCC U UCCAAUGC	676	GCAUUGGA CUGAUGAG X CGAA IGCUGGAA	1812
1280	AGCCUAAC A AUGCAGGC	677	GCCUGCAU CUGAUGAG X CGAA IUUAGGCU	1813
1283	CUAACAUC C CAGGCAAG	678	CUUGCCUG CUGAUGAG X CGAA IAUGUUAG	1814
1284	UAACAUCC A AGGCAAGG	679	CCUUGCCU CUGAUGAG X CGAA IGAUGUUA	1815
1289	UCCAAUGC A AGGAAAAU	680	AUUUUCCU CUGAUGAG X CGAA ICAUUGGA	1816
1293	AUGCAGGC A AAAUAAAA	681	UUUUAUUU CUGAUGAG X CGAA ICCUGCAU	1817
1312	AAGAUUUC C ACAGAAAA	682	UUUUCUGU CUGAUGAG X CGAA IAAAUCUU	1818
1313	AGAUUUCC A CAGAAAAA	683	UUUUUCUG CUGAUGAG X CGAA IGAAAUCU	1819
1319	CCAGUGAC A AAUAUAUU	684	AAUAUAUU CUGAUGAG X CGAA IUCACUGG	1820
1335	AUAUUAUC U UAUUUUUU	685	AAAAAAUA CUGAUGAG X CGAA IAUAAUAU	1821
1337	AUUAUCUC A UUUUUUAA	686	UUAAAAAA CUGAUGAG X CGAA IAGAUAAU	1822
1364	AUGAAUUC U CCAAAUAU	687	AUAUUUGG CUGAUGAG X CGAA IAAUUCAU	1823
1366	GAAUUCUC U AAAUAUUA	688	UAAUAUUU CUGAUGAG X CGAA IAGAAUUC	1824
1368	AUUCUCUC U AUAUUAAC	689	GUUAAUAU CUGAUGAG X CGAA IAGAGAAU	1825
1370	UCUCUCUC C AUUAACUA	690	UAGUUAAU CUGAUGAG X CGAA IAGAGAGA	1826
1371	CUCUCUCC A UUAACUAA	691	UUAGUUAA CUGAUGAG X CGAA IGAGAGAG	1827
1381	AUAUUAAC U AUUAGAUU	692	AAUCUAAU CUGAUGAG X CGAA IUUAAUAU	1828
1410	AAAUGAAC U GGCCCAUC	693	GAUGGGCC CUGAUGAG X CGAA IUUCAUUU	1829
1418	UUGUUGGC C UAUUACAU	694	AUGUAAUA CUGAUGAG X CGAA ICCAACAA	1830
1419	UGUUGGCC C AUUACAUC	695	GAUGUAAU CUGAUGAG X CGAA IGCCAACA	1831
1420	GUUGGCCC A UUACAUCU	696	AGAUGUAA CUGAUGAG X CGAA IGGCCAAC	1832
1423	GGCCCAUC U CAUCUACA	697	UGUAGAUG CUGAUGAG X CGAA IAUGGGCC	1833
1429	UCUAUUAC A CAGCUGAC	698	GUCAGCUG CUGAUGAG X CGAA IUAAUAGA	1834
1432	AUUACAUC U CUGACCCU	699	AGGGUCAG CUGAUGAG X CGAA IAUGUAAU	1835
1435	ACAUCUAC A ACCCUUGA	700	UCAAGGGU CUGAUGAG X CGAA IUAGAUGU	1836
1438	UCUACAGC U CUUGAACA	701	UGUUCAAG CUGAUGAG X CGAA ICUGUAGA	1837
1442	CAGCUGAC C AACAUGGG	702	CCCAUGUU CUGAUGAG X CGAA IUCAGCUG	1838
1443	AGCUGACC C ACAUGGGG	703	CCCCAUGU CUGAUGAG X CGAA IGUCAGCU	1839
1444	GCUGACCC U CAUGGGGG	704	CCCCCAUG CUGAUGAG X CGAA IGGUCAGC	1840
1450	CCUUGAAC A GGUUAGGG	705	CCCUAACC CUGAUGAG X CGAA IUUCAAGG	1841
1467	AGGGGAGC U AUUCGUGG	706	CCACGAAU CUGAUGAG X CGAA ICUCCCCU	1842
1471	GAGCUGAC A GUGGGUCC	707	GGACCCAC CUGAUGAG X CGAA IUCAGCUC	1843
1483	CGUGGGUC C AAUCUUAA	708	UUAAGAUU CUGAUGAG X CGAA IACCCACG	1844
1486	GGGUCCGC A CUUAACUA	709	UAGUUAAG CUGAUGAG X CGAA ICGGACCC	1845
1492	GCAAAAUC U UACCUAAU	710	AUUAGGUA CUGAUGAG X CGAA IAUUUUGC	1846
1497	AUCUUAAC U AAUAGCCU	711	AGGCUAUU CUGAUGAG X CGAA IUUAAGAU	1847
1500	UUAACUAC C AGCCUACU	712	AGUAGGCU CUGAUGAG X CGAA IUAGUUAA	1848

Table 25

1501	UAACUACC U GCCUACUA	713	UAGUAGGC CUGAUGAG X CGAA IGUAGUUA	1849
1508	CUAAUAGC C AUUGACCA	714	UGGUCAAU CUGAUGAG X CGAA ICUAUUAG	1850
1509	UAAUAGCC U UUGACCAU	715	AUGGUCAA CUGAUGAG X CGAA IGCUAUUA	1851
1512	UAGCCUAC U ACCAUAAA	716	UUUAUGGU CUGAUGAG X CGAA IUAGGCUA	1852
1519	CUAUUGAC C ACCUUACU	717	AGUAAGGU CUGAUGAG X CGAA IUCAAUAG	1853
1520	UAUUGACC A CCUUACUG	718	CAGUAAGG CUGAUGAG X CGAA IGUCAAUA	1854
1526	CCAUAAAC C UGAUAACA	719	UGUUAUCA CUGAUGAG X CGAA IUUUAUGG	1855
1527	CAUAAACC U GAUAACAU	720	AUGUUAUC CUGAUGAG X CGAA IGUUUAUG	1856
1531	AACCUUAC U ACAUAAAC	721	GUUUAUGU CUGAUGAG X CGAA IUAAGGUU	1857
1538	CUGAUAAC A CAGUAAAU	722	AUUUACUG CUGAUGAG X CGAA IUUAUCAG	1858
1544	ACAUAAAC A AUUAACAC	723	GUGUUAAU CUGAUGAG X CGAA IUUUAUGU	1859
1555	AAAUUAAC A UUUUGCGU	724	ACGCAAAA CUGAUGAG X CGAA IUUAAUUU	1860
1557	AUUAACAC A UUGCGUGU	725	ACACGCAA CUGAUGAG X CGAA IUGUUAAU	1861
1584	UAUUAUAC A AUUCCUAC	726	GUAGGAAU CUGAUGAG X CGAA IUAUAAUA	1862
1586	UUAUACAC U UCCUACAA	727	UUGUAGGA CUGAUGAG X CGAA IUGUAUAA	1863
1593	CUAUAUUC C AUAAAGUA	728	UACUUUAU CUGAUGAG X CGAA IAAUAUAG	1864
1594	UAUAUUCC U UAAAGUAA	729	UUACUUUA CUGAUGAG X CGAA IGAAUAUA	1865
1597	AUUCCUAC A AGUAAGCU	730	AGCUUACU CUGAUGAG X CGAA IUAGGAAU	1866
1609	AAGUAAGC U AAAAUGUU	731	AACAUUUU CUGAUGAG X CGAA ICUUACUU	1867

Input Sequence = PLN. Cut Site = CH/.

Stem Length = 8 . Core Sequence = CUGAUGAG X CGAA (X = GCCGUUAGGC or other stem II) PLN (Homo sapiens phospholamban (PLN) mRNA.; 1635 bp)

Table 26

Table 26: Human Phospholamban (PLN) G-cleaver Ribozyme and Target Sequence

Substrate	Seq ID	Ribozyme	Rz Seq ID
G UGAUGAUC	732	GAUCAUCA UGAUG GCAUGCACUAUGC GCG AGUAUAGA	1868
UNUACUGU G AUGAUCAC	733	GUGAUCAU UGAUG GCAUGCACUAUGC GCG ACAGUAUA	1869
ACUGUGAU G AUCACAGC	734	GCUGUGAU UGAUG GCAUGCACUAUGC GCG AUCACAGU	1870
UCACAGCU G CCAAGGCU	735	AGCCUUGG UGAUG GCAUGCACUAUGC GCG AGCUGUGA	1871
AUUUGGCU G CCAGCUUU	736	AAAGCUGG UGAUG GCAUGCACUAUGC GCG AGCCAAAU	1872
UNICUCUC G ACCACUUA	737	UAAGUGGU UGAUG GCAUGCACUAUGC GCG GAGAGAAA	1873
GACTUDOCU G UCCUGOUG	738	CAGCAGGA UGAUG GCAUGCACUAUGC GCG AGGAAGUC	1874
ccuguccu e cuaguauc	739	GAUACCAG UGAUG GCAUGCACUAUGC GCG AGGACAGG	1875
ccucacuc e cucaecua	740	UAGCUGAG UGAUG GCAUGCACUAUGC GCG GAGUGAGG	1876
CAACCAUU G AAAUGCCU	741	AGGCAUUU UGAUG GCAUGCACUAUGC GCG AAUGGUUG	1877
AUUGAAAU G CCUCAACA	742	UGUUGAGG UGAUG GCAUGCACUAUGC GCG AUTUCAAU	1878
CAAUTUCU G UCUCAUCU	743	AGAUGAGA UGAUG GCAUGCACUAUGC GCG AGAAAUUG	1879
CUUAAUAU G UCUCUUGC	744	GCAAGAGA UGAUG GCAUGCACUAUGC GCG AUAUUAAG	1880
UGUCUCUU G CUGAUCUG	745	CAGAUCAG UGAUG GCAUGCACUAUGC GCG AAGAGACA	1881
cucuugeu a aucuguau	746	AUACAGAU UGAUG GCAUSCACUAUGC GCG AGCAAGAG	1882
SCUGAUCU G UAUCAUCS	747	CGAUGAUA UGAUG GCAUGCACUAUGC GCG AGAUCAGC	1883
AUCAUCGU G AUGCUUCU	748	AGANGCAU UGAUG GCAUGCACUAUGC GCG ACGAUGAU	1884
AUCGUGAU G CUUCUCUG	749	CAGAGAAG UGAUG GCAUGCACUAUGC GCG AUCACGAU	1885
SCUUCUCU G AAGUUCUG	750	CAGAACUU UGAUG GCAUGCACUAUGC GCG AGAGAAGC	1886
GAAGUUCU G CUACAACC	751	GGUUGUAG UGAUG GCAUGCACUAUGC GCG AGAACUUC	1887
CUAGAUCU G CAGCUUGC	752	GCAAGCUG UGAUG GCAUGCACUAUGC GCG AGAUCUAG	1888
uccascuu s ccacauca	753	UGAUGUGG UGAUG GCAUGCACUAUGC GCG AAGCUGCA	1889
UAAAAUCU G UCAUCCCA	754	UGGGAUGA UGAUG GCAUGCACUAUGC GCG AGAUUUUA	1890
CAUCCCAU G CAGACAGG	755	CCUGUCUS UGAIG GCAUGCACUAUGC GCG AUGGGAUG	1891
ACAAUAUU G UAUAACAG	756	CUGUDADA UGADG GCAUGCACUADGC GCG AADADDGD	1892
CACUUCCU G AGUAGAAG	757	CUUCUACU UGAUG GCAUGCACUAUGC GCG AGGNAGUG	1893
SUUUCUUU G UGAAAAGG	758	CCUUUUCA UGAUG GCAUGCACUAUGC GCG AAAGAAAC	1894
Uncoungu G AAAAGGUC	759	GACCUUUU UGAUG GCAUGCACUAUGC GCG ACAAAGAA	1895

492	AACUUAUU G UUACCAUA	160	UAUGGUAA UGAUG GCAUGCACUAUGC GCG AAUAAGUU	1896
205	UACCAUAU G UAUUCAUC	191	GAUGAAUA UGAUG GCAUGCACUAUGC GCG AUAUGGUA	1897
512	AUUCAUCU G UUGGAUCU	762	AGAUCCAA UGAUG GCAUGCACUAUGC GCG AGAUGAAU	1898
522	UGGAUCUU G UAAACAUG	763	CAUGUUUA UGAUG GCAUGCACUAUGC GCG AAGAUCCA	1899
530	GURAACAU G AAAAGGGC	764	GCCCUIUU UGAUG GCAUGCACUAUGC GCG AUGUUUAC	1900
570	AAAUAAGU G UAUAAAAU	765	AUTUTIANA UGAUG GCAUGCACUAUGC GCG ACUUAUTU	1901
579	UAUAAAAU G CAACUGUU	994	AACAGUUG UGAUG GCAUGCACUAUGC GCG AUUUUAUA	1902
585	AUGCAACU G UUGAUUUC	767	GAAAUCAA UGAUG GCAUGCACUAUGC GCG AGUUGCAU	1903
588	CAACUGUU G AUUUCCUC	768	GAGGAAAU UGAUG GCAUGCACUAUGC GCG AACAGUUG	1904
633	UCUIUUCU G AAGAUGAA	769	UUCAUCUU UGAUG GCAUGCACUAUGC GCG AGAAAAGA	1905
639	CUGAAGAU G AAGAGUUU	170	ANACUCUU UGAUG GCAUGCACUAUGC GCG AUCUUCAG	1906
099	UNAMARCU G CACUGCCA	771	UBGCAGUG UGAUG GCAUGCACUAUGC GCG AGUUUUAA	1907
999	ACUGCACU G CCAACAAG	772	CUUGUUGG UGAUG GCAUGCACUAUGC GCG AGUGCAGU	1908
710	ACUCUUUU G AGGUGAAU	773	AUTICACCU UGAUG GCAUGCACUAUGC GCG AAAAGAGU	1909
715	UNUGAGGU G AAUAUAAU	774	AUJANAUU UGAUG GCAUGCACUAUGC GCG ACCUCAAA	1910
736	AUUACAAU G UAAAAGCU	775	AGCUUUUA UGAUG GCAUGCACUAUGC GCG AUUGUAAU	1911
802	ACACAAAU G AAGUGUCA	176	UGACACUU UGAUG GCAUGCACUAUGC GCG AUUUGUGU	1912
807	AAUGAAGU G UCAUUAUU	777	AAUNAUGA UGAUG GCAUGCACUAUGC GCG ACUUCAUU	1913
830	AGUCCACU G ACUCCUCA	178	UGAGGAGU UGAUG GCALIGCACUAUGC GCG AGUGGACU	1914
844	UCACAUCU G UUAUCUUA	611	UNAGAUNA UGAUG GCAUGCACUAUGC GCG AGAUGUGA	1915
869	AACUAUUU G UAGUAACU	780	AGUJACUA UGAUG GCAUGCACUAUGC GCG AAAUAGUU	1916
907	CAGAAAUU G UAUUUUUU	781	MANANAUA UGAUG GCAUGCACUAUGC GCG AAUUUCUG	1917
920	UUUUCUAU G CCACAUUA	782	UNAUGUGG UGAUG GCAUGCACUAUGC GCG AUAGAAAA	1918
944	UDAAAGUU G AUGAGAAU	783	AUTOCICAU UGAUG GCAUGCACUAUGC GCG NACUUUNA	1919
947	AAGUUGAU G AGAAUCAA	784	UUGAUUCU UGAUG GCAUGCACUAUGC GCG AUCAACUU	1920
1039	UAGUACAU G UAGGUAAA	785	UUUACCUA UGAUG GCAUGCACUAUGC GCG AUGUACUA	1921
1058	AUAAAUCU G UUCUAAGA	786	UCUUAGAA UGAUG GCAUGCACUAUGC GCG AGAUUUAU	1922
1072	AGACAUAU G AUCAACAG	787	CUGUUGAU UGAUG GCAUGCACUAUGC GCG AUAUGUCU	1923
1083	CAACAGAU G AGAACUGG	788	CCAGUICU UGAUG GCAUGCACUAUGC GCG AUCUGUIG	1924
1102	GUUAAUAU G UGACAGUG	789	CACUGUCA UGAUG GCAUGCACUAUGC GCG AUAUUAAC	1925
1104	UNAUAUGU G ACAGUGAG	190	CUCACUGU UGAUG GCAUGCACUAUGC GCG ACAUAUUA	1926

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1927	1928	1929	1930	1931	1932	1933	1934	1935	1936	1937	1938	1939	1940	1941	1942	1943	1944	1945	1946	1947	1948	1949	1950
ACUGUCAC	AGUGCCUU	ACUACAGU	AGAUAAUU	* AUGAUUCC	AUUCUGAA	. AAAAUCAU	S AACCUGCA	S AUUGGAUG	ACUGGAAA	NAUAUNU S	S AAAUAUA	AUUUCAAA	3 AAGUUCAU	3 AGCUGUAG	AAGGGUCA	* AGCUCCCC	GGACCCAC	3 AAUAGUAG	3 AGUAAGGU	AAAAUAUG	3 ACGCAAAA	3 AUAUAACA	3 AUTUUCUC
ACUAAUCU UGAUG GCAUGCACUAUGC GCG ACUGUCAC	AUUCACUA UGAUG GCAUGCACUAUGC GCG AGUGCCUU	AGAUAAUU UGAUG GCAUGCACUAUGC GCG ACUACAGU	CUCUAGCU UGAUG GCAUGCACUAUGC GCG AGAUAAUU	UAAGGUUU UGAUG GCAUGCACUAUGC GCG AUGAUUCC	UGCAAAAU UGAUG GCAUGCACUAUGC GCG AUUCUGAA	ACAACCUG UGAUG GCAUGCACUAUGC GCG AAAAUCAU	AUGGAAGA UGAUG GCAUGCACUAUGC GCG AACCUGCA	CUUGCCUG UGAUG GCAUGCACUAUGC GCG AUUGGAUG	UUUUCUGU UGAUG GCAUGCACUAUGC GCG ACUGGAAA	AGAGAAUU UGAUG GCAUGCACUAUGC GCG AUAUAUUU	GUUCAUUU UGAUG GCAUGCACUAUGC GCG AAAAUAUA	AACAAGUU UGAUG GCAUGCACUAUGC GCG AUUUCAAA	UGGGCCAA UGAUG GCAUGCACUAUGC GCG AAGUUCAU	UCAAGGGU UGAUG GCAUGCACUAUGC GCG AGCUGUAG	CCCAUGUU UGAUG GCAUGCACUAUGC GCG AAGGGUCA	CGAAUUGU UGAUG GCAUGCACUAUGC GCG AGCUCCCC	AGAUUTUG UGAUG GCAUGCACUAUGC GCG GGACCCAC	UUUAUGGU UGAUG GCAUGCACUAUGC GCG AAUAGUAG	UAUGUUAU UGAUG GCAUGCACUAUGC GCG AGUAAGGU	AUAACACG UGAUG GCAUGCACUAUGC GCG AAAAUAUG	ACAUAUAA UGAUG GCAUGCACUAUGC GCG ACGCAAAA	GUAUAAUA UGAUG GCAUGCACUAUGC GCG AUAUAACA	CUARAUMA UGAUG GCAUGCACUAUGC GCG AUTUUCUC
ACUAAUCU UGAUG G	AUUCACUA UGAUG G	AGAUAAUU UGAUG C	CUCUAGCU UGAUG G	UAAGGUUU UGAUG	UGCAAAAU UGAUG O	ACAACCUG UGAUG O	AUGGRAGA UGAUG	CUUGCCUG UGAUG	UUUUCUGU UGAUG (AGAGAAUU UGAUG	GUUCAUUU UGAUG (AACAAGUU UGAUG	UGGGCCAA UGAUG	UCAAGGGU UGAUG	CCCAUGUU UGAUG (CGAAUUGU UGAUG C	AGAUUTUG UGAUG (UUUAUGGU UGAUG (UAUGUUAU UGAUG	AUAACACG UGAUG	ACAUAUAA UGAUG	GUAUAAUA UGAUG (CUAAAUAA UGAUG
191	792	793	794	795	796	797	798	199	800	801	802	803	804	805	908	807	808	809	810	811	812	813	814
GUGACAGU G AGAUUAGU	AAGGCACU G UAGUGAAU	ACUGUAGU G AAUUAUCU	AAUUAUCU G AGCUAGAG	GGAAUCAU G AAACCUUA	UUCAGAAU G AUUUUGCA	AUGAUUUU G CAGGUUGU	UGCAGGUU G UCUUCCAU	CAUCCAAU G CAGGCAAG	UUUCCAGU G ACAGAAAA	AAAUAUAU G AAUUCUCU	UAUAUUUU G AAAUGAAC	UUUGAAAU G AACUUGUU	AUGAACUU G UUGGCCCA	CUACAGCU G ACCCUUGA	UGACCCUU G AACAUGGG	GGGGAGCU G ACAAUUCG	GUGGGUCC G CAMMAUCU	CUACUAUU G ACCAUAAA	ACCUUACU G AUAACAUA	CAUAUUUU G CGUGUUAU	UNUUGCGU G UNAUAUGU	UGUUAUAU G UAUUAUAC	GAGAAAU G UUAUUUAG
1110	1168	1173	1182	1226	1247	1253	1260	1287	1316	1358	1401	1406	1412	1439	1446	1468	1484	1516	1532	1564	1568	1575	1619

Input Sequence = PLN. Cut Site = YGM or UG/U.
Stem Length = 8. Core Sequence = UGAUG GCAUGCACUAUGC GCG
PLN (Homo sapiens phospholamban (PLN) mRNA; 1635 bp)

Table 27: Human Phospholamban (PLN) zinzyme Ribozyme and Target Sequence

3	Substrate	Seq ID	Ribozyme	Rz Seq ID
64	UCUAUACU G UGAUGAUC	732	GAUCAUCA GCCGAAAGGCGAGUCAAGGUCU AGUAUAGA	1981
19	UCACAGCU G CCAAGGCU	735	AGCCUUGG GCCGAAGGCGAGUCAAGGUCU AGCUGUGA	1952
121	AUUUGGCU G CCAGCUUU	736	AAAGCUGG GCCGAAAGGCGAGUCAAGGUCU AGCCAAAU	1953
168	GACUUCCU G UCCUGCUG	738	CAGCAGGA GCCGAAAGGCGAGUCAAGGUCU AGGAAGUC	1954
173	ceneuceu e eugenaue	739	GAUACCAG GCCGAAAGGCGAGUCAAGGUCU AGGACAGG	1955
207	CCUCACUC G CUCAGCUA	740	UNGCUGAG GCCGAAAGGCGAGGUCAAGGUCU GAGUGAGG	1956
241	AUUGAAAU G CCUCAACA	742	UGUUGAGG GCCGAAAGGCGAGUCAAGGUCU AUUUCAAU	1957
288	CAAUTUCU G UCUCAUCU	743	AGNUGAGA GCCGAAAGGCGAGUCAAGGUCU AGAAAUUG	1958
303	CUUAAUAU G UCUCUUGC	744	GCAAGAGA GCCGAAAGGCGAGUCAAGGUCU AUAUUAAG	1959
310	UGUCUCUU G CUGAUCUG	745	CAGAUCAG GCCGAAAGGCGAGUCAAGGUCU AAGAGACA	1960
318	GCUGAUCU G UAUCAUCG	747	CGAUGAUA GCCGAAAGGCGAGUCAAGGUCU AGAUCAGC	1961
331	AUCGUGAU G CUUCUCUG	749	CAGAGAAG GCCGAAAGGCGAGUCAAGGUCU AUCACGAU	1962
347	GAAGUUCU G CUACAACC	751	GGUUGUAG GCCGAAAGGCGAGUCAAGGUCU AGAACUUC	1963
365	CUAGAUCU G CAGCUUGC	752	GCAAGCUG GCCGAAAGGCGAGUCAAGGUCU AGAUCUAG	1964
372	UGCAGCUU G CCACAUCA	753	UGAUGUGG GCCGAAAGGCGAGUCAAGGUCU AAGCUGCA	1965
392	UNANAUCU G UCAUCCCA	754	UGGGAUGA GCCGAAGGCGAGUCAAGGUCU AGAUUUUA	1966
402	CAUCCCAU G CAGACAGG	755	CCUGUCUG GCCGAAAGGCGAGUCAAGGUCU AUGGGAUG	1961
422	ACAAUAUU G UAUAACAG	756	CUGUDADA GCCGAAAGGCGAGUCAAGGUCU AADAUUGU	1968
459	GUUUCUUU G UGAAAGG	758	CCUUUUCA GCCGAAAGGCGAGUCAAGGUCU AAAGAAAC	1969
492	AACUUAUU G UUACCAUA	260	UNUGGUAA GCCGAAAGGCGAGUCAAGGUCU AAUAAGUU	1970
502	UACCAUAU G UAUUCAUC	761	GAUGAAUA GCCGAAAGGCGAGUCAAGGUCU AUAUGGUA	1971
512	AUUCAUCU G UNGGAUCU	762	AGAUCCAA GCCGAAAGGCGAGUCAAGGUCU AGAUGAAU	1972
522	UGGAUCUU G UAAACAUG	763	CAUGUUUA GCCGAAAGGCGAGUCAAGGUCU AAGAUCCA	1973
570	AAAUAAGU G UAUAAAAU	765	AUDUDADA GCCGAAAGGCGAGUCAAGGUCU ACUDAUDU	1974
579	UNUADADU G CAACUGUU	994	AACAGUUG GCCGAAAGGCGAGUCAAGGUCU AUUUUAUA	1975
585	AUGCAACU G UUGAUUUC	167	GAAAUCAA GCCGAAAGGCGAGUCAAGGUCU AGUUGCAU	1976
099	UUAAAACU G CACUGCCA	171	UGGCAGUG GCCGAAAGGCGAGGUCU AGUUUUAA	1977
200	CARCAGO O TOROGONA	222	AND ACCOUNTS A REPORT OF A PROPERTY OF A PRO	0000

736	AUUACAAU G UAAAAGCU	775	AGCUUUUA GCCGAAAGGCGAGUCAAGGUCU AUUGUAAU	1979
807	AAUGAAGU G UCAUUAUU	117	AAUAAUGA GCCGAAAGGCGAGUCAAGGUCU ACUUCAUU	1980
844	UCACAUCU G UDAUCUUA	179	UAAGAUAA GCCGAAAGGCGAGUCAAGGUCU AGAUGUGA	1981
869	AACUAUUU G UAGUAACU	780	AGUUACUA GCCGAAAGGCGAGUCAAGGUCU AAAUAGUU	1982
907	CAGAAAUU G UAUUUUUU	781	AAAAAUA GCCGAAAGGCGAGUCAAGGUCU AAUUUCUG	1983
920	UNUUCUAU G CCACAUUA	782	UAAUGUGG GCCGAAAGGCGAGUCAAGGUCU AUAGAAAA	1984
1039	UAGUACAU G UAGGUAAA	785	UUJACCUA GCCGAAAGGCGAGUCAAGGUCU AUGUACUA	1985
1058	AUAAAUCU G UUCUAAGA	786	UCUUAGAA GCCGAAAGGCGAGUCAAGGUCU AGAUUUAU	1986
1102	GUUAAUAU G UGACAGUG	789	CACUGUCA GCCGAAAGGCGAGUCAAGGUCU AUAUUAAC	1987
1168	AAGGCACU G UAGUGAAU	792	AUUCACUA GCCGAAAGGCGAGUCAAGGUCU AGUGCCUU	1988
1253	AUGAUUUU G CAGGUUGU	197	ACAACCUG GCCGAAAGGCGAGUCAAGGUCU AAAAUCAU	1989
1260	UGCAGGUU G UCUUCCAU	798	AUGGAAGA GCCGAAAGGCGAGUCAAGGUCU AACCUGCA	1990
1287	CAUCCAAU G CAGGCAAG	199	CUIGCCUG GCCGAAAGGCGAGUCAAGGUCU AUUGGAUG	1991
1412	AUGAACUU G UUGGCCCA	804	UGGGCCAA GCCGAAAGGCGAGUCAAGGUCU AAGUUCAU	1992
1484	GUGGGUCC G CAAAAUCU	808	AGAUTUUG GCCGAAAGGCGAGUCAAGGUCU GGACCCAC	1993
1564	CAUAUUUU G CGUGUUAU	811	AUAACACG GCCGAAAGGCGAGUCAAGGUCU AAAAUAUG	1994
1568	UNUUGCGU G UNAUAUGU	812	ACAUAUAA GCCGAAAGGCGAGUCAAGGUCU ACGCAAAA	1995
1575	UGUNAUAU G NAUNANAC	813	GUAUAAUA GCCGAAAGGCGAGUCAAGGUCU AUAUAACA	1996
1619	GAGAAAAU G UUAUUUAG	814	CUANAUAA GCCGAAAGGCGAGUCAAGGUCU AUUUUCUC	1997
21	ACUCCCCA G CUANACAC	815	GUGUUUAG GCCGAAAGGCGAGUCAAGGUCU UGGGGAGU	1998
32	AAACACCC G DAAGACUU	816	AAGUCUUA GCCGAAAGGCGAGUCAAGGUCU GGGUGUUU	1999
9/	UGAUCACA G CUGCCAAG	817	CUUGGCAG GCCGAAGGCGAGUCAAGGUCU UGUGAUCA	2000
82	CUGCCAAG G CUACCUAA	818	UNAGGUAG GCCGAAAGGCGAGUCAAGGUCU CUUGGCAG	2001
103	AGAAGACA G UDAUCUCA	819	UGAGAUAA GCCGAAAGGCGAGUCAAGGUCU UGUCUUCU	2002
118	CAUAUTUG G CUGCCAGC	820	GCUGGCAG GCCGAAAGGCGAGUCAAGGUCU CAAAUAUG	2003
125	GGCUGCCA G CUUUUNUAU	821	AUAAAAAG GCCGAAAGGCGAGUCAAGGUCU UGGCAGCC	2004
177	uccuecue e naucause	822	CCAUGAUA GCCGAAAGGCGAGUCAAGGUCU CAGCAGGA	2005
191	UGGAGAAA G UCCAAUAC	823	GUAUUGGA GCCGAAAGGCGAGUCAAGGUCU UUUCUCCA	2006
212	CUCGCUCA G CUAUAAGA	824	UCUJAJAG GCCGAAAGGCGAGUCAAGGUCU UGAGCGAG	2007
224	UAAGAAGA G CCUCAACC	825	GGUUGAGG GCCGAAAGGCGAGUCAAGGUCU UCUUCUUA	2008
251	CUCAACAA G CACGUCAA	826	UNGACGUG GCCGAAAGGCGAGUCAAGGUCU UUGUUGAG	2009

2040

GAGUAUGG GCGGAAAGGCGAGUCU CUIACUUU
AAAAAUUA GCGGAAAGGCGAGUCAAGGUCU UUAAAAGG
UACAUGUA GCGGAAAGGCGAGUCAAGGUCU UAGAAUUC

2035

CUCAUCAA GCCGAAAGGCBAGUCAAGGUCU UUUAAAAG UUUCCAUA GCCGAAAGGCBAGUCAAGGUCU UUGAUUCU UGGCCUUA GCCGAAAGGCBAGUCAAGGUCA UUUUCCAU

852 854 854 855 856

CUUUUAAA G UUGAUGAAA AGAAACAA G UAAGGCCA AAAGUAAG G CCAUACUC CCUUUUAA G UAAUUUUU GAAUUCUA G UACAUGUA

> 956 966 971 1003

941

2036 2037 2038 2039

2034	GAUAGUUA GCCGAAAGGCGAGUCAAGGUCU UACAAAUA	851	UAUUUGUA G UAACUAUC	872
2033	UCAGUGGA GCCGAAAGGCGAGUCAAGGUCU UAUUUUGA	850	UCAAAAUA G UCCACUGA	823
2032	UAAUGACA GCCGAAAGGCGAGUCAAGGUCU UUCAUUUG	849	CAAAUGAA G UGUCAUUA	805
2031	UGUJAUDA GCCGAAAGGCGAGUCAAGGUCU UUUGAUAC	848	GUAUCAAA G UAAUAACA	788
2030	CUUJGAUA GCCGAAAGGCGAGUCAAGGUCU UJGGUGAA	847	UUCACCAA G UAUCAAAG	780
2029	GGUGAAGA GCCGAAAGGCGAGUCAAGGUCU CUGAAAAA	846	UUUUUCAG G UCUUCACC	769
2028	GAAAAAUA GCCGAAAAGGCGAGUCAAGGUCU UUAGUAUU	845	AAUACUAA G UAUUUUUC	758
2027	UAAAGAAG GCCGAAAGGCGAGUCAAGGUCU UUUUACAU	844	AUGUAAAA G CUUCUUUA	742
2026	UNUAUUCA GCCGAAAGGCGAGUCAAGGUCU CUCAAAAG	843	CUUUUGAG G UGAAUAUA	713
2025	AAAUAAUG GCCGAAAGGCGAGUCAAGGUCU UUUAUAUA	842	UAUAUAAA G CAUUAUUU	169
2024	GAAGUGAA GCCGAAAGGCGAGUCAAGGUCU UUGUUGGC	841	GCCAACAA G UUCACUUC	673
2023	UUUUAAAA GCCGAAAGCCGAGUCAAGGUCU UAAACUCU	840	AGAGUUUA G UUUUAAAA	649
2022	AAACUAAA GCCGAAAGGCGAGUCAAGGUCU UCUUCAUC	839	GAUGAAGA G UUUAGUUU	644
2021	UUUGUGAG GCCGAAAGGCGAGUCAAGGUCU CAUGUUGA	838	UCAACAUG G CUCACAAA	603
2020	UUUAUACA GCCGAAGCGAGUCAAGGUCU UUAUUUUG	837	CAAAAUAA G UGUAUAAA	268
2019	AAAUAAAG GCCGAAAGGCGAGUCAAGGUCU CCUUUUCA	836	UGAAAAGG G CUUUAUUU	537
2018	AAUCUUGA GCCGAAAGGCGAGUCAAGGUCU CUUUUCAC	835	GUGAAAAG G UCAAGAUU	467
2017	CAAAGAAA GCCGAAAGGCGAGUCAAGGUCU UCUUCUAC	834	GUAGAAGA G UJUCUUUG	451
2016	CUCUUCUA GCCGAAAGGCGAGUCAAGGUCU UCAGGAAG	833	CUUCCUGA G DAGAAGAG	443
2015	AUTUDAAG GCCGAAAGGCGAGUCAAGGUCU UGAUGUGG	832	CCACAUCA G CUUAAAAU	381
2014	GUGGCAAG GCCGAAAGGCGAGUCAAGGUCU UGCAGAUC	831	GAUCUGCA G CUUGCCAC	368
2013	UAGCAGAA GCCGAAAGGCGAGUCAAGGUCU UUCAGAGA	830	UCUCUGAA G UUCUGCUA	342
2012	AAGCAUCA GCCGAAAGGCGAGUCAAGGUCU GAUGAUAC	829	GUAUCAUC G UGAUGCUU	326
2011	UUCUGUAG GCCGAAAGCCGAGUCAAGGUCU UUUUGACG	828	CGUCAAAA G CUACAGAA	262
2010	GCUUUUGA GCCGAAAGGCGAGUCAAGGUCU GUGCUUGU	827	ACAAGCAC G UCAAAAGC	255

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1043	ACAUGUAG G UAAAUCAU	858	AUGAUTUNA GCCGAAAGGCGAGUCAAGGUCU CUACAUGU	2041
1001	GAGAACUG G UGGUUAAU	859	AUUAACCA GCCGAAAGGCGAGUCAAGGUCU CAGUUCUC	2042
1094	AACUGGUG G UUAAUAUG	860	CAUAUUAA GCCGAAAGGCGAGUCAAGGUCU CACCAGUU	2043
1108	AUGUGACA G UGAGAUUA	198	UNAUCUCA GCCGAAAGGCGAGUCAAAGGUCU UGUCACAU	2044
1117	UGAGAUUA G UCAUAUCA	862	UGAUAUGA GCCGAAAGGCGAGUCAAGGUCU UAAUCUCA	2045
1163	CAUUUAAG G CACUGUAG	863	CUACAGUG GCCGAAAGGCGAGUCAAGGUCU CUUAAAUG	2046
1111	GCACUGUA G UGAAUUAU	864	AUAAUUCA GCCGAAAGGCGAGUCAAGGUCU UACAGUGC	2047
1184	UNAUCUGA G CUAGAGUU	865	AACUCUAG GCCGAAAGGCGAGUCAAGGUCU UCAGAUAA	2048
1190	GAGCUAGA G UUACCUAG	998	CUAGGUAA GCCGAAAGGCGAGUCAAGGUCU UCUAGCUC	2049
1198	GUUACCUA G CUUACCAU	867	AUGGUAAG GCCGAAAGGCGAGUCAAGGUCU UAGGUAAC	2050
1257	UUUUGCAG G UUGUCUUC	898	GAAGACAA GCCGAAAGGCGAGUCAAGGUCU CUGCAAAA	2051
1273	CCAUUCCA G CCUAACAU	869	AUGUDAGG GCCGAAAGGCGAGUCAAGGUCU UGGAAUGG	2022
1291	CAAUGCAG G CAAGGAAA	870	UUUCCUUG GCCGAAAGGCGAGUCAAGGUCU CUGCAUUG	2053
1314	GAUUUCCA G UGACAGAA	871	UUCUGUCA GCCGAAAGGCGAGUCAAGGUCU UGGAAAUC	2054
1339	UAUCUCAA G UAUTUTUTU	872	AAAAAAUA GCCGAAAGGCGAGUCAAGGUCU UUGAGAUA	2055
1416	ACUUGUUG G CCCAUCUA	873	UAGAUGGG GCCGAAAGGCGAGUCAAGGUCU CAACAAGU	2056
1436	CAUCUACA G CUGACCCU	874	AGGGUCAG GCCGAAAGGCGAGUCAAGGUCU UGUAGAUG	2057
1456	ACAUGGGG G UUAGGGGA	875	UCCCCUAA GCCGAAAGGCGAGUCAAGGUCU CCCCAUGU	2058
1465	UNAGGGGA G CUGACAAU	876	AUTGUCAG GCCGAAAGGCGAGUCAAGGUCU UCCCCUAA	2059
1476	GACAAUUC G UGGGUCCG	877	CGGACCCA GCCGAAAGGCGAGUCAAGGUCU GAAUUGUC	2060
1480	AUUCGUGG G UCCGCAAA	878	UUUGCGGA GCCGAAAGGCGAGUCAAGGUCU CCACGAAU	2061
1506	ACCUANUA G CCUACUAU	879	AUAGUAGG GCCGAAAGGCGAGUCAAGGUCU UAUUAGGU	2902
1545	CAUAAACA G UAAAUUAA	880	UUAAUUUA GCCGAAAGGCGAGUCAAGGUCU UGUUUAUG	2063
1566	UAUUUUGC G UGUUAUAU	881	AUAUAACA GCCGAAAGGCGAGUCAAGGUCU GCAAAAUA	2064
1603	ACAAUAAA G UAAGCUAG	882	CUAGCUUA GCCGAAAGGCGAGUCAAGGUCU UUUAUUGU	2065
1607	HAAAGHAA G CHAGAGAA	883	INCUCUAG GCCGAAAGGCGAGUCAAGGUCU UUACUUUA	2066

Input Sequence = PLN. Cut Site = G/Y
Stem Length = 8. Core Sequence = GCogaaagGCGaGuCaaGGuCu
PLN (Homo saplens phospholamban (PLN) mRNA; 1635 bp)

Table 28: Human Phospholamban (PLN) DNAzyme and Target Sequence

Pos	Substrate	Seq ID	Ribozyme	Rz Seq ID
44	GACUUCAU A CAACACAA	6	TTGTGTTG GGCTAGCTACAACGA ATGAAGTC	2067
54	AACACAAU A CUCUAUAC	7	GTATAGAG GGCTAGCTACAACGA ATTGTGTT	2068
59	AAUACUCU A UACUGUGA	9	TCACAGTA GGCTAGCTACAACGA AGAGTATT	2069
61	UACUCUAU A CUGUGAUG	10	CATCACAG GGCTAGCTACAACGA ATAGAGTA	2070
88	CCAAGGCU A CCUAAAAG	12	CTTTTAGG GGCTAGCTACAACGA AGCCTTGG	2071
106	AGACAGUU A UCUCAUAU	15	· ATATGAGA GGCTAGCTACAACGA AACTGTCT	2072
113	UAUCUCAU A UUUGGCUG	18	CAGCCAAA GGCTAGCTACAACGA ATGAGATA	2073
132	AGCUUUUU A UCUUUCUC	25	GAGAAAGA GGCTAGCTACAACGA AAAAAGCT	2074
179	CUGCUGGU A UCAUGGAG	39	CTCCATGA GGCTAGCTACAACGA ACCAGCAG	2075
198	AGUCCAAU A CCUCACUC	42	GAGTGAGG GGCTAGCTACAACGA ATTGGACT	2076
215	GCUCAGCU A UAAGAAGA	46	TCTTCTTA GGCTAGCTACAACGA AGCTGAGC	2077
265	CAAAAGCU A CAGAAUCU	52	AGATTCTG GGCTAGCTACAACGA AGCTTTTG	2078
274	CAGAAUCU A UUUAUCAA	54	TTGATAAA GGCTAGCTACAACGA AGATTCTG	2079
278	AUCUAUUU A UCAAUUUC	57	GAAATTGA GGCTAGCTACAACGA AAATAGAT	2080
301	AUCUUAAU A UGUCUCUU	67	AAGAGACA GGCTAGCTACAACGA ATTAAGAT	2081
320	UGAUCUGU A UCAUCGUG	72	CACGATGA GGCTAGCTACAACGA ACAGATCA	2082
350	GUUCUGCU A CAACCUCU	80	AGAGGTTG GGCTAGCTACAACGA AGCAGAAC	2083
419	AAAACAAU A UUGUAUAA	91	TTATACAA GGCTAGCTACAACGA ATTGTTTT	2084
424	AAUAUUGU A UAACAGAC	93	GTCTGTTA GGCTAGCTACAACGA ACAATATT	2085
489	UAAAACUU A UUGUUACC	108	GGTAACAA GGCTAGCTACAACGA AAGTTTTA	2086
495	UUAUUGUU A CCAUAUGU	111	ACATATGG GGCTAGCTACAACGA AACAATAA	2087
500	GUUACCAU A UGUAUUCA	112	TGAATACA GGCTAGCTACAACGA ATGGTAAC	2088
504	CCAUAUGU A UUCAUCUG	113	CAGATGAA GGCTAGCTACAACGA ACATATGG	2089
542	AGGGCUUU A UUUUCAAA	123	- TTTGAAAA GGCTAGCTACAACGA AAAGCCCT	2090
572	AUAAGUGU A UAAAAUGC	133	GCATTTTA GGCTAGCTACAACGA ACACTTAT	2091
617	AAAUUUCU A UCCCAAAU	144	ATTTGGGA GGCTAGCTACAACGA AGAAATTT	2092
684	CACUUCAU A UAUAAAGC	162	GCTTTATA GGCTAGCTACAACGA ATGAAGTG	2093
686	CUUCAUAU A UAAAGCAU	163	ATGCTTTA GGCTAGCTACAACGA ATATGAAG	2094
696	AAAGCAUU A UUUUUACU	166	AGTAAAAA GGCTAGCTACAACGA AATGCTTT	2095
702	UUAUUUUU A CUCUUUUG	171	CAAAAGAG GGCTAGCTACAACGA AAAAATAA	2096
719	AGGUGAAU A UAAUUUAU	176	ATAAATTA GGCTAGCTACAACGA ATTCACCT	2097
726	UAUAAUUU A UAUUACAA	180	TTGTAATA GGCTAGCTACAACGA AAATTATA	2098
728	UAAUUUAU A UUACAAUG	181	CATTGTAA GGCTAGCTACAACGA ATAAATTA	2099
731	UUUAUAUU A CAAUGUAA	183	TTACATTG GGCTAGCTACAACGA AATATAAA	2100
753	UCUUUAAU A CUAAGUAU	190	ATACTTAG GGCTAGCTACAACGA ATTAAAGA	2101
760	UACUAAGU A UUUUUCAG	192	CTGAAAAA GGCTAGCTACAACGA ACTTAGTA	2102
782	CACCAAGU A UCAAAGUA	201	TACTTTGA GGCTAGCTACAACGA ACTTGGTG	2103
813	GUGUCAUU A UUCAAAAU	207	ATTTTGAA GGCTAGCTACAACGA AATGACAC	2104
847	CAUCUGUU A UCUUAUUA	216	TAATAAGA GGCTAGCTACAACGA AACAGATG	2105
852	GUUAUCUU A UUAUAAAG	219	CTTTATAA GGCTAGCTACAACGA AAGATAAC	2106
855	AUCUUAUU A UAAAGAAC	221	GTTCTTTA GGCTAGCTACAACGA AATAAGAT	2107
865	AAAGAACU A UUUGUAGU	223	ACTACAAA GGCTAGCTACAACGA AGTTCTTT	2108
878	UAGUAACU A UCAGAAUC	228	GATTCTGA GGCTAGCTACAACGA AGTTACTA	2109
888	CAGAAUCU A CAUUCUAA	231	TTAGAATG GGCTAGCTACAACGA AGATTCTG	2110

Table 28

999 GAAAJUUJ A UUUUUUGU 236 AGAAAAAA GUTTACCTACAACGA ACANTTC 2111 918 UUUUUUGU A UGGAAAAA 243 ATTGGGCA GCTGACTCAACGA ACAATTC 2113 976 AAGGCAAU A CUCUUACA 255 TGTAAGGA GCTGACTCAACGA ACTGATT 2113 976 AAGGCAAU A CUCUUACA 255 TGTAAGGA GCTTACCTACAACGA ACTGACT 2114 978 AUACUCUU A CAUAAUAA 258 TGTATATGA GCCTTACCAACGA AGGATT 2114 979 AUACUCUU A CAUAAUAA 258 TGTATATGA GCCTTACCAACGA AAGGATT 2115 1035 AUTCUTACU A CAUGUAGG 279 CCTCACTA GCCTTACCAACGA AAGGATT 2116 1070 UAAGCAU A UGAUCAAC 287 CTTCACTA GCCTTACCAACGA AAGGATT 2116 1100 UGAGUAAU A UGUCAACA 295 CTTCACTA GCCTTACCAACGA AAGATTA 2117 1110 UGACUAAA U UGCAUAAC 298 TTTTATGA GCCTACCTACAACGA ATGACTTA 2117 1121 UUAGUCAU A UCACUAAC 299 TTTTATGA GCCTACCTACAACGA ATTAACCA 2118 1122 UUAGUCAU A UCACACA 299 TTTTATGA GCCTACTACAACGA ATTAACCA 2119 1133 ACUAAUAU A CUACACA 299 TTTTATGA GCCTACTACAACGA ATTAACTA 2120 1139 AUGAGAU A UCUAGACA 299 TTTTATGA GCCTACTACAACGA ATTAACTA 2121 1139 AUGAGAUU A UCUAGACA 299 TTTTATGA GCCTACTACAACGA ATTCACT 2122 1139 CUAGAGUU A CUAGACA 298 TTTTATGA GCCTACTACAACGA ATTCACT 2122 1202 CCUAGCUU A CCUAGCUU 315 AAGCTAGA GCCTACCACCAA AACTCAAC 2124 1207 CUULACCAU A UCUAUGUU 315 AAGATTATGA GCCTACCTACAACGA AACTCAAC 2124 1207 CUULACCAU A UCUAUGAC 318 TAGTATGA GCCTACCTACAACGA AACTCAAC 2124 1207 CUULACCAU A UCUAUGAC 320 CAAAGATA GCCTACCTACAACGA ACTTCAAC 2125 1212 CAUACUAU A UCUCUAGA 321 TAGTATGA GCCTACCTACAACGA ACTTCAAC 2126 1212 CAUACUAU A UCUCUAGA 321 TAGTATGA GCCTACCTACAACGA ACTTTATT 2127 1227 CAUACUAU A UCUCUAGA 321 TAGTATGA GCCTACCTACAACGA ATTATTT 2129 1228 AAAAAUAU A UUAUAUCU 348 ACTTGAGA GCCTACCTACAACGA ATTATTT 2129 1239 AAAAAUAU A UUAUAUCU 348 ACTTGAGA GCCTACCTACAACGA ATTATTTT 2129 1231 AUGAGAUU A UUACAACA 396 TAGTATA GCCTACCTACAACGA ATTATTTT 2121 1231						
958 ANICANGU A UGGANANG 253 CTTTTCCA GGCTAGCTACAACGA ACTGATT 2113 976 ANGCCAU A CUCUURCA 255 TGTAAGGG GGCTAGCTACAACGA ATGGCCTT 2114 9782 AUGUCUU A CAUJAUJAN 255 TGTAAGGG GGCTAGCTACAACGA ATGGCCTT 2114 1035 AUJCULGU A CAUJAUJAN 255 TGTAAGGG GGCTAGCTACAACGA AAGGATT 2116 1079 UAAGACAU A UGUGACACA 287 GCTAGCTACAACGA AAGGATT 2116 1070 UAAGACAU A UGUGACACA 291 CCTGCACA GGCTAGCTACAACGA ACTAGAAT 2116 1122 UULAGUCAU A UCACUAAU 295 ATTAGTCA GGCTAGCTACAACGA ATTAGATA 2117 1130 ACUANAU A UGUCACACA 299 TGTGTACA GGCTAGCTACAACGA ATTAGATA 2119 1131 ACUANAU A UCUACACA 299 TGTGTAG GGCTAGCTACAACGA ATTAGGTA 2120 1132 AGUGAUAU A UCUAGACA 299 TGTGTAG GGCTAGCTACAACGA ATTAGGTA 2121 1178 AGUGANU A UCUAGACA 299 TGTGTAG GGCTAGCTACAACGA ATTAGGTA 2121 1179 AGUGANU A UCUAGACA 299 TGTGTAG GGCTAGCTACAACGA ATTCACT 2122 1133 CUAGAGUU A CCUAGCU 311 AGCTCAGA GGCTAGCTACAACGA ATTCACT 2122 1134 CUULACCAU A UCUAUACU 318 TAGTATGG GGCTTAGCTACAACGA AATTCACT 2122 1202 CCUAGCUU A CCUAGCU 318 AGCTAGG GGCTAGCTACAACGA AATTCACT 2122 1210 ACCAIACU A UAUCUUG 319 AGATATTAG GGCTAGCTACAACGA AATTCACT 2123 1211 ACCAIACU A UAUCUUGA 319 AGATATTAG GGCTAGCTACAACGA AATTCACT 2123 1212 CAUACAU A UAUCUUGA 321 TAGTATGG GGCTAGCTACAACGA ATTCATT 2126 1213 CAUACAU A UAUCUUGA 321 TAGTATGG GGCTAGCTACAACGA ATTCATT 2126 1327 AGAAAAAU A UAUCUUGA 321 TCCAAAGA GGCTAGCTACAACGA ATTGATG 2127 1327 AGAAAAAU A UAUCUUGA 345 AGTAGATA GGCTAGCTACAACGA ATTGATT 2127 1328 AAAAAUAU A UAUCUCAA 346 TGAGATA GGCTAGCTACAACGA ATTGATT 2128 1329 AAAAAUAU A UAUCUCAA 346 TGAGATA GGCTAGCTACAACGA ATTGTTT 2129 1331 AGAUAAUA A UAUCUCAA 346 TGAGATA GGCTAGCTACAACGA ATTGTTT 2129 1321 AGAAAAUA A UAUCUCAA 346 TGAGATA GGCTAGCTACAACGA ATTGTTTT 2129 1322 AAAAAUAU A UAUCUCAA 346 TGAGATA GGCTAGCTACAACGA ATTGTTTT 2129 1324 AGAUAGUU A UAUCUCAA 346 TGAGATA AGCTAGCTACAACGA ATTGTTTT 2129 1325 AAAAAUAU A UAUCUCAA 346 TGAGATA AGCTAGCTACAACGA ATTGTTTT 2129 1326 AAAAAUAU A UAUCUCAA 346 TGAGATA AGCTAGCTACAACGA ATTGTTTT 2129 1327 AGAAAAUAU A UAUCUCAA 346 TGAGATA AGCTAGCACAA ATTGTTTT 2129 1328 AAAAUAUA UAUCUCAA 346 TGAGATA AGCTAGAGA ATT		909	GAAAUUGU A UUUUUUCU	236	AGAAAAA GGCTAGCTACAACGA ACAATTTC	2111
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1035		976	AAGGCCAU A CUCUUACA	255	TGTAAGAG GGCTAGCTACAACGA ATGGCCTT	2114
1070		982	AUACUCUU A CAUAAUAA	258	TTATTATG GGCTAGCTACAACGA AAGAGTAT	2115
1100		1035	AUUCUAGU A CAUGUAGG	278	CCTACATG GGCTAGCTACAACGA ACTAGAAT	2116
1122 UULGUCAU A UCACUAAU 299 ATTAGTGA GCTRACTICACACGA ATGACTRA 2119 1111 UCACUAAU A UACUACACA 299 TGTTAGTA GCTRACTICACACGA ATTAGTGA 2120 1113 ACUAAUAU A UCUACACA 299 GTGTTAGTA GCTRACTICACACGA ATTAGTGA 2120 11178 AGUAAUAU A UCUACACCU 311 AGCTCAGA GCTRACTICACACGA ATTAGTAGT 2121 11791 CUQAGGUU A CUAGACUU 311 AGCTCAGA GGCTRACTICACACGA ATTCTAGT 2122 11202 CCUAGCUU A CUAUAUCUU 319 AGATTAGG GCTGACTACACCGA ATTCTAGT 2122 11202 CCUAGCUU A CUAUAUCUU 319 AGATTAGG GCTGACTACACGA AACTTAGG 2124 1207 CUULACCAU A CUAUAUCUU 319 AGATTATG GGCTGACTACACGA AACTTAGG 2125 1210 ACCUACAU A CUAUAUCUU 319 AGATTATG GGCTGACTACACGA ATGTAGG 2126 1211 CAUACUAU A UCUUUGGA 320 CNAAGATG GGCTGACTACACGA ATGTAGG 2127 1212 CAUACUAU A UCUUUGGA 321 TCCAAAGA GGCTGACTACACGA ATGTATGG 2127 1213 CAUACUAU A UCUUUGGA 321 TCCAAAGA GGCTGACTACACGA ATGTATGG 2127 1214 CAUACUAU A UCUUUGGA 345 MATAGATA GGCTGACTACACGA ATTATTTT 2129 1322 AAAAAUAU A UULUGUCU 348 ACTTGAGG AGCTGACTACACGA ATTATTTT 2129 1332 AAAAAUAU A UULUGUCU 348 ACTTGAGG GGCTGACTACACGA ATTATTTT 2129 1332 AAAAAUAU A UULUGUCU 348 ACTTGAGG GGCTGACTACACGA ATTATTTT 2129 1334 UUCAAAGAU A UUUGUAGA 359 ACTTGAGG GGCTGACTACACGA ATTATTTT 2129 1335 AUGAAAUAU A UUAGANUCU 359 AATTCATA GGCTGACTACACGA ATTATTTT 2129 1336 UUAAAAAUA A UAGAAUU 359 AATTCATA GGCTGACTACACGA ATTATTTT 2121 1356 CUCCAAGU A UUUUGAA 359 TATACTAA GGCTTACCACCACA ATTTTTTA 2121 1357 CUCCAAGU A UUUGAAUCA 359 AATTCATA GGCTTACCACCA ATTTTTTA 2121 1358 AUGAAUAUA U UUAGAUCU 370 TAATCTAA GGCTTACCACCAA ATTTTTTT 2121 1359 CUCCAAGU A UUUUGAA 359 TAATCATA GGCTTACCACCAA ATTTTTTT 2121 1351 AUGACUAU A UUACAUCU 370 TAATCTAA GGCTTACCACCAA ATTTTTTT 2121 1351 AUGACUAU A UUACAUCU 370 TAATCTAA GGCTTACCACCAA ATTTTTTT 2121 1351 AUGACUAU A UUUGAAUCA 365 TAATCTTAA GGCTTACCACCAA ATTGTATT 2135 1359 CUCCAAUC U UUUGAAUCA 370 TAATCTAA GGCTTACCACCAA ATTGTATT 2135 1359 CUCCAAUC U UUUGAAUCA 370 TAATCTAA GGCTTACCACCAA ATTGTATT 1351 AUGACUAU A CAGCUGAC 375 TAATCTAA GGCTTACCACCAA ATTGTATT 1351 AUGACUAU A CAGCUGAC 375 TAATCTAA GGCTTACCACCAA ATTGTATT 1351 CUCCAAGUAU A UUACACCU 410 ACTACACC		1070	UAAGACAU A UGAUCAAC	287	GTTGATCA GGCTAGCTACAACGA ATGTCTTA	2117
1131		1100	UGGUUAAU A UGUGACAG	291	CTGTCACA GGCTAGCTACAACGA ATTAACCA	2118
1133 ACUAAUAU A CUAACUAC 299 GTTOTTAG GGCTAGCTACAACGA ATTATAT 2121		1122	UUAGUCAU A UCACUAAU	295	ATTAGTGA GGCTAGCTACAACGA ATGACTAA	2119
1178 AGUGAAJU A UCUGAGCU 311 AGCTCAGA GGCTAGCTACAACGA AATTCACT 2122 1193 CUAGAGUU A CUAGCUU 315 AAGCTAGG GGCTAGCTACAACGA AATTCACT 2123 1202 CCUAGCUU A CCUAGCUA 318 TAGATAGG GGCTAGCTACAACGA AACTCTAG 2123 1207 CUULACCAU A CUAGAUCU 319 AGATATAG GGCTAGCTACAACGA AGGTAGG 2125 1210 ACCAUACU A UAUCUUUG 320 CAAAGATA GGCTAGCTACAACGA AGTATGGT 2126 1212 CAUACUAU A UAUCUUUG 320 CAAAGATA GGCTAGCTACAACGA AGTATGGT 2126 1212 CAUACUAU A UAUCUUUG 321 TCCAAAGA GGCTAGCTACAACGA AGTATGGT 2126 1212 CAUACUAU A UCUUUGGA 321 TCCAAAGA GGCTAGCTACAACGA AGTATGGT 2126 1327 AGAAAAUA A UAUUAUCU 345 AGATATAT 325 GCTAGCTACAACGA ATTATTT 2128 1328 AAUAUAUU A UCUCAAGU 348 ACTTGGATA GGCTAGCTACAACGA ATTATTT 2130 1341 UCUCAAGU A UUUUUUAA 351 TTAAAAUA GGCTAGCTACAACGA ATTATTT 2130 1354 AUUAAAAU A UAUACUCA 355 AATTCATA GGCTAGCTACAACGA ATTTTTA 2131 1355 AAAAAUAU A UAUAACUA 355 AATTCATA GGCTAGCTACAACGA ATTTTTA 2131 1356 AAAAAUAU A UAUGACUA 355 AATTCATA GGCTAGCTACAACGA ATTTTTTA 2131 1357 CUCCAAU A UUUAACUA 355 AATTCATA GGCTAGCTACAACGA ATTTTTTA 2131 1358 AAAAUAU A UUAACUA 355 TAGATTAA GGCTAGCTACAACGA ATTTTTTA 2131 1359 CUCCAAAU A UUUAACUA 355 TAGATTAA GGCTAGCTACAACGA ATTTTTTA 2131 1354 AUUAGAUU A UUAGAUU 370 TAATCTAA GGCTAGCTACAACGA ATTTTTTA 2131 1355 CAUCCAAU A UUAGAUUA 370 TAATCTAA GGCTAGCTACAACGA ATTTTTTA 2131 1354 AUUAGAUUA UUUGAAA 375 TTAAAATA GGCTAGCTACAACGA ATTTGGAG 2131 1354 AUUAGAUUA UUUGAAA 376 TCAAAATA GGCTAGCTACAACGA ATTTGGAG 2131 1354 AUUAGAUUA UUUGAAA 376 TCAAAATA GGCTAGCTACAACGA ATTTGGAG 2131 1355 UUACAUUA CAUCUUAGA 374 TCAAAATA GGCTAGCTACAACGA AATTGGT 2135 1356 AACUAUUA CAUCUAUA 375 TTAAAATA GGCTAGCTACAACGA AATTGGT 2135 1357 CUCCAAU A UUACAUCU 382 AAATTGAA GGCTAGCTACAACGA AATTGGT 2135 1358 UUACAUUA CAUCUACU 386 TCAACTAA GGCTAGCTACAACGA AATTGGT 2136 1427 CAUCUAUU A CAUCUACU 386 TCAACGA AGCTAACGA AATTGGT 2136 1428 GCCAUCU A UUACAUCU 386 TCAACGA GGCTAGCTACAACGA AATTGGT 2136 1433 UUACAUCU A CAUCUACU 386 TCAACGA AGCTAACGA AATTGGT 2136 1433 UUACAUCU A CAUCUACU 386 TCAACGA AGCTAACGA AATTGATA 2140 1559 UAAACCUU A UUACACCU 400 ATGGTAG GGCTAGCTACAACGA A		1131	UCACUAAU A UACUAACA	298	TGTTAGTA GGCTAGCTACAACGA ATTAGTGA	2120
1193		1133	ACUAAUAU A CUAACAAC	299	GTTGTTAG GGCTAGCTACAACGA ATATTAGT	2121
1202 CCUAGCUU A CCAUACUCU 318		1178	AGUGAAUU A UCUGAGCU	311	AGCTCAGA GGCTAGCTACAACGA AATTCACT	2122
1207 CUUNCCAU A CUNDINCU 319 AGRATATIA GOCTAGCTACACGA ATTOGTAMG 2125	i	1193	CUAGAGUU A CCUAGCUU	315	AAGCTAGG GGCTAGCTACAACGA AACTCTAG	2123
1210	ĺ	1202	CCUAGCUU A CCAUACUA	318	TAGTATGG GGCTAGCTACAACGA AAGCTAGG	2124
1212		1207	CUUACCAU A CUAUAUCU	319	AGATATAG GGCTAGCTACAACGA ATGGTAAG	2125
1327 AGAAAAU A UAUUAUCU 345 AGATAATA GGCTAGCTACAACGA ATTTTTCT 2128		1210	ACCAUACU A UAUCUUUG	320	CAAAGATA GGCTAGCTACAACGA AGTATGGT	2126
1332 ANANAUMI A UNINUCCIA 346 TORGATRA GOCTRACTACAGA ATRITTIT 2139 1332 ANUNINU A UCUCANGU 348 ACTIGUAG GOCTRACTACAGA ATRATTIT 2130 2131 21	ı	1212	CAUACUAU A UCUUUGGA	321	TCCAAAGA GGCTAGCTACAACGA ATAGTATG	2127
1332 ANUMANU A UCUCAAGU 348 ACTTGAGA GGCTAGCTACAACGA AATATATT 2130 1341		1327	AGAAAAAU A UAUUAUCU	345	AGATAATA GGCTAGCTACAACGA ATTTTTCT	2128
1341 UCUCAAGU A UUUUUNA 351		1329	AAAAAUAU A UUAUCUCA	346	TGAGATAA GGCTAGCTACAACGA ATATTTTT	2129
1354 UUAAAAAU A UAUGAAUU 358	ı	1332		348	ACTTGAGA GGCTAGCTACAACGA AATATATT	2130
1356		1341				
1315	i	1354	UUAAAAAU A UAUGAAUU	358	AATTCATA GGCTAGCTACAACGA ATTTTTAA	2132
1386		1356	AAAAAUAU A UGAAUUCU	359	AGAATTCA GGCTAGCTACAACGA ATATTTTT	2133
1394		1375		365		
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1424 GCCCAUCU A UUACAUCU 382 AGATGTAA GGCTAGCTACAACGA AGATGGGC 2138 1427 CANCUNAU A CANCUACA 384 TGTRAGRG GGCTAGCTACAACGA AGATGGGC 2139 1433 UUACAUCU A CAGCUGAC 386 GTCAGCTG GGCTAGCTACAACGA AGATGGAC 2139 1438 UCUUAACU A CAGCUGAC 386 GTCAGCTG GGCTAGCTACAACGA AGATGAGAC 2141 1510 AAUAGCCU A CUMUUGAC 399 GTCATTAGG GGCTAGCTACAACGA AGATGAGCT 2142 1513 AGCCUACU A UUGACCAU 400 ATGGTCAA GGCTAGCTACAACGA AGATGGGCT 2143 1529 UAAACCAU A UUUGACGU 401 ATGGTCAA GGCTACCTACAACGA AGATGGCT 2143 1529 UAAACCAU A UUUGAGGU 401 AGCGAAAA GGCTAGCTACAACGA AGATGGTTA 2144 1529 UAAACCAU A UUUGAGGU 410 AGCGAAAA GGCTAGCTACAACGA AGAGGTTA 1521 UGCGUGUU A UAUGUGAU 415 AATACCAT GGCTAGCTACAACGA AGACGCA 2146 1527 UUAUAUGU A UUAUACAC 417 GTTATAA GGCTAGCTACAACGA ATACAGC 2147 1528 UUAUGUUACA UUAUACAC 417 GTTATAA GGCTAGCTACAACGA ATACAGC 2147 1529 UAUAGUU A UUAUACAC 417 GTTATAA GGCTAGCTACAACGA ATACAGC 2147 1520 UAUGUAUAU A CACUUAU 419 ATAGTGTA GGCTAGCTACAACGA ATACAGT 2149 1520 UAUGUAUAU A CACUUAU 420 ATAGTGTG GGCTAGCTACAACGA ATACAGT 2149 1520 UAUGUAUAU A CACUUAU 420 ATAGTGTG GGCTAGCTACAACGA ATACATA 2149 1520 UAUGUAUAU A CACUUAU 421 ATAGTAGT GGCTAGCTACAACGA ATACATA 2150 1521 UAUACACU A UUUCCUAC 422 ATAGTGTG GGCTAGCTACAACGA ATACATA 2151 1522 AAAAUGUU A UUUAGAAA 430 TTTCTAAA GGCTAGCTACAACGA ATACATA 2151 1523 AAAUGUCU A CAAUAAAG 425 CTTATTAT GGCTAGCTACAACGA ATACAC 2152 1524 AAAAUGUU A UUUAGAAA 430 TTTCTAAA GGCTAGCTACAACGA ATACATTT 2154 1522 AAAAUGUU A UUAUAGAAC 425 CTTATTAT GGCTAGCTACAACGA ATACATTT 2154 1522 AAAAUGUU A UUAUAGAAC 426 CTTATTAT GGCTAGCTACAACGA ATACATTT 2154 1523 AAAAUGUU A UUAUAGAAC 426 CTTATTAT GGCTAGCTACAACGA ATACATTT 2154 1524 AAAAUGUU A UUAUAGAAC 427 CTTATTAT GGCTAGCTACAACGA ATACATTT 2154 1527 AAAAUGUU A UUAUAGAAC 428 CTTATTAT GGCTAGCTACAACGA ATACATTTT 2154 1528 AAAAUGUU A UUAUAGAA	- 1	1394				
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1571 UGCQUUUU A UMUGUAUU 415 AATACATA GGCTAGCTACACAA AACACGCA 2146 1573 CGUGUUUU A UGUAUUU 416 ATAATACA GGCTAGCTACACAA AACACGCA 2147 1577 UUAUMUGU A UGUAUCAC 417 GTOTATAA GGCTAGCTACAACGA ATAACACG 2147 1580 UANGGUAUU A UACACUAU 419 ATAGTGTA GGCTAGCTACAACGA AATACATA 2149 1582 CGUAUUAU A CACUUGUA 420 ATATACTA GGCTAGCTACAACGA AATACATA 2150 1587 UAUACACU A UAUUCCUA 421 TAGGAATA GGCTAGCTACAACGA AGTGTATA 2151 1589 UACACUAU A UUCCUACA 422 TGTAGGAA GGCTAGCTACAACGA AGTGTATA 2151 1599 UALUUCCU A CAAUAAAG 425 CTTATATTG GGCTAGCTACAACGA AGAATAT 2151 1591 AAAAUGUU A UUUAGAAA 430 TTTCTAAA GGCTAGCTACAACGA AGAATAT 2154 64 UCUAUACU G UGAUGAUC 732 GATCATCA GGCTAGCTACAACGA AGATTT 2154 65 UCUAUACU G UGAUGAUC 732 GATCATCA GGCTAGCTACAACAA AGAATAT 2154 66 UCUAUACU G UGAUGAUC 732 GATCATCA GGCTAGCTACAACAA AGAATAT 2154 67 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACAA AGCTGTGA 2155 79 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACAA AGCTGTGA 2156						
1573 CGUGUUAU A UGUAJUAU 416 ATAATACA GGCTAGCTACAACGA ATAACACG 2147 1577 UUAUAUGU A UUAUACCC 417 GTOTATAA GGCTAGCTACAACGA ACTATAA 2148 1580 UAUGUAUA UACACUTAU 419 ATAGTGTA GGCTAGCTACAACGA ACATATAA 2148 1582 UGUAUUAU A CACUAUAU 420 ATATAGTG GGCTAGCTACAACGA ATAATACA 2150 1587 UAUACACUA UAUUCCUA 421 TAGGAATA GGCTAGCTACAACGA AGTGTATA 2151 1589 UACACUAUA UUCCUACA 422 TOTAGGAA GGCTAGCTACAACGA AGTGTATA 2151 1589 UAUACACUA CAUAUAAG 425 CTTTATTG GGCTAGCTACAACGA AGGATAT 2153 1622 AAAAUGUU A UUUAGAAA 430 TTTCTAAA GGCTAGCTACAACGA AACATTTT 2154 440 UCUAUACU G UGAGGAUC 732 GGTCAGCTAC GGCTAGCTACAACGA AGTATATGA 2155 79 UCACAGGU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGTATATGA 2156 440 4						
1577 UUAUUNUGU A UUNUACAC 417 GTGTATAA GGCTAGCTACAACGA ACATATAA 2148 1580 UNIGUNUU A UKACKUMU 419 ATAGGTAT GGCTGACTACAACGA ACATATAA 2149 1582 GUGAUUAU A CACUMUAU 420 ATATAGTA GGCTGACTACAACGA ATATACA 2150 1587 UNIACACU A UNUCCUA 421 TRGGAATA GGCTAGCTACAACGA ATGTATA 2151 1589 URACKUMU A UUCUACA 422 TGTAGGAA GGCTAGCTACAACGA ATGATGTA 2151 1595 AUAUUCCU A CAAUAAAG 425 CTTTATTG GGCTGACAACGA ATGATGTA 2153 1622 AAAAUGUU A UUUAGAAA 430 TTTCTAAA GGCTGACTACAACGA AGGAATTT 2154 64 UCUAUACU G UGAUGAUC 732 GATCATCA GGCTAGCTACAACGA AGTATAGA 2155 79 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACACGA AGCTGTGA 2156						
1580						
1582 UGUAUUAU A CACUAUAU 420 ATATAGTG GGCTAGCTACAACGA ATAATACA 2150 1587 UANUACAU A UAUUCCUA 421 TAGGAATA GGCTAGCTACAACGA AGTGTATA 2151 1589 UAUCCUALA 422 TOTRAGAA GGCTAGCTACAACGA AGTGTATA 2151 1595 AUAUUCCU A CAMUAAAG 425 CTTTATTG GGCTAGCTACAACGA AGATGTTA 2153 1622 AAAAUGUU A UUUAGAAA 430 TTTCTAAA GGCTAGCTACAACGA AGATTTT 2154 44 UCUAUACU G UAUGAGAU 732 GGTCAGTCA GGCTAGCTACAACGA AGATTTT 2154 59 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGATTTT 2154 59 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTGTGA 2155 50 CCAAGGCU CACAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTGTGA 2156 50 CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTGTGA 735						
1587 UNUACACU A UNUUCCUA 421 TAGGAATA GGCTAGCTACAACGA AGTGTATA 2151 1599 UACACUAU A UUCCUACA 422 TGTAGGAA GGCTAGCTACAACGA ATAGTGTA 2152 1595 AUQUUCCU A CAAUAAAG 425 CTITATTO GGCTAGCTACAACGA AGAATAT 2153 1622 AAAAUGUU A UUUAGAAA 430 TTTCTAAA GGCTAGCTACAACGA AGAATTT 2154 64 UCUAUACU G UGAUGAUC 732 GATCATCA GGCTAGCTACAACGA AGATATTAGA 79 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTATGA 2156 79 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTGTGA 2157 79 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTGTGA 2158 79 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTGTGA 2159 79 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTGTGA 2150 70 70 70 70 70 70 70						
1589						
1595 AUAUUCCU A CAMUANAG 425 CTTTATTG GGCTAGCTACAACGA AGGARTAT 2153 1622 ABAABUGU A UUUAGAAA 430 TTTCTAAA GGCTAGCTACAACGA AACATTTT 2154 UUCAUAACU G UAGAGAUC 732 GARCATCA GGCTAGCTACAACGA AACATTATAGA 2155 79 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTGTGA 2156 2						
1622 AAAAUGUU A UUUAGAAA 430 TTTCTAAA GGCTAGCTACAACGA AACATTTT 2154 64 UCUAUACU G UGAUGAUC 732 GATCATCA GGCTAGCTACAACGA AGTATAGA 2155 79 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTGTGA 2156						
64 UCUAUACU G UGAUGAUC 732 GATCATCA GGCTAGCTACAACGA AGTATAGA 2155 79 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTGTGA 2156						
79 UCACAGCU G CCAAGGCU 735 AGCCTTGG GGCTAGCTACAACGA AGCTGTGA 2156						
121 AUUUGGCU G CCAGCUUU 736 AAAGCTGG GGCTAGCTACAACGA AGCCAAAT 2157						
		121	AUUUGGCU G CCAGCUUU	736	AAAGUTGG GGUTAGCTACAACGA AGCCAAAT	2157

Table 28

173 CCUUCCU G CUGGUAIC 739 GATACCA GIGCTAGCTACAACGA AGAGATC 2159	168	GACUUCCU G UCCUGCUG	738	G10G1G31 G20M1G0M1G111G1 1GG110MG	
207 CCUCACUE G CUCAGCIA 740 TAGCTOAG GGCTAGCTACAACGA GAGTGAGG 2156 241 ANUSAAN G CCUCAACA 742 TOTTGAGG GGCTAGCTACACGA ATTCCAAT 2151 288 CAANUUCU G UCCUCUCA 743 AAGTGAGA GGCTAGCTACACGA ATTCCAAT 2152 303 CUNANUMU G UCUCUUCU 744 GGCAGGAG GGCTAGCTACACGA ATTATAAG 2153 310 UGURCUCU G CURCUCU 749 COATGAG GGCTAGCTACACACACA ATTATAAG 2163 311 AUCUGUAL G CUCUCUG 749 COATGATA GGCTAGCTACACACAA AGATCAGCA 2166 331 AUCUGUAL G CUCUCUG 749 COATGATA GGCTAGCTACACACAACGA AGATCTAG 2166 347 GARQUUCU G CUCACACC 751 GGTTGATCACACACAACAA AGACTCAACA 2166 356 CUAGAUCU G CACACUCA 752 GGCAGGTG GGCTAGCTACACGA AGACTCAG 2168 392 UANAAUCU G UCAUCCCA 754 TOGGATAG GACTACACACGA AGATTTA 2170 402 CALUCCAU G CAGACAGG 755 CCTOTTATA GGCTAGCTACACGA AGATTTA 2171 402 CALUAULU G UCAUCACA 754 TOGGATAGCTACACACGA ATTTGT 2171				CAGCAGGA GGCTAGCTACAACGA AGGAAGTC	2158
241 MUUGAANU G CCUCAACA 742 TOTTGRGG GUCTAGCTACACAGA ATTTCAAT 2161 288 CARJUUGU G UCUCAUCU 743 MARTGRAG GUCTAGCTACACAGA AGRAATTG 2162 303 CUUANANU G UCUCUUGC 744 GCAAGAGA GUCTAGCTACACAGA AGRAATTG 2163 310 UGUCUUU G CUGAUCUG 745 CAGATCAG GGCTAGCTACACAGA AGAGACA 2164 318 GUUGUCUU G CUGAUCUG 749 CAGAGAGA GUCTAGCTACACAGA AGACAGA 2166 331 AUCUGACU G CUACACC 751 CAGAGAGA GUCTACCTACACGA AGACACAGA 2166 347 GAGAGUU G CUACACC 752 GCAGACTCA GGCTAGCTACACAGA AGACTCAG 2169 352 UGCAGCUU G CCACAUCA 753 TORTGTGG GGCTAGCTACACGA AGACTCAG 2169 392 UANANUCU G UCACACAG 755 CCTUTCTG GGCTAGCTACACGA AGATTTTA 2170 402 CALUCCAU G UCACACAG 755 CCTUTCTG GGCTAGCTACACGA ATATTGT 2172 422 ACAULUU G UGAACAG 756 CCTTTATA GGCTAGCTACAACGA ATATTGT 2174 459 GUUUCUU G UGAACAG 756 CCTTTATA GGCTAGCTACAACGA ATATAGTT 2174 <t< td=""><td></td><td></td><td></td><td></td><td></td></t<>					
288 CANUUUCU G UCUCAUCU 743 AGATGRGA GGCTAGCTACAACGA AGAAATTG 2162 300 CUUJANUAG G UCUCUUGC 744 GCAAGGAG GGCTAGCTACAACGA AGAAATTGA 2163 310 USUGUCUG G CUSALICUG 747 CAGATGAG GGCTAGCTACAACGA AGAGGACA 2164 318 GCUGANUCI G LUCAUCUG 747 CAGATGATA GGCTAGCTACAACGA AGATCAGC 2165 321 AUCUGUUG G CUACAACC 751 GGTTGAGCTACAACGA AGACCACGA 2166 347 GAGAGGAG GGCTAGCTACACGA AGACCTACA 2167 365 CUAGAUCU G CACACCC 751 GGTTGAGCTACACGA AGACCTACACA 2167 365 CUAGAUCU G CACACCC 751 GGTAGCTACACACAACA AGACCTACACA 2169 372 UGCAGUU G CACACACA 753 TOATGTGG GGCTAGCTACACGA AGATCTACA 2169 392 UANANUCU G UCUACACA 754 TOGGATGA 754 TOGGATGA 402 ACACUAUU G UAUCACACA 755 CCTUTTACA GGCTAGCTACACGA AAAGAAACAC 2172 459 GUUUCUU G UACAACAG 756 CTUTTACA GGCTAGCTACACGA AAAGAAACAC 2175 522 UACAUAU G UAUCAUC <td></td> <td></td> <td></td> <td></td> <td></td>					
303 CUUANNUU G UCUCUUU					
310					
331	303		744	GCAAGAGA GGCTAGCTACAACGA ATATTAAG	2163
331 AUCQUANU G CUUCUCU 749 CAGAGANG GGCTAGCTACACACA ATCACGAT 2166 347 GAAGUUCU G CUACAACC 751 GGTTUTAG GGCTAGCTACACGA AGACCTC 2167 365 CUAGACU G CACCUUCC 752 GCAMGCTG GGCTAGCTACACGA AGACCTCG 2168 372 UGCAGCUU G CCACAUCA 753 TGATGTGG GGCTAGCTACACGA AGACCTCG 2168 372 UGCAGCUU G CCACAUCA 753 TGATGTGG GGCTAGCTACACGA AGACCTCG 2169 392 UANAANCU G GUACACCCA 754 TGGGGTAG GGCTAGCTACACGA AGACTUCA 2169 422 CARAUGUU G CACACCGA 755 TGGGTAG GGCTAGCTACACGA AGACTUCA 2169 422 CACAUCCCA G CAGACACG 755 CCTUTCTG GGCTAGCTACACGA AGACTUCA 2171 422 ACAAUAU G UAUAACAG 756 CCTUTCTG GGCTAGCTACACGA AGACTUCA 2173 422 ACAAUAU G UAUACACGA 756 CCTUTCTG GGCTAGCTACACGA AATAACAT 2174 429 AACUUAUU G UGAAAAGG 758 CCTUTCTG GGCTAGCTACACGA AATAACAT 2174 429 AACUUAUU G UGAAAAGG 758 CCTUTCTG GGCTAGCTACACGA AATAACAT 2174 429 AACUUAUU G UGAAAAGG 758 CCTUTCTG GGCTAGCTACACGA AATAACAT 2174 422 AACUUAUU G UGAAACGU 761 GATGGTAA GGCTAGCTACACGA AATAACAT 2174 422 AACUUAUU G UGAAACGU 762 AGATCCAA GGCTAGCTACACGA AATAACAT 2176 522 UGGAUCUU G UAGAACGU 762 AGATCCAA GGCTAGCTACACGA AATAACAT 2176 522 UGGAUCUU G UAAAACGU 763 AGATCCAA GGCTAGCTACACGA AATAACAT 2176 522 UGGAUCUU G UAAAACGU 766 AACAGTTG GGCTAGCTACACGA AGTTTAT 2178 579 VANIAAAGU G CAACUGUU 766 AACAGTTG GGCTAGCTACACGA ACTTTATT 2178 588 AUGACACU G UAUAAAG 772 CTTGTTGG GGCTAGCTACACGA ACTTTATT 2178 588 AUGACACU G UAUAAAG 772 CTTGTTGG GGCTAGCTACACGA ACTTTATT 2180 665 ACUGACU G CCAACAG 771 TGGCAGT GGCTAGCTACACGA ACTTCAT 2180 665 ACUGACU G CCAACAG 772 CTTGTTGG GGCTAGCTACACGA ACTTCAT 2181 665 ACUGACU G CCAACAG 772 CTTGTTGG GGCTAGCTACACGA ACTTCAT 2181 665 AAUACAGU G UAUAAGAU 780 AATAATGA GGCTAGCTACACGA ACTTCAT 2181 665 AAUACAGU G UAUAUGUU 775 AACAGTG GGCTAGCTACACGA ACTTCAT 2181 670 670 670 670 670 670 670 670 670 670 670 670 670 670 6	310	UGUCUCUU G CUGAUCUG	745	CAGATCAG GGCTAGCTACAACGA AAGAGACA	2164
347	318	GCUGAUCU G UAUCAUCG	747	CGATGATA GGCTAGCTACAACGA AGATCAGC	2165
375	331	AUCGUGAU G CUUCUCUG	749	CAGAGAAG GGCTAGCTACAACGA ATCACGAT	2166
372 UQCAGCUU G CCACAUCA 753 TQATOTGQ GUCTAGCTACAACGA AAGCTUCA 2169 392 UAAAADUU G UCAUCCCA 754 TUGGATGA GUCTAGCTACAACGA AAGCTUCA 2169 402 CALUCCCAU G CAACACAG 755 CCTUTCTG GUCTAGCTACAACGA AAGATTTA 2170 422 ACAAUAUU G UALAACAG 756 CCTUTCTG GUCTAGCTACAACGA AATATTGT 2172 459 GUUUCUU G UGAAAAGG 756 CCTTTTCA GGCTAGCTACAACGA AAAGAAAC 2173 502 UACCAUAU G UUACCAUA 760 TATOGTAA GGCTAGCTACAACGA AAAGAAAC 2174 502 UACCAUAU G UUACCAUA 761 GATGAATA GGCTAGCTACAACGA AATATGAT 2174 512 AUUCAUCU G UUACCAUA 761 GATGAATA GGCTAGCTACAACGA ATATGATA 2175 512 AUUCALU G UUACCAUA 763 CATOTTTA GGCTAGCTACAACGA ATATGATA 2176 522 UUACAUAU 763 CATOTTTA GGCTAGCTACAACGA ATTATTAT 2176 570 AAAAAGU G CAACAA 766 AACAGTTA GGCTAGCTACAACGA ATTATTAT 2177 571 AAAAAACU G CAACAAG 771 TUGCAGTTAGCTACAACGA AGTTCATTATA 2180	347	GAAGUUCU G CUACAACC	751	GGTTGTAG GGCTAGCTACAACGA AGAACTTC	2167
392	365	CUAGAUCU G CAGCUUGC	752	GCAAGCTG GGCTAGCTACAACGA AGATCTAG	2168
ADDITION	372	UGCAGCUU G CCACAUCA	753	TGATGTGG GGCTAGCTACAACGA AAGCTGCA	2169
422 ACAAUAUU G UAUAACAG 756 CTOTTATA GGCTAGCTACAACGA AATATTGT 2172 459 GUUUGUUU G UGAAAAGG 758 CCTTTTCA GGCTAGCTACAACGA AATATTGT 2174 492 AACUUAUU G UAUACACA 760 TATOGTAA GGCTAGCTACAACGA AATAATGT 2174 502 UACCAUU G UAUACAUC 761 TATOGTAA GGCTAGCTACAACGA AATAATGT 2174 502 UACCAUU G UAUACAUC 761 GATGAATA GGCTAGCTACAACGA AATAATGT 2175 512 AUUCAUU G UUGAACAUG 762 AGATCCAA GGCTAGCTACAACGA AATATGGTA 2175 520 UUGAAUCUU G UUGAACAUG 763 CATOTTTA GGCTAGCTACAACGA AAGATCAA 2176 570 AAAUAAGG G UAUAAAAU 765 ATTTTATA GGCTAGCTACAACGA AGATCAAT 2176 579 UAUAAAAU G UAUAAAAU 765 ATTTTATA GGCTAGCTACAACGA AGATCAAT 2176 585 AUGCAACU G UUGAUUCC 767 GAAATCCAA GGCTAGCTACAACGA AGTTTATA 2179 585 AUGCAACU G UUGAUUCC 767 TUGCAGTG GGCTAGCTACAACGA AGTTTATA 2180 660 UUAAAACU G CACACAAG 772 CTTGTTGG GGCTAGCTACAACGA AGTTTATA 2181 661 AUUACAAU G UAUAAAGU 775 AGCTTTA GGCTAGCTACAACGA ATTGTAT 2181 662 AUUACAAU G UAUACUU 777 AATAATGA GGCTAGCTACAACGA ATTGTAT 2181 663 AUUACAAU G UAUACUU 777 AATAATGA GGCTAGCTACAACGA ATTGTAT 2181 664 UUUACAUC G UUUAUCUU 777 AATAATGA GGCTAGCTACAACGA AGTTCTAT 2181 665 ACUUACUU G UUUAUCUU 777 AATAATGA GGCTAGCTACAACGA AGTGTAT 2181 666 AACUUAUU G UUUUCUU 778 AATAATGA GGCTAGCTACAACGA AATTGTAT 2181 667 AACUUAUU G CACCAUU 780 AOTTACTA GGCTAGCTACAACGA AATTGTAT 2181 668 AACUUAUU G UUUUCUU 781 AAAAAGA GGCTAGCTACAACGA AATTGTAT 2181 669 AACUUAUUU G CACCAUU 782 AATAGGG GGCTAGCTACAACGA AATTGTAT 2181 660 AACUUACUU G CACCAUU 782 AATAGGG GGCTAGCTACAACGA AATTGTT 2180 670 AUGAAAUU G UUCUAAGA 785 TTACACCA GGCTAGCTACAACGA AATTGTT 2180 670 AUGAACU G UUGUAAGA 785 TTACACCA GGCTAGCTACAACGA AATTGTT 2180 670 AUGACAU G UUCUAAGA 786 TCTTGAAG GGCTAGCTACAACGA AATTGTT 2180 670 AUGACAU G UUCUAAGA 786 TCTTGAAG GGCTAGCTACAACGA AATTGTT 2190 670 CAGAAAUU G UUCUAAGA 786 TCTTGAAG GGCTAGCTACAACGA AATTGTT 2190 670 CAGAAAUU G UUGUAAGA 786 TCTTGAAG GGCTAGCTACAACGA AATTGTT 2190 670 CAGAAAUU G UUGUAAGA 786 TCTTGAAG GGCTAGCTACAACGA AATTGTT 2190 670 CAGAAAUU G UUGUAAGA 786 TCTTGAAG GGCTAGCTACAACGA AATTGTT 2190 670 CAGAAAUU G UUGUAAGA 786 TCTTGAAG GGCTAGCTACAACGA AATTGT	392	UAAAAUCU G UCAUCCCA	754	TGGGATGA GGCTAGCTACAACGA AGATTTTA	2170
459 GUULCUUU G UGAAAAGG 758 CCTTTTCA GGCTAGCTACAACGA AAAGAAC 2173 492 AACUUAUU G UUACCAUA 760 TATGGTAA GGCTAGCTACAACGA AAAGAAC 2174 592 UACCAUAU G UUAUCAUC 761 GATGGTAA GGCTAGCTACAACGA AATAAGTT 2174 512 AUUCAUCU G UUGGAUCU 762 AAATACAT 3GCTAGCTACAACGA AATACATT 2176 522 UUGGAUCU G UUGGAUCU 762 AAATACAT 2176 570 AAAUAAGU G UAUAAAAU 765 ATTTATA GGCTAGCTACAACGA AATACATT 2176 570 AAAUAAGU G UAUAAAAU 765 AACAGTT GGCTAGCTACAACGA AATACAT 2178 570 AAAUAAGU G UAUAAAAU 765 AACAGTT GGCTAGCTACAACGA AATACAT 2178 570 UAUAAAACU G CACUGUU 766 AACAGTT GGCTAGCTACAACGA AATTTATA 2179 585 AUGACACU G UUAAAACU 767 GAAATACA GGCTAGCTACAACGA AATTTATA 2179 660 UUAAAACU G CACUGCCA 771 TOGCAGT GGCTAGCTACAACGA AGTTTTAA 2181 665 ACUUACAU G CACUGCCA 771 TOGCAGT GGCTAGCTACAACGA AGTTTTAA 2181 673 AAUAAAU G UNAAAGCU 775 AACAGTT GGCTAGCTACAACGA ATTTTATA 2181 880 AAAUAAUU G UNAAAGCU 775 AACAGTTA GGCTAGCTACAACGA ATTTTATA 2181 884 UACACAUC G UUAUAUU 777 AATAATGA GGCTAGCTACAACGA ATTGTAT 2181 884 UACACAUC G CACUUCUA 779 TAAAATGA GGCTAGCTACAACGA ATTGTAT 2184 884 UACACAUC G UUAUCUU 779 TAAAATGA GGCTAGCTACAACGA AATTGTAT 2185 884 UACACAUC G UUAUCUU 780 AATTACTA GGCTAGCTACAACGA AATTGTAT 2186 886 AACUUAUU G UAGACU 780 AATTACTA GGCTAGCTACAACGA AATTGTAT 2186 887 AACUUAUU G CACAUUA 780 AATTACTA GGCTAGCTACAACGA AATTGTAT 2186 888 AACUUAUU G CACAUUA 780 AATTACTA GGCTAGCTACAACGA AATTGTTA 2189 907 CAGAAAUT G UUAUCUUA 782 TAATGTOG GGCTAGCTACAACGA AATTGTTA 2189 1039 UAGACAU G UAGAGUG 789 ATTACCTA GGCTAGCTACAACGA AATTGTTA 2189 1058 AUAAAAUC G UUCUAAGA 785 TTTACCTA GGCTAGCTACAACGA AATTGTT 2189 1058 AUAAAAUC G UUCUAAGA 786 TTTACCTA GGCTAGCTACAACGA AATTGTTA 2189 1058 AUAAAAUC G UUCUAAGA 786 TTTACCTA GGCTAGCTACAACGA AATTGTTA 2190 1058 AUAAAAUC G UUCUAAGA 786 TTTACCTA GGCTAGCTACAACGA AATTGTTA 2190 1058 AUAAAAUC G UUCUAAGA 787 TTACCTA GGCTAGCTACAACGA AATTGTTA 2190 1058 AUAAAACC G UUAAAACC 799 ACAACCTG GGCTAGCTACAACGA AATTGTTA 2191 1168 AAGCACG G GAGCAG 799 CTCCCC GCTAGCTACAACGA AATTGTTA 2191 1169 GUCAAGUU G UUCUCAU 798 AATTGTA GGCTAGCTACAACGA ATTGTTACA 2191 1169 UUCAAGUU G U	402	CAUCCCAU G CAGACAGG	755	CCTGTCTG GGCTAGCTACAACGA ATGGGATG	2171
492	422	ACAAUAUU G UAUAACAG	756	CTGTTATA GGCTAGCTACAACGA AATATTGT	2172
SO2	459	GUUUCUUU G UGAAAAGG	758	CCTTTCA GGCTAGCTACAACGA AAAGAAAC	2173
512 AUUCALICU G UUGGALCU 762 AGATCCAA GGCTAGCTACAACGA AGATGAT 2176 522 UUGALUCU G UAAACAUG 763 ACATGTTA GGCTAGCTACAACGA AGATCCA 2177 570 ANALNAGG G UAUANAAU 765 ATTTTATA GGCTAGCTACAACGA AGATCCA 2177 579 UAUANAAUG G CAACUGUU 766 AACAGTTG GGCTAGCTACAACGA AGTTCAT 2180 585 AUGCAACU G UUGAUUC 767 GANATCAA GGCTAGCTACAACGA AGTTCAT 2180 666 UUAAAACU G CCAACCAG 771 TUGCAGTG GGCTAGCTACAACGA AGTTCAT 2181 665 ACUGCACU G CCAACCAG 772 CTTGTTGG GGCTAGCTACAACGA AGTTCAT 2182 736 AJUCACAU G CCAACCAG 772 CTTGTTGG GGCTAGCTACAACGA AGTCCAT 2182 807 AAUGAAGU G UCAUUUU 777 AATAATAA GGCTAGCTACAACGA AGTCCATT 2184 807 AAUGAAGU G UUAUCUU 779 AATAATAA GGCTAGCTACAACGA AGTCCATT 2186 907 CAGAAAUU G UUUUUUU 781 AAAAAATA GGCTAGCTACAACGA AATTCCT 2187 920 UUUUCUAU G CCACAUUA 782 AATTCACA GGCTAGCTACAACGA ATTCCT 2187 <	492	AACUUAUU G UUACCAUA	760	TATGGTAA GGCTAGCTACAACGA AATAAGTT	2174
522 UUGAUCUU G UNAACAUG 763 CATUTTTA GGCTAGCTACAACGA AAGATCCA 2177 570 AAADMAGG G UNIAAAAU 765 ATTTTATA GGCTAGCTACAACGA ACTTATTA 2179 579 UAJAAAU G CAACUGUU 766 AACAGTTG GGCTAGCTACAACGA ACTTATTA 2179 585 AUGCAACU G UUGAUUUC 767 GAAATCAA GGCTAGCTACAACGA AGTTGCAT 2180 660 UUJAAACU G CACUGCA 771 TUGCAGTG GGCTAGCTACACGA AGTTGCAT 2181 665 ACUGCACU G CCAACCAG 772 CTTGTTGG GGCTAGCTACACGA AGTTGTAT 2181 867 AAUGAAGU G UAACAGU 775 AAGCATTTA GGCTAGCTACACGA ATTGTAT 2183 867 AAUGAAGU G UAUCUUA 777 AATAGTAG GGCTAGCTACACGA AGTTGTAT 2184 869 AACUAUUU G UAUCUUA 779 TAAGATAA GGCTAGCTACACGA AGTTGTA 2185 869 AACUAUUU G UAUCUUA 780 AGTTACTA GGCTAGCTACACGA AGTTGTA 2186 907 CABABUU G UAUGUUA 781 AAAGAATA GGCTAGCTACACGA ATTGTA 2186 920 UUUUCUUA G CCACAUUA 782 TAATGTGG GGCTAGCTACACGA ATTGTA 2189	502	UACCAUAU G UAUUCAUC	761	GATGAATA GGCTAGCTACAACGA ATATGGTA	2175
522 UGGAUCUU G UDANACANU 763 CATOTTTA GGGTAGCTACAACGA AAGATCCA 2177 570 MANUARU G URUNANAU 765 ATTTTATA GGGTAGCTACAACGA AAGATCCA 2177 579 MUARAAU G URUNANAU 766 AACAGTIG GGCTAGCTACAACGA AGTTGCAT 2120 585 AUGCAACU G UUGABUUU 767 GAAATCAA GGCTAGCTACAACGA AGTTGCAT 2180 669 UUAAAACU G CACACCAA 771 TÜGGGAGTG GGCTAGCTACAACGA AGTTGCAT 2180 669 ACUGCACU G CCAACAAG 772 CTTGTTGG GGCTAGCTACAACGA AGTGCAT 2182 736 AUUACAAD G UAAAAGU 775 AGCTTTTA GGCTAGCTACAACGA ATTGTAAT 2183 807 AAUAGAGU G UAACUUAU 777 AATAATGA GGCTAGCTACAACGA AGTGCAT 2183 869 AACUAUUU G UAUCUUA 779 AATAATGA GGCTAGCTACAACGA AGATGTAA 2185 869 AACUAUUU G UAUGUUA 780 AGTTACTA GGCTAGCTACAACGA AGATGTAA 2186 907 CASAADU G UAUUUUU 781 AAAAAATA GGCTAGCTACAACGA AATTGTA 2186 920 UUUUCUAU G CCACAUUA 782 TAATTGTG GGCTAGCTACAACGA ATTGTAT 2189	512	AUUCAUCU G UUGGAUCU	762		
STO	522	UGGAUCUU G UAAACAUG	763	CATGTTTA GGCTAGCTACAACGA AAGATCCA	
S79					L
585 AUGCARCU G UUGAUUUC 767 GAMATCAA GUCTAGCTACAACGA AGTTGCAT 2180 660 UUNAANGU G CACUGCCA 771 TUGCARCU GGCTAGCTACACGA AGTTTTAA 2181 665 AUUCAGAU G CACACAGA 772 CTTGTTGG GGCTAGCTACACGA AGTTGTAA 2181 736 AUUCAGAU G UNAANGCU 775 AGCTTTA GGCTAGCTACACGA ATGTAAT 2183 807 AMIGABUJ G UNACUUU 777 ANTAAGU GOCTAGCTACACGA AGTGTAAT 2184 844 UCACAUCU G UUAUCUU 779 TAAGATAA GGCTAGCTACACGA AGTGTTAA 2185 869 AACUMUU G UAGUUAUU 780 AGTTACTA GGCTAGCTACACGA AATTGTT 2186 907 CAGAANU G UAUUUUU 781 AAAAAATA GGCTAGCTACACGA AATTGTT 2187 920 UUUUCUU G CACAUUA 782 TAATGTGG GGCTAGCTACACGA ATGTACAA 2189 1039 UAGAACU G UUCUAAGA 785 TTTACCTA GGCTAGCTACACGA ATGTACAA 2189 1102 GUUAAGAU G UCUAAGA 785 TTTACCTA GGCTAGCTACACGA ATGTACAA 2190 1102 GUUAAGAU G UCUAAGA 785 TTTACCTA GGCTAGCTACACGA ATGTACA 2191					
660 UUNAAACU G CRCUGCCA 771 TUGCRITT GUGCAGTACTACACGA AGTTTAA 2181 665 ACUGCACU G CCAACAAG 772 CTTGTTGG GGCTAGCTACACGA AGTGCAGT 2182 716 AUUCACAU G CCAACAAG 775 ACCTTTTA GGCTAGCTACACGA AGTGCAGT 2182 807 ANIGARGU G CACAUCAU 777 AACTATTA GGCTAGCTACACGA AGTGCAT 2184 844 UCACAUCU G UUAUCUUA 779 TAAGATAA GGCTAGCTACAACGA AGATGAT 2186 869 AACUAUUU G UUAUUACU 780 AGTTACTACACGA AAATTGTT 2186 907 CAGAAAUU G UAUUUUU 781 AAAAAATA GGCTAGCTACAACGA AATTGTT 2186 920 UUUUCUMU G CCACAUUA 782 TAAGTGG GGCTAGCTACAACGA ATTGCTA 2187 1039 UAGUACAU G UAGUAAA 785 TTTACCTA GGCTAGCTACAACGA ATTGCTA 2189 1058 AUAAAUCU G UUCUAUAA 785 TTTACCTA GGCTAGCTACAACGA AGATTTAA 2189 1102 GUIULAGAU G UUGUAAUA 789 CACTGTCA GGCTAGCTACACGA AGATTTAA 2191 1168 AAGGCAU G UAUUGAU 792 ATTCACTA GGCTAGCTACACGA AGATCTTA 2192					1
665 ACUGCACU G CCAACAGA 772 CTTGTTGG GGCTAGCTACAACGA AUTGCAGT 2182 736					
736					
807 AAUGAAGU G UCAUUAUU 777 AATAATGA GGCTAGCTACAACGA ACTTCATT 2184 844 UCACADUC G UUAUCUUA 779 TAGGATAA GGCTAGCTACAACGA ACTTCATT 2186 869 AACUAUUU G UUAUACU 780 AGTTACTA GGCTAGCTACAACGA AATTGTT 2186 907 CAGAAAUU G UAUUUUU 781 AAAAAATA GGCTAGCTACAACGA AATTGTT 2187 920 UUUUCUAU G CCACAUUA 782 TARTGTGG GGCTAGCTACAACGA AATTGTT 2189 1039 UAGUCAU G CUCUANGA 785 TTTACCTA GGCTAGCTACAACGA ATGTACT 2189 1058 AUAAAUCG G UUCUANGA 786 TCTTAGAA GGCTAGCTACAACGA AGATTTAC 2190 1102 GUUALAGA GUGG 789 CACTGTCA GGCTAGCTACAACGA AGATTTAC 2191 1168 AAGGACU G UAUGUAAU 792 ATTCACTA GGCTAGCTACAACGA ACTCCCT 2191 1253 AUGAUUU G CAGGUUGU 797 ACAACCTA GGCTAGCTACAACGA AACTCCT 2192 1260 UGAGGOU G UUUCAU 798 ATGGAGAA GGCTAGCTACAACGA AACTCCT 2194 1287 CAUCCAAU G CAGGCAAG 799 CTTGCCTG GGCTAGCTACAACGA ACTCCAC 2195 <tr< td=""><td></td><td></td><td></td><td></td><td></td></tr<>					
844					
869 AACUAUJUU G UAGUAACU 780 AGTTACTA GGCTAGCTACAACGA AAATAGTT 2186 907 CAGAAAUJ G UAUUUUUU 781 AAAAAATA GGCTAGCTACAACGA AAATAGTT 2187 920 UUUUCUAU G CACAUUA 782 TAAATGGG GGCTAGCTACAACGA AATTTCTG 2187 1039 UAGUACAU G UAGUAAAA 785 TATACCTG GGCTAGCTACAACGA ATGTACTA 2188 1058 AUAAAUCU G UUCUAAGA 786 TCTTAGAA GGCTAGCTACAACGA ATGTACTA 2190 1102 GUUAAUAU G UAGACAUG 789 CACTGTCA GGCTAGCTACAACGA AGATTTAA 2191 1168 AAGGCACU G UAGUGAAU 792 ATTCACTA GGCTAGCTACAACGA AAATTTAA 2191 1253 AUGAUUUU G CAGGUUGU 797 ACAACCTG GGCTAGCTACAACGA AAAATCAT 2193 1260 UGCAGGUU G UCUUCCAU 798 ATGGAAGA GGCTAGCTACAACGA AAACTCAC 2194 1287 CAUCCAAU G CAGGCAG 799 CTTUCCTG GGCTAGCTACAACGA AAACTCAC 2194 1287 CAUCCAAU G CAGGCAG 799 CTTUCCTG GGCTAGCTACAACGA AAGTTCAT 2195 1412 AUGAACUU G UUGUCCCAU 804 TGGGCCAA GGCTAGCTACAACGA AAGTTCAT 2196 1484 GUGGGUC G CAAAAUCU 808 AGATTTTG GGCTAGCTACAACGA AAGTTCAT 2196 1568 UUUUGGU G UUGUUCU 812 ACATATAA GGCTAGCTACAACGA AAAATCAT 2198 1568 UUUUGGU G UUUUUUCC 812 ACATATAA GGCTAGCTACAACGA AAAATCAT 2198 1575 UUUUAUAU G UUUUUCC 813 GTATAATA GGCTAGCTACAACGA AAATCAT 2200 1619 GAGAAAU G UUAUUUCC 814 GTATATAA GGCTAGCTACAACGA AATTTCCT 2201 1619 GAGAAAU G UUAUAUAC 814 GTATATAA GGCTAGCTACAACGA AATTTCCT 2201 1610 AAACACCC G UAAAACCC 815 GTGTTAG GGCTAGCTACAACGA ATTTTCCT 2201 1610 AAACACCC G UAAAACCU 816 CAAATTCTA GGCTAGCTACAACGA ATTTTCCT 2201 1610 AAACACCC G UAAAACCC 815 GTGTTAG GGCTAGCTACAACGA AGGTAGTT 2202 1610 AAACACCC G UAAAACCU 816 AAAGTCTACA GGCTAGCTACAACGA AGGTAGTT 2202 1610 AAACACCC G UAAAACCC 815 GTGTTAG GGCTAGCTACAACGA AGGGATAT 2202 1610 AAACACCC G UAAAACCC 815 GTGTTAG GGCTAGCTACAACGA AGGGATAT 2202 1610 AAACACC G GCAAACCC 815 GTGTTAG GGCTAGCTACACGA CGGA AGGTACT 2202 1610 AAACACC G GCAAACCC 815 GTGTTAG GGCTAGCTACACCA					
907 CAGAAAUU G UAUUUUUU 781 AAAAATA GGCTAGCTACAACGA AATTCTG 2187 920 UUUUCUAU G CCACAUUA 782 TAATUTGG GGCTAGCTACAACGA ATTCATAA 2188 1039 UAGAACAU G UGAGAAA 785 TTTACCTA GGCTAGCTACAACGA ATTGATAAA 2188 1058 AUAAAGCG G UUCUAAGA 785 TCTTACATA GGCTAGCTACAACGA ATTGATAT 2189 1058 AUAAAGCG G UUCUAAGA 786 TCTTAGAA GGCTAGCTACAACGA ATTTTAT 2190 1102 GUUAAGAU G UGACAGUG 789 CACTGTCA GGCTAGCTACAACGA ATATTAAC 2191 1168 AAGGCACU G UAGUGAAU 792 ATTCACTA GGCTAGCTACAACGA ATATTCAT 2191 1253 AUGAUUU G CAGGUUGU 797 ACAACCTG GGCTAGCTACAACGA ATATCAT 2193 1260 UGAGGGUG G UCUCCAU 798 ATGGGAAGA GGCTAGCTACAACGA ATATCATC 2193 1287 CAUCCAAU G CAGGCAAG 799 CTTGCCTG GGCTAGCTACAACGA AAATCAT 2195 1412 AUGAACUU G UUGAGCCA 804 TUGGCCAA GGCTAGCTACAACGA AAATCAT 2196 1484 GUGGGUC G CAAAAUCU 808 AAATTTTG GGCTAGCTACAACGA AAATCAT 2196 1564 CAUAUUUU G CGUGUUU 811 ATAACACG GGCTAGCTACAACGA AAAATCT 2198 1568 UUUUGCGU G UUAUAUGU 812 ACATATTAA GGCTAGCTACAACGA AAAATCT 2198 1569 UUUUGCGU G UUAUAUGU 812 ACATATTAA GGCTAGCTACAACGA AAAATCT 2200 1519 GAGAAAAU G UUAUAUGC 813 GTATATAA GGCTAGCTACAACGA ATATTAACA 2200 1619 GAGAAAAG UUAUAUAC 813 GTATAATAA GGCTAGCTACAACGA ATATTAACA 2200 1619 GAGAAAAU G UUAUAUAC 813 GTATAATAA GGCTAGCTACAACGA ATATTAACA 2200 1619 GAGAAAAU G UUAUAUAC 813 GTATAATAA GGCTAGCTACAACGA ATATTAACA 2200 1619 GAGAAAAU G UUAUAUAC 813 GTATAATAA GGCTAGCTACAACGA ATATTACCA 2200 1619 GAGAAAAU G UUAAUAUAC 814 GTATATAA GGCTAGCTACAACGA ATATTACCA 2200 1619 GAGAAAAU G UUAAUAUC 814 CTAAATTAA GGCTAGCTACAACGA ATATTACCA 2200 1619 GAGAAAAU G UUAAUAUC 815 GTATTAAG GGCTAACTACAACGA ATTTTACCA 2200 1619 AAACACCC G UAAAACACU 815 GTGTTTAG GGCTACCTACACGA AGGTTACTACACGA 2003GGATT 2202					
920 UUUUCUNU G CCACAUUA 782 TAATGTGG GGCTAGCTACAACGA ATAGAAAA 2188 1039 UAGAGACU G UAGGUAAA 785 TITACCTA GGCTAGCTACAACGA ATATTATA 2189 1058 AUAAAUCG G UGUAAGA 786 TETTAGAA GGCTAGCTACAACGA ATATTATA 2189 1102 GUUAAGUG G UGUAGAG 789 CACTGTCA GGCTAGCTACAACGA ATATTAAC 2191 1168 AAGGCACG G LOBUGUAU 792 ATTGACTA GGCTAGCTACAACGA ATATTAAC 2191 1253 AUGAUUUU G CAGGUUGU 797 ACAACCTG GGCTAGCTACAACGA AAAATCAT 2193 1260 UGCAGGUU G UCULCCAU 798 ATGGAAGA GGCTAGCTACAACGA AAAATCAT 2193 1287 CACACCTG GGCTAGCTACAACGA AAAATCAT 2194 1187 CACACCAAU G CAGGAAA 799 CTTGACCTG GGCTAGCTACAACGA AAAATCAT 2195 1412 AUGAACUU G UUGAGCCA 804 TUGGGCCA GGCTAACTACAACGA AAAATCAT 2196 1484 GUGGGUCC G CAAAAUCU 808 AGATTTG GGCTAGCTACAACGA AAAATCAT 2196 1564 CAUAUUUU G CGUGUUUU B 81 AACATTAA GGCTAGCTACAACGA AAAATATG 2198 1575 CUUUAUGC G UUAUAUGU					
1039					
1058					
1102 GUUANDAU G UGACAGUG 789 CACTGTCA GGCTAGCTACAACGA ATATTAAC 2191					
1168					
1253 AUGAUUUU G CAGGUUGU 797 ACAACCTG GGCTAGCTACAACGA AAAATCAT 2193 1260 UGCAGGUU G UCUUCCAU 798 ATGGAAGA GGCTAGCTACAACGA AAAATCAT 2194 1287 CAAUCCAAU G CAGGAAG 799 CTTGCCTG GGCTAGCTACAACGA ACCTGCA 2194 1412 AUGAACUU G UUGGCCCA 804 TUGGGCCAA GGCTAGCTACAACGA AAAATCAT 2196 1484 GUUGGGUC G CAAAAACUU 808 AGATTTTG GGCTAGCTACAACGA GAAACTAT 2196 1564 CAUAUUUU G CGUGUUAU 811 ATAACACG GGCTAGCTACAACGA AAAATATG 2198 1568 UUUUGGCU G UUUAUGUG 812 ACATATAA GGCTAGCTACAACGA AAAATATG 2198 1575 UUUUUAUG G GUUUAUG 813 GTATAATA GGCTAGCTACAACGA ATATTACA 2200 1519 GAGAAAAI G UUAUUUG 814 CTAAATAA GGCTAGCTACAACGA ATATTACA 2200 1519 GAGAAAAI G UUAUUUG 814 CTAAATAA GGCTAGCTACAACGA ATTTTCTC 2201 21 ACUCCCCA G CUAAGACUU 815 GTGTTAG GGCTAGCTACAACGA ATGTTCTC 2201 32 AAACACCC G UAAGACUU 816 AAGTCTTA GGCTAGCTACAACGA GGGTTTT 2203 33 AAACACCC G UAAGACUU 816 AAGTCTTA GGCTAGCTACAACGA GGGTTTT 2203					
1260					
1287					
1412 AUGARCUU G UUGGCCCA 804 TUGGCCAA GGCTAGCTACAACGA AAGTTCAT 2196 1484 GUGGGUCC G CAAAAUCU 808 AGATTTTG GGCTAGCTACAACGA GGACCCAC 2197 1564 CAUAUUUU G CGUGUUAU 811 ATAACACG GGCTAGCTACAACGA AAAATATG 2198 1568 UUUUGGGU G UUAUAUGU 812 ACATATAA GGCTAGCTACAACGA ACGCAAAA 2199 1575 UUUUGUU G UUAUAUGU 813 GTATAATA GGCTAGCTACAACGA ACGCAAAA 2200 1619 GAGAAAAU G UUAUUUAG 814 CTAAATAA GGCTAGCTACAACGA ATTTTCC 2201 1619 ACCCCCA G CUAAGACU 815 GTGTTATG GGCTAGCTACAACGA ATTTCCC 2202 32 AAACACCC G UAAGACU 816 AAGTCTTA GGCTAGCTACAACGA GGGTGTTT 2203					
1484 GURGGUCC G CAAAAUCU 808 AGATTTT GGCTAGCTACAACGA GGACCCAC 2197 1564 CAUAUUUU G CGUGUUAU 811 ATRACAGG GGCTAGCTACCACGA ARAATATG 2198 1568 UUUNGGGU G UUAUAUGU 812 ACACTATAA GGCTAGCTACAACGA AGCCAAAA 2199 1575 UGUUAUAU G UUAUAUAC 813 GTATAATA GGCTAGCTACAACGA ACACAAAA 2200 1519 GAGAAAAU G UUAUUUAG 814 CTAAATAA GGCTAGCTACAACGA ATTTTCTC 2201 21 ACUCCCA G CUAAAACAC 815 GTGTTAG GGCTAGCTACAACGA AGGGGGT 2202 32 AAACACCC G UAAGACUU 816 AAGTCTAA GGCTAGCTACAACGA GGGTGTTT 2203					
1564 CAUAUUUU G COUGUUAU 811 ATAACACG GGCTAGCTACAACGA AAAATATG 2198					
1568 UUUUQCGU G UUAUAUGU 812 ACATATAA GGCTAGCTACAACGA ACGCAAAA 2199 1575 UGUUAUAU G UUAUUAUC 813 GTATAATA GGCTAGCTACAACGA ATATTAACA 2200 1619 GAGAAAAU G UUAUUUAG 814 CTAAATAA GGCTAGCTACAACGA ATTTTCTC 2201 21 ACUCCCCA G CUAAACAC 815 GTGTTTAG GGCTAGCTACAACGA TGGGAGT 2202 32 AAACACCC G UAAGACUU 816 AAGTCTTA GGCTAGCTACAACGA GGGTGTTT 2203					
1575 UGUUAUAU G UAUUAUAC 813 GTATAATA GGCTAGCTACAACGA ATATAACA 2200 1519 GAGAAAAU G UUAUUUAG 814 CTAAATAA GGCTAGCTACAACGA ATTTTCTC 2201 21 ACUCCCCA G CUAAAACAC 815 GGCTGTGTG GGCTAGCTACAACGA GGGGGGT 2202 32 ANACACCC G UAAGACUU 816 AAGTCTTA GGCTAGCTACAACGA GGGTGTT 2203					
1619 GAGAANAU G UUAUUUAG 814 CTAAATAA GGCTAGCTACAACGA ATTTTCTC 2201 21 ACUCCCCA G CUANACAC 815 GTGTTTAG GGCTAGCTACAACGA TGGGGAGT 2202 32 AAACACCC G UAAGACUU 816 AAGTCTTA GGCTAGCTACAACGA GGGTGTTT 2203					
21 ACUCCCCA G CUAAACAC 815 GTGTTTAG GGCTAGCTACAACGA TGGGGAGT 2202 32 AAACACCC G UAAGACUU 816 AAGTCTTA GGCTAGCTACAACGA GGGTGTTT 2203					
32 AAACACCC G UAAGACUU 816 . AAGTCTTA GGCTAGCTACAACGA GGGTGTTT 2203					
76 UGAUCACA G CUGCCAAG 817 CTTGGCAG GGCTAGCTACAACGA TGTGATCA 2204					
	76	UGAUCACA G CUGCCAAG	817	CTTGGCAG GGCTAGCTACAACGA TGTGATCA	2204

Table 28

85	CUGCCAAG G CUACCUAA	818	TTAGGTAG GGCTAGCTACAACGA CTTGGCAG	2205
103	AGAAGACA G UUAUCUCA	819	TGAGATAA GGCTAGCTACAACGA TGTCTTCT	2206
118	CAUAUUUG G CUGCCAGC	820	GCTGGCAG GGCTAGCTACAACGA CAAATATG	2207
125	GGCUGCCA G CUUUUUAU	821	ATAAAAAG GGCTAGCTACAACGA TGGCAGCC	2208
177	UCCUGCUG G UAUCAUGG	822	CCATGATA GGCTAGCTACAACGA CAGCAGGA	2209
191	UGGAGAAA G UCCAAUAC	823	GTATTGGA GGCTAGCTACAACGA TTTCTCCA	2210
212	CUCGCUCA G CUAUAAGA	824	TCTTATAG GGCTAGCTACAACGA TGAGCGAG	2211
224	UAAGAAGA G CCUCAACC	825	GGTTGAGG GGCTAGCTACAACGA TCTTCTTA	2212
251	CUCAACAA G CACGUCAA	826	TTGACGTG GGCTAGCTACAACGA TTGTTGAG	2213
255	ACAAGCAC G UCAAAAGC	827	GCTTTTGA GGCTAGCTACAACGA GTGCTTGT	2214
262	CGUCAAAA G CUACAGAA	828	TTCTGTAG GGCTAGCTACAACGA TTTTGACG	2215
326	GUAUCAUC G UGAUGCUU	829	AAGCATCA GGCTAGCTACAACGA GATGATAC	2216
342	UCUCUGAA G UUCUGCUA	830	TAGCAGAA GGCTAGCTACAACGA TTCAGAGA	2217
368	GAUCUGCA G CUUGCCAC	831	GTGGCAAG GGCTAGCTACAACGA TGCAGATC	2218
381	CCACAUCA G CUUAAAAU	832	ATTTTAAG GGCTAGCTACAACGA TGATGTGG	2219
443	CUUCCUGA G UAGAAGAG	833	CTCTTCTA GGCTAGCTACAACGA TCAGGAAG	2220
451	GUAGAAGA G UUUCUUUG	834	CAAAGAAA GGCTAGCTACAACGA TCTTCTAC	2221
467	GUGAAAAG G UCAAGAUU	835	AATCTTGA GGCTAGCTACAACGA CTTTTCAC	2222
537	UGAAAAGG G CUUUAUUU	836	AAATAAAG GGCTAGCTACAACGA CCTTTTCA	2223
568	CAAAAUAA G UGUAUAAA	837	TTTATACA GGCTAGCTACAACGA TTATTTTG	2224
603	UCAACAUG G CUCACAAA	838	TTTGTGAG GGCTAGCTACAACGA CATGTTGA	2225
644	GAUGAAGA G UUUAGUUU	839	AAACTAAA GGCTAGCTACAACGA TCTTCATC	2226
649	AGAGUUUA G UUUUAAAA	840	TTTTAAAA GGCTAGCTACAACGA TAAACTCT	2227
673	GCCAACAA G UUCACUUC	841	GAAGTGAA GGCTAGCTACAACGA TTGTTGGC	2228
691	UAUAUAAA G CAUUAUUU	842	AAATAATG GGCTAGCTACAACGA TTTATATA	2229
713	CUUUUGAG G UGAAUAUA	843	TATATTCA GGCTAGCTACAACGA CTCAAAAG	2230
742	AUGUAAAA G CUUCUUUA	844	TAAAGAAG GGCTAGCTACAACGA TTTTACAT	2231
758	AAUACUAA G UAUUUUUC	845	GAAAATA GGCTAGCTACAACGA TTAGTATT	2232
769	UUUUUCAG G UCUUCACC	846	GGTGAAGA GGCTAGCTACAACGA CTGAAAAA	2233
780	UUCACCAA G UAUCAAAG	847	CTTTGATA GGCTAGCTACAACGA TTGGTGAA	2234
788	GUAUCAAA G UAAUAACA	848	TGTTATTA GGCTAGCTACAACGA TTTGATAC	2235
805	CAAAUGAA G UGUCAUUA	849	TAATGACA GGCTAGCTACAACGA TTCATTTG	2236
823	UCAAAAUA G UCCACUGA	850	TCAGTGGA GGCTAGCTACAACGA TATTTTGA	2237
872	UAUUUGUA G UAACUAUC	851	GATAGTTA GGCTAGCTACAACGA TACAAATA	2238
941	CUUUUAAA G UUGAUGAG	852	CTCATCAA GGCTAGCTACAACGA TTTAAAAG	2239
956	AGAAUCAA G UAUGGAAA	853	TTTCCATA GGCTAGCTACAACGA TTGATTCT	2240
966	AUGGAAAA G UAAGGCCA	854	TGGCCTTA GGCTAGCTACAACGA TTTTCCAT	2241
971	AAAGUAAG G CCAUACUC	855	GAGTATGG GGCTAGCTACAACGA CTTACTTT	2242
1003	CCUUUUAA G UAAUUUUU	856 857	AAAAATTA GGCTAGCTACAACGA TTAAAAGG TACATGTA GGCTAGCTACAACGA TAGAATTC	2243
1033	GAAUUCUA G UACAUGUA			
1043	ACAUGUAG G UAAAUCAU	858	ATGATTTA GGCTAGCTACAACGA CTACATGT ATTAACCA GGCTAGCTACAACGA CAGTTCTC	2245
1091	GAGAACUG G UGGUUAAU		CATATTAA GGCTAGCTACAACGA CACCAGTT CATATTAA GGCTAGCTACAACGA CACCAGTT	2246
1094	AACUGGUG G UUAAUAUG	860		
1108	AUGUGACA G UGAGAUUA	861 862	TAATCTCA GGCTAGCTACAACGA TGTCACAT TGATATGA GGCTAGCTACAACGA TAATCTCA	2248
1117	UGAGAUUA G UCAUAUCA			
1163	CAUUUAAG G CACUGUAG	863	CTACAGTG GGCTAGCTACAACGA CTTAAATG ATAATTCA GGCTAGCTACAACGA TACAGTGC	2250
1171	GCACUGUA G UGAAUUAU	864	ATARTTUA GGCTAGCTACAACGA TACAGTGC	2251

Table 28

1184	UUAUCUGA G CUAGAGUU	865	AACTCTAG GGCTAGCTACAACGA TCAGATAA	2252
1190	GAGCUAGA G UUACCUAG	866	CTAGGTAA GGCTAGCTACAACGA TCTAGCTC	2253
1198	GUUACCUA G CUUACCAU	867	ATGGTAAG GGCTAGCTACAACGA TAGGTAAC	2254
1257	UUUUGCAG G UUGUCUUC	868	GAAGACAA GGCTAGCTACAACGA CTGCAAAA	2255
1273	CCAUUCCA G CCUAACAU	869	ATGTTAGG GGCTAGCTACAACGA TGGAATGG	2256
1291	CAAUGCAG G CAAGGAAA	870	TTTCCTTG GGCTAGCTACAACGA CTGCATTG	2257
1314	GAUUUCCA G UGACAGAA	871	TTCTGTCA GGCTAGCTACAACGA TGGAAATC	2258
1339	UAUCUCAA G UAUUUUUU	872	AAAAATA GGCTAGCTACAACGA TTGAGATA	2259
1416	ACUUGUUG G CCCAUCUA	873	TAGATGGG GGCTAGCTACAACGA CAACAAGT	2260
1436	CAUCUACA G CUGACCCU	874	AGGGTCAG GGCTAGCTACAACGA TGTAGATG	2261.
1456	ACAUGGGG G UUAGGGGA	875	TCCCCTAA GGCTAGCTACAACGA CCCCATGT	2262
1465	UJJAGGGGA G CUGACAAU	876	ATTGTCAG GGCTAGCTACAACGA TCCCCTAA	2263
1476	GACAAUUC G UGGGUCCG	877	CGGACCCA GGCTAGCTACAACGA GAATTGTC	2264
1480	AUUCGUGG G UCCGCAAA	878	TTTGCGGA GGCTAGCTACAACGA CCACGAAT	2265
1506	ACCUANUA G CCUACUAU	879	ATAGTAGG GGCTAGCTACAACGA TATTAGGT	2266
1545	CAUAAACA G UAAAUUAA	880	TTAATTTA GGCTAGCTACAACGA TGTTTATG	2267
1566	UAUUUUGC G UGUUAUAU	881	ATATAACA GGCTAGCTACAACGA GCAAAATA	2268
1603	ACAAUAAA G UAAGCUAG	882	CTAGCTTA GGCTAGCTACAACGA TTTATTGT	2269
1607	UAAAGUAA G CUAGAGAA	883	TTCTCTAG GGCTAGCTACAACGA TTACTTTA	2270
13	GUCAGAAA A CUCCCCAG	884	CTGGGGAG GGCTAGCTACAACGA TTTCTGAC	2271
26	CCAGCUAA A CACCCGUA	885	TACGGGTG GGCTAGCTACAACGA TTAGCTGG	2272
28	AGCUAAAC A CCCGUAAG	886	CTTACGGG GGCTAGCTACAACGA GTTTAGCT	2273
37	CCCGUAAG A CUUCAUAC	887	GTATGAAG GGCTAGCTACAACGA CTTACGGG	2274
42	AAGACUUC A UACAACAC	888	GTGTTGTA GGCTAGCTACAACGA GAAGTCTT	2275
47	UUCAUACA A CACAAUAC	889	GTATTGTG GGCTAGCTACAACGA TGTATGAA	2276
49	CAUACAAC A CAAUACUC	890	GAGTATTG GGCTAGCTACAACGA GTTGTATG	2277
52	ACAACACA A UACUCUAU	891	ATAGAGTA GGCTAGCTACAACGA TGTGTTGT	2278
67	AUACUGUG A UGAUCACA	892	TGTGATCA GGCTAGCTACAACGA CACAGTAT	2279
70	CUGUGAUG A UCACAGCU	893	AGCTGTGA GGCTAGCTACAACGA CATCACAG	2280
73	UGAUGAUC A CAGCUGCC	894	GGCAGCTG GGCTAGCTACAACGA GATCATCA	2281
100	AAAAGAAG A CAGUUAUC	895	GATAACTG GGCTAGCTACAACGA CTTCTTTT	2282
111	GUUAUCUC A UAUUUGGC	896	GCCAAATA GGCTAGCTACAACGA GAGATAAC	2283
144	UUCUCUCG A CCACUUAA	897	TTAAGTGG GGCTAGCTACAACGA CGAGAGAA	2284
147	UCUCGACC A CUUAAAAC	898	GTTTTAAG GGCTAGCTACAACGA GGTCGAGA	2285
154	CACUUAAA A CUUCAGAC	899	GTCTGAAG GGCTAGCTACAACGA TTTAAGTG	2286
161	AACUUCAG A CUUCCUGU	900	ACAGGAAG GGCTAGCTACAACGA CTGAAGTT	2287
182	CUGGUAUC A UGGAGAAA	901	TTTCTCCA GGCTAGCTACAACGA GATACCAG	2288
196	AAAGUCCA A UACCUCAC	902	GTGAGGTA GGCTAGCTACAACGA TGGACTTT	2289
203	AAUACCUC A CUCGCUCA	903	TGAGCGAG GGCTAGCTACAACGA GAGGTATT	2290
230	GAGCCUCA A CCAUUGAA	904	TTCAATGG GGCTAGCTACAACGA TGAGGCTC	2291
233	CCUCAACC A UUGAAAUG	905	CATTICAA GGCTAGCTACAACGA GGTTGAGG	2292
239	CCAUUGAA A UGCCUCAA	906	TTGAGGCA GGCTAGCTACAACGA TTCAATGG	2293
247	AUGCCUCA A CAAGCACG	907	CGTGCTTG GGCTAGCTACAACGA TGAGGCAT	2294
253	CAACAAGC A CGUCAAAA	908	TTTTGACG GGCTAGCTACAACGA GCTTGTTG	2295
270	GCUACAGA A UCUAUUUA	909	TAAATAGA GGCTAGCTACAACGA TCTGTAGC	2296
282	AUUUAUCA A UUUCUGUC	910	GACAGAAA GGCTAGCTACAACGA TGATAAAT	2297
293	UCUGUCUC A UCUUAAUA	911	TATTAAGA GGCTAGCTACAACGA GAGACAGA	2298

Table 28

299	UCAUCUUA A UAUGUCUC	912	GAGACATA GGCTAGCTACAACGA TAAGATGA	2299
314	UCUUGCUG A UCUGUAUC	913	GATACAGA GGCTAGCTACAACGA CAGCAAGA	2300
3 2 3	UCUGUAUC A UCGUGAUG	914	CATCACGA GGCTAGCTACAACGA GATACAGA	2301
329	UCAUCGUG A UGCUUCUC	915	GAGAAGCA GGCTAGCTACAACGA CACGATGA	2302
353	CUGCUACA A CCUCUAGA	916	TCTAGAGG GGCTAGCTACAACGA TGTAGCAG	2303
361	ACCUCUAG A UCUGCAGC	917	GCTGCAGA GGCTAGCTACAACGA CTAGAGGT	2304
375	AGCUUGCC A CAUCAGCU	918	AGCTGATG GGCTAGCTACAACGA GGCAAGCT	2305
377	CUUGCCAC A UCAGCUUA	919	TAAGCTGA GGCTAGCTACAACGA GTGGCAAG	2306
388	AGCUUAAA A UCUGUCAU	920	ATGACAGA GGCTAGCTACAACGA TTTAAGCT	2307
395	AAUCUGUC A UCCCAUGC	921	GCATGGGA GGCTAGCTACAACGA GACAGATT	2308
400	GUCAUCCC A UGCAGACA	922	TGTCTGCA GGCTAGCTACAACGA GGGATGAC	2309
406	CCAUGCAG A CAGGAAAA	923	TTTTCCTG GGCTAGCTACAACGA CTGCATGG	2310
414	ACAGGAAA A CAAUAUUG	924	CAATATTG GGCTAGCTACAACGA TTTCCTGT	2311
417	GGAAAACA A UAUUGUAU	925	ATACAATA GGCTAGCTACAACGA TGTTTTCC	2312
427	AUUGUAUA A CAGACCAC	926	GTGGTCTG GGCTAGCTACAACGA TATACAAT	2313
431	UAUAACAG A CCACUUCC	927	GGAAGTGG GGCTAGCTACAACGA CTGTTATA	2314
434	AACAGACC A CUUCCUGA	928	TCAGGAAG GGCTAGCTACAACGA GGTCTGTT	2315
473	AGGUCAAG A UUAAGACU	929	AGTCTTAA GGCTAGCTACAACGA CTTGACCT	2316
479	AGAUUAAG A CUAAAACU	930	AGTTTTAG GGCTAGCTACAACGA CTTAATCT	2317
485	AGACUAAA A CUUAUUGU	931	ACAATAAG GGCTAGCTACAACGA TTTAGTCT	2318
498	UUGUUACC A UAUGUAUU	932	AATACATA GGCTAGCTACAACGA GGTAACAA	2319
508	AUGUAUUC A UCUGUUGG	933	CCAACAGA GGCTAGCTACAACGA GAATACAT	2320
517	UCUGUUGG A UCUUGUAA	934	TTACAAGA GGCTAGCTACAACGA CCAACAGA	2321
526	UCUUGUAA A CAUGAAAA	935	TTTTCATG GGCTAGCTACAACGA TTACAAGA	2322
528	UUGUAAAC A UGAAAAGG	936	CCTTTCA GGCTAGCTACAACGA GTTTACAA	2323
552	UUUCAAAA A UUAACUUC	937	GAAGTTAA GGCTAGCTACAACGA TTTTGAAA	2324
556	AAAAAUUA A CUUCAAAA	938	TTTTGAAG GGCTAGCTACAACGA TAATTTTT	2325
564	ACUUCAAA A UAAGUGUA	939	TACACTTA GGCTAGCTACAACGA TTTGAAGT	2326
577	UGUAUAAA A UGCAACUG	940	CAGTTGCA GGCTAGCTACAACGA TTTATACA	2327
582	AAAAUGCA A CUGUUGAU	941	ATCAACAG GGCTAGCTACAACGA TGCATTTT	2328
589	AACUGUUG A UUUCCUCA	942	TGAGGAAA GGCTAGCTACAACGA CAACAGTT	2329
598	UUUCCUCA A CAUGGCUC	943	GAGCCATG GGCTAGCTACAACGA TGAGGAAA	2330
600	UCCUCAAC A UGGCUCAC	944	GTGAGCCA GGCTAGCTACAACGA GTTGAGGA	2331
607	CAUGGCUC A CAAAUUUC	945	GAAATTTG GGCTAGCTACAACGA GAGCCATG	2332
611	GCUCACAA A UUUCUAUC	946	GATAGAAA GGCTAGCTACAACGA TTGTGAGC	2333
624	UAUCCCAA A UCUUUUCU	947	AGAAAGA GGCTAGCTACAACGA TTGGGATA	2334
637	UUCUGAAG A UGAAGAGU	948	ACTOTTCA GGCTAGCTACAACGA CTTCAGAA	2335
657	GUUUUAAA A CUGCACUG	949	CAGTGCAG GGCTAGCTACAACGA TTTAAAAC	2336
662	AAAACUGC A CUGCCAAC	950	GTTGGCAG GGCTAGCTACAACGA GCAGTTTT	2337
669	CACUGCCA A CAAGUUCA	951	TGAACTTG GGCTAGCTACAACGA TGGCAGTG	2338
677	ACAAGUUC A CUUCAUAU	952	ATATGAAG GGCTAGCTACAACGA GAACTTGT	2339
682	UUCACUUC A UAUAUAAA	953	TTTATATA GGCTAGCTACAACGA GAAGTGAA	2340
693	UAUAAAGC A UUAUUUUU	954	AAAAATAA GGCTAGCTACAACGA GCTTTATA	2341
717	UGAGGUGA A UAUAAUUU	955	AAATTATA GGCTAGCTACAACGA TCACCTCA	2342
722	UGAAUAUA A UUUAUAUU	956	AATATAAA GGCTAGCTACAACGA TATATTCA	2343
734	AUAUUACA A UGUAAAAG	957	CTTTTACA GGCTAGCTACAACGA TGTAATAT	2344
751	CUUCUUUA A UACUAAGU	958	ACTTAGTA GGCTAGCTACAACGA TAAAGAAG	2345
			·	

Table 28

775	AGGUCUUC A CCAAGUAU	959	ATACTTGG GGCTAGCTACAACGA GAAGACCT	2346
791	UCAAAGUA A UAACACAA	960	TTGTGTTA GGCTAGCTACAACGA TACTTTGA	2347
794	AAGUAAUA A CACAAAUG	961	CATTIGTG GGCTAGCTACAACGA TATTACTT	2348
796	GUAAUAAC A CAAAUGAA	962	TTCATTTG GGCTAGCTACAACGA GTTATTAC	2349
800	UAACACAA A UGAAGUGU	963	ACACTTCA GGCTAGCTACAACGA TTGTGTTA	2350
810	GAAGUGUC A UUAUUCAA	964	TTGAATAA GGCTAGCTACAACGA GACACTTC	2351
820	UAUUCAAA A UAGUCCAC	965	GTGGACTA GGCTAGCTACAACGA TTTGAATA	2352
827	AAUAGUCC A CUGACUCC	966	GGAGTCAG GGCTAGCTACAACGA GGACTATT	2353
831	GUCCACUG A CUCCUCAC	967	GTGAGGAG GGCTAGCTACAACGA CAGTGGAC	2354
838	GACUCCUC A CAUCUGUU	968	AACAGATG GGCTAGCTACAACGA GAGGAGTC	2355
840	CUCCUCAC A UCUGUUAU	969	ATAACAGA GGCTAGCTACAACGA GTGAGGAG	2356
862	UAUAAAGA A CUAUUUGU	970	ACAAATAG GGCTAGCTACAACGA TCTTTATA	2357
875	UUGUAGUA A CUAUCAGA	971	TCTGATAG GGCTAGCTACAACGA TACTACAA	2358
884	CUAUCAGA A UCUACAUU	972	AATGTAGA GGCTAGCTACAACGA TCTGATAG	2359
890	GAAUCUAC A UUCUAAAA	973	TTTTAGAA GGCTAGCTACAACGA GTAGATTC	2360
898	AUUCUAAA A CAGAAAUU	974	AATTTCTG GGCTAGCTACAACGA TTTAGAAT	2361
904	AAACAGAA A UUGUAUUU	975	AAATACAA GGCTAGCTACAACGA TTCTGTTT	2362
923	UCUAUGCC A CAUUAACA	976	TGTTAATG GGCTAGCTACAACGA GGCATAGA	2363
925	UAUGCCAC A UUAACAUC	977	GATGTTAA GGCTAGCTACAACGA GTGGCATA	2364
929	CCACAUUA A CAUCUUUU	978	AAAAGATG GGCTAGCTACAACGA TAATGTGG	2365
931	ACAUUAAC A UCUUUUAA	979	TTAAAAGA GGCTAGCTACAACGA GTTAATGT	2366
945	UAAAGUUG A UGAGAAUC	980	GATTCTCA GGCTAGCTACAACGA CAACTTTA	2367
951	UGAUGAGA A UCAAGUAU	981	ATACTTGA GGCTAGCTACAACGA TCTCATCA	2368
974	GUAAGGCC A UACUCUUA	982	TAAGAGTA GGCTAGCTACAACGA GGCCTTAC	2369
984	ACUCUUAC A UAAUAAAA	983	TTTTATTA GGCTAGCTACAACGA GTAAGAGT	2370
987	CUUACAUA A UAAAAUUC	984	GAATTTTA GGCTAGCTACAACGA TATGTAAG	2371
992	AUAAUAAA A UUCCUUUU	985	AAAAGGAA GGCTAGCTACAACGA TTTATTAT	2372
1006	UUUAAGUA A UUUUUUCA	986	TGAAAAA GGCTAGCTACAACGA TACTTAAA	2373
1019	UUCAAAGA A UCACAGAA	987	TTCTGTGA GGCTAGCTACAACGA TCTTTGAA	2374
1022	AAAGAAUC A CAGAAUUC	988	GAATTCTG GGCTAGCTACAACGA GATTCTTT	2375
1:027	AUCACAGA A UUCUAGUA	989	TACTAGAA GGCTAGCTACAACGA TCTGTGAT	2376
1037	UCUAGUAC A UGUAGGUA	990	TACCTACA GGCTAGCTACAACGA GTACTAGA	2377
1047	GUAGGUAA A UCAUAAAU	991	ATTTATGA GGCTAGCTACAACGA TTACCTAC	2378
1050	GGUAAAUC A UAAAUCUG	992	CAGATTTA GGCTAGCTACAACGA GATTTACC	2379
1054	AAUCAUAA A UCUGUUCU	993	AGAACAGA GGCTAGCTACAACGA TTATGATT	2380
1066	GUUCUAAG A CAUAUGAU	994	ATCATATG GGCTAGCTACAACGA CTTAGAAC	2381
1068	UCUAAGAC A UAUGAUCA	995	TGATCATA GGCTAGCTACAACGA GTCTTAGA	2382
1073	GACAUAUG A UCAACAGA	996	TCTGTTGA GGCTAGCTACAACGA CATATGTC	2383
1077	UAUGAUCA A CAGAUGAG	997	CTCATCTG GGCTAGCTACAACGA TGATCATA	2384
1081	AUCAACAG A UGAGAACU	998	AGTICTCA GGCTAGCTACAACGA CTGTTGAT	2385
1087	AGAUGAGA A CUGGUGGU	999	ACCACCAG GGCTAGCTACAACGA TCTCATCT	2386
1098	GGUGGUUA A UAUGUGAC	1000	GTCACATA GGCTAGCTACAACGA TAACCACC	2387
1105	AAUAUGUG A CAGUGAGA	1001	TCTCACTG GGCTAGCTACAACGA CACATATT ATGACTAA GGCTAGCTACAACGA CTCACTGT	2388
1113	ACAGUGAG A UUAGUCAU			
1120	GAUUAGUC A UAUCACUA	1003	TAGTGATA GGCTAGCTACAACGA GACTAATC	2390
1125	UAUCACUA A UAUACUAA	1004	TATATTAG GGCTAGCTACAACGA GATATGAC TTAGTATA GGCTAGCTACAACGA TAGTGATA	2391
1179	DADCACOA A UNUACUAA	1002	TIAGTATA GGCTAGCTACAACGA TAGTGATA	2332

Table 28

1137	AUAUACUA A CAACAGAA	1006	TTCTGTTG GGCTAGCTACAACGA TAGTATAT	2393
1140	UACUAACA A CAGAAUCU	1007	AGATTCTG GGCTAGCTACAACGA TGTTAGTA	2394
1145	ACAACAGA A UCUAAUCU	1008	AGATTAGA GGCTAGCTACAACGA TCTGTTGT	2395
1150	AGAAUCUA A UCUUCAUU	1009	AATGAAGA GGCTAGCTACAACGA TAGATTCT	2396
1156	UAAUCUUC A UUUAAGGC	1010	GCCTTAAA GGCTAGCTACAACGA GAAGATTA	2397
1165	UUUAAGGC A CUGUAGUG	1011	CACTACAG GGCTAGCTACAACGA GCCTTAAA	2398
1175	UGUAGUGA A UUAUCUGA	1012	TCAGATAA GGCTAGCTACAACGA TCACTACA	2399
1205	AGCUUACC A UACUAUAU	1013	ATATAGTA GGCTAGCTACAACGA GGTAAGCT	2400
1221	UCUUUGGA A UCAUGAAA	1014	TTTCATGA GGCTAGCTACAACGA TCCAAAGA	2401
1224	UUGGAAUC A UGAAACCU	1015	AGGTTTCA GGCTAGCTACAACGA GATTCCAA	2402
1229	AUCAUGAA A CCUUAAGA	1016	TCTTAAGG GGCTAGCTACAACGA TTCATGAT	2403
1237	ACCUUAAG A CUUCAGAA	1017	TTCTGAAG GGCTAGCTACAACGA CTTAAGGT	2404
1245	ACUUCAGA A UGAUUUUG	1018	CAAAATCA GGCTAGCTACAACGA TCTGAAGT	2405
1248	UCAGAAUG A UUUUGCAG	1019	CTGCAAAA GGCTAGCTACAACGA CATTCTGA	2406
1267	UGUCUUCC A UUCCAGCC	1020	GGCTGGAA GGCTAGCTACAACGA GGAAGACA	2407
1278	CCAGCCUA A CAUCCAAU	1021	ATTGGATG GGCTAGCTACAACGA TAGGCTGG	2408
1280	AGCCUAAC A UCCAAUGC	1022	GCATTGGA GGCTAGCTACAACGA GTTAGGCT	2409
1285	AACAUCCA A UGCAGGCA	1023	TGCCTGCA GGCTAGCTACAACGA TGGATGTT	2410
1300	CAAGGAAA A UAAAAGAU	1024	ATCTTTTA GGCTAGCTACAACGA TTTCCTTG	2411
1307	AAUAAAAG A UUUCCAGU	1025	ACTGGAAA GGCTAGCTACAACGA CTTTTATT	2412
1317	UUCCAGUG A CAGAAAAA	1026	TTTTTCTG GGCTAGCTACAACGA CACTGGAA	2413
1325	ACAGAAAA A UAUAUUAU	1027	ATAATATA GGCTAGCTACAACGA TTTTCTGT	2414
1352	UUUUAAAA A UAUAUGAA	1028	TTCATATA GGCTAGCTACAACGA TTTTAAAA	2415
1360	AUAUAUGA A UUCUCUCU	1029	AGAGAGAA GGCTAGCTACAACGA TCATATAT	2416
1373	CUCUCCAA A UAUUAACU	1030	AGTTAATA GGCTAGCTACAACGA TTGGAGAG	2417
1379	AAAUAUUA A CUAAUUAU	1031	ATAATTAG GGCTAGCTACAACGA TAATATTT	2418
1383	AUUAACUA A UUAUUAGA	1032	TCTAATAA GGCTAGCTACAACGA TAGTTAAT	2419
1391	DUUAUAUU A DAUUAUUU	1033	AAATATAA GGCTAGCTACAACGA CTAATAAT	2420
1404	AUUUUGAA A UGAACUUG	1034	CAAGTTCA GGCTAGCTACAACGA TTCAAAAT	2421
1408	UGAAAUGA A CUUGUUGG	1035	CCAACAAG GGCTAGCTACAACGA TCATTTCA	2422
1420	GUUGGCCC A UCUAUUAC	1036	GTAATAGA GGCTAGCTACAACGA GGGCCAAC	2423
1429	UCUAUUAC À UCUACAGO	1037	GCTGTAGA GGCTAGCTACAACGA GTAATAGA	2424
1440	UACAGCUG A CCCUUGAA	1038	TTCAAGGG GGCTAGCTACAACGA CAGCTGTA	2425
1448	ACCCUUGA A CAUGGGGG	1039	CCCCCATG GGCTAGCTACAACGA TCAAGGGT	2426
1450	CCUUGAAC A UGGGGGUU	1040	AACCCCCA GGCTAGCTACAACGA GTTCAAGG	2427
1469	GGGAGCUG A CAAUUCGU	1041	ACGAATTG GGCTAGCTACAACGA CAGCTCCC	2428
1472	AGCUGACA A UUCGUGGG	1042	CCCACGAA GGCTAGCTACAACGA TGTCAGCT	2429
1489	UCCGCAAA A UCUUAACU	1043	AGTTAAGA GGCTAGCTACAACGA TTTGCGGA	2430
1495	AAAUCUUA A CUACCUAA	1044	TTAGGTAG GGCTAGCTACAACGA TAAGATTT	2431
1503	ACUACCUA A UAGCCUAC	1045	GTAGGCTA GGCTAGCTACAACGA TAGGTAGT	2432
1517	UACUAUUG A CCAUAAAC	1046	GTTTATGG GGCTAGCTACAACGA CAATAGTA	
1520	UAUUGACC A UAAACCUU	1047	AAGGTTTA GGCTAGCTACAACGA GGTCAATA	2434
1524	GACCAUAA A CCUUACUG	1048	CAGTAAGG GGCTAGCTACAACGA TTATGGTC	2435
1533	CCUUACUG A UAACAUAA	1049	TTATGTTA GGCTAGCTACAACGA CAGTAAGG	2436
1536	UACUGAUA A CAUAAACA	1050	TGTTTATG GGCTAGCTACAACGA TATCAGTA	2437
1538	CUGAUAAC A UAAACAGU	1051	ACTGTTTA GGCTAGCTACAACGA GTTATCAG	2438
1542	UAACAUAA A CAGUAAAU	1052	ATTTACTG GGCTAGCTACAACGA TTATGTTA	2437

Table 28

1549	AACAGUAA A UUAACACA	1053	TGTGTTAA GGCTAGCTACAACGA TTACTGTT	2440
1553	GUAAAUUA A CACAUAUU	1054	AATATGTG GGCTAGCTACAACGA TAATTTAC	2441
1555	AAAUUAAC A CAUAUUUU	1055	AAAATATG GGCTAGCTACAACGA GTTAATTT	2442
1557	AUUAACAC A UAUUUUGC	1056	GCAAAATA GGCTAGCTACAACGA GTGTTAAT	2443
1584	UAUUAUAC A CUAUAUUC	1057	GAATATAG GGCTAGCTACAACGA GTATAATA	2444
1598	UUCCUACA A UAAAGUAA	1058	TTACTTTA GGCTAGCTACAACGA TGTAGGAA	2445
1617	UAGAGAAA A UGUUAUUU	1059	AAATAACA GGCTAGCTACAACGA TTTCTCTA	2446

Input Sequence = PLN. Cut Site = R/Y
Stem Length = 8 . Core Sequence = GGCTAGCTACAACGA
PLN (Homo sapiens phospholamban (PLN) mRNA.; 1635 bp)

Table 29: Human Phospholamban (PLN) amberzyme Ribozyme and Target Sequence

GCUGUGAU GGAGGAACUCC CU UCAAGGACAUCUCGGG AUCACAGO
Adeciding gangamatric of ucaagaacine age Adecaaa
1
738
739
740
741
742
743
744
745
746
747
748
749
750
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753
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757
758

2475	2476	2477	2478	2479	2480	2481	2482	2483	2484	2485	2486	2487	2488	2489	2490	2491	2492	2493	2494	2495	2496	2497	2498	2499	2500	2501	2502	2503	2504	2505
UAUGGUAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUAAGUU	GAUGAAUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAUGGUA	AGAUCCAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAUGAAU	CAUGUUUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGAUCCA	GCCCUUUU GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG AUGUUUAC	AUTUDADA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUUAUTU	AACAGUUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUUUUAUA	GAAAUCAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUUGCAU	GAGGAAAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACAGUUG	UNCAUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAAAAGA	AAACUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCUUCAG	UGGCAGUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUJUUAA	CUUGUUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUGCAGU	AUUCACCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAAGAGU	AUUAUAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCUCAAA	AGCUUUUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUUGUAAU	UGACACUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUUUGUGU	AAUAAUGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUUCAUU	UGAGGAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUGGACU	UNAGAUNA GGAGGNANCUCC CU UCNAGGNCAUCGUCCGGG AGAUGUGN	AGUUACUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAUAGUU	APABABUN GGAGGNAACUCC CU UCNAGGNCAUCGUCCGGG AAUUUCUG	UNAUGUGG GGAGGANACUCC CU UCNAGGACAUCGUCCGGG AUAGAAAA	AUTICUCAU GGAGGANACUCC CU UCAAGGACAUCGUCCGGG AACUUUAA	UUGAUUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCAACUU	UUUACCUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGUACUA	UCUUAGAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAUUUAU	CUGUUGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAUGUCU	CCAGUUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCUGUUG	CACUGUCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAUUAAC	CUCACUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAUAUUA
160	191	762	763	764	765	992	767	768	694	770	771	772	773	774	775	176	777	778	179	780	781	782	783	784	785	786	787	788	789	790
AACTUIAUU G UUACCAUA	UACCAUAU G UAUUCAUC	AUUCAUCU G UUGGAUCU	UGGAUCUU G UAAACAUG	GUAAACAU G AAAAGGGC	AAAUAAGU G UAUAAANU	UAUAAAAU G CAACUGUU	AUGCAACU G UUGAUUUC	CAACUGUU G AUTUCCUC	UCUUUUCU G AAGAUGAA	CUGAAGAU G AAGAGUUU	UUAAAACU G CACUGCCA	ACUGCACU G CCAACAAG	ACUCUUUU G AGGUGAAU	UUUGAGGU G AAUAUAAU	AUUACAAU G UAAAAGCU	ACACAAAU G AAGUGUCA	AAUGAAGU G UCAUUAUU	AGUCCACU G ACUCCUCA	UCACAUCU G UUAUCUUA	AACUAUUU G UAGUAACU	CAGAAAUU G UAUUUUUU	UUUUCUAU G CCACAUUA	UUAAAGUU G AUGAGAAU	AAGUUGAU G AGAAUCAA	UAGUACAU G UAGGUAAA	AUAAAUCU G UUCUAAGA	AGACAUAU G AUCAACAG	CAACAGAU G AGAACUGG	GUUAAUAU G UGACAGUG	UAAUAUGU G ACAGUGAG
492	502	512	522	530	570	579	585	588	633	689	099	999	710	715	736	802	807	830	844	698	206	920	944	947	1039	1058	1072	1083	1102	1104

1110	GUGACAGU G AGAUUAGU	164	ACUMANCE GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUGUCAC	2506
1168	AAGGCACU G UAGUGAAU	792	AUUCACUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUGCCUU	2507
1173	ACUGUAGU G AAUUAUCU	793	AGAUDANU GGAGGAAACUCC CU UCAAGGACAUGGUCCGGG ACUACAGU	2508
1182	AAUUAUCU G AGCUAGAG	794	CUCUAGEU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAUAAUU	2509
1226	GGAAUCAU G AAACCUUA	795	UAAGGUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGAUUCC	2510
1247	UUCAGAAU G AUUUUGCA	964	UGCAAAAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUUCUGAA	2511
1253	AUGAUUTU G CAGGUUGU	797	ACAACCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAAUCAU	2512
1260	UGCAGGUU G UCUUCCAU	798	AUGGAAGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACCUGCA	2513
1287	CAUCCAAU G CAGGCAAG	199	CUUBCCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUUGGAUG	2514
1316	UUUCCAGU G ACAGAAAA	800	UUUUCUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUGGAAA	2515
1358	AAAUAUAU G AAUUCUCU	801	AGAGAAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAUAUUU	2516
1401	UAUAUUUU G AAAUGAAC	802	GUUCAUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAAUAUA	2517
1406	UUUGAAAU G AACUUGUU	803	AACAAGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUUUCAAA	2518
1412	AUGRACUU G UUGGCCCA	804	UGGGCCAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGUUCAU	2519
1439	CUACAGCU G ACCCUUGA	805	UCANGGGU GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG AGCUGUAG	2520
1446	UGACCCUU G AACAUGGG	908	CCCAUGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGGGUCA	2521
1468	GGGGAGCU G ACAAUUCG	807	CGAAUUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCUCCCC	2522
1484	GUGGGUCC G CAAAAUCU	808	AGAUJUJUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGACCCAC	2523
1516	CUACUAUU G ACCAUAAA	608	UNUAUGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUAGUAG	2524
1532	ACCUUACU G AUAACAUA	810	UNUGUUNU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUAAGGU	2525
1564	CAUAUUUU G CGUGUUAU	811	AUNACACS GGAGGNAACUCC CU UCAAGGNCAUCGUCCGGG AAAAUAUG	2526
1568	UNUUGCGU G UNAUAUGU	812	ACAUNUAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGCAAAA	2527
1575	UGUDADAD G DADDADAC	813	GUAUAAUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAUAACA	2528
1619	GAGAAAU G UUAUUUAG	814	CUANAUNA GGAGGANACUCC CU UCANGGACAUCGUCCGGG AUTUUCUC	2529
21	ACUCCCCA G CUANACAC	815	GUGUTUNG GGAGGAAACUCC CU UCAAGGACAUGGUCCGGG UGGGGAGU	2530
32	AAACACCC G UAAGACUU	816	AAGUCUUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGUGUUU	2531
9.	UGAUCACA G CUGCCAAG	817	CUUGGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUGAUCA	2532
88	CUGCCAAG G CUACCUAA	818	UUNGGUNG GGNGGNAACUCC CU UCAAGGNCAUCGUCCGGG CUUGGCAG	2533
103	AGAAGACA G UUAUCUCA	819	UGAGAUNA GGAGGANACUCC CU UCNAGGACAUCGUCCGGG UGUCUUCU	2534
118	CAUAUTUG G CUGCCAGC	820	GCUGGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAAUAUG	2535
125	GGCUGCCA G CUUTUUAU	821	AUNANANG GGNGGANACUCC CU UCANGGACAUCGUCCGGG UGGCAGCC	2536

2537	2538	2539	2540	2541	2542	2543	2544	2545	2546	2547	2548	2549	2550	2551	2552	2553	2554	2555	2556	2557	2558	2559	2560	2561	2562	2563	2564	2565	2566	2567
CCAUGAUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGCAGGA	GUAUNGGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUCUCCA	UCUUAUNG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAGCGAG	GGUUGAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCUUCUUA	UNGACGUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGUUGAG	GCUUUUGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUGCUUGU	UNCUGUAG GGAGGAAACUCC CU UCAAGGACAUCGUCGGG UUUUGACG	AAGCAUCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAUGAUAC	UAGCAGAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCAGAGA	GUGGCAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCAGAUC	AUDUDAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAUGUGG	CUCUUCUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCAGGAAG	CAAAGAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCUUCUAC	AAUCUUGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUUUUCAC	AAAUAAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUUUUCA	UUUAUACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUAUUUUG	UUUGUGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUGUUGA	AAACUAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCUUCAUC	UUUUNAANA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAAACUCU	GAAGUGAA GGAGGAAACUCC CU UCAAGGACAUCGUCGGG UUGUUGGC	AAAUAAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUAUAUA	DADADUCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUCAAAAG	UAAAGAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUUACAU	GNAAAAUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUAGUAUU	GGUGAAGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGAAAAA	CUUUGAUA GGAGGAMACUCC CU UCAAGGACAUCGUCCGGG UUGGUGAA	UGUDAUDA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUGAUAC	UMANGACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCAUUUG	UCAGUGGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAUUUUGA	GAUAGUUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UACAAAUA	CUCAUCAA GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG UUUAAAAG
822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852
TICCHGCTIG G DAUCAUGG	UGGAGAAA G UCCAAUAC	CILCOCITCA G CUADAAGA	HARGAGA G CCUCAACC	CHICARCEA G CACGUCAA	ACAAGCAC G UCAAAAGC	CGUCAAAA G CUACAGAA	GUAUCAUC G UGAUGCUU	UCUCUGAA G UUCUGCUA	GAUCUGCA G CUUGCCAC	CCACAUCA G CUUNAAAU	CUUCCUGA G UAGAAGAG	GUNGAAGA G UUUCUUUG	GUGAAAAG G UCAAGAUU	UGARAGG G CUUUAUUU	CAAAAUAA G UGUAUAAA	UCAACAUG G CUCACAAA	GAUGAAGA G UUUAGUUU	AGAGILIUA G UUUDAAAA	GCCAACAA G UUCACUUC	UAUAUAAA G CAUUAUUU	CUUUUGAG G UGAAUAUA	AUGUAAAA G CUUCUUUA	AAUACUAA G UAUUUUUC	UUUUUCAG G UCUUCACC	UUCACCAA G UAUCAAAG	GUAUCAAA G UAAUAACA	CAAAUGAA G UGUCAUUA	UCAAAAUA G UCCACUGA	DAUTUGUA G DAACUAUC	CUUUDAAA G UUGAUGAG
127	101	212	224	261	255	262	326	342	368	381	443	451	467	537	568	603	644	649	673	169	713	742	758	169	780	788	805	823	872	941

2568	2569	2570	2571	2572	2573	2574	2575	2576	2577	2578	2579	2580	2581	25.82	2002	2583	2584	2585	2586	2587	2588	2589	2590	2591	2592	2593	2594	2595	2596	2597	1002	2330
UNUCCAUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGAUUCU	UGGCCUUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUUCCAU	CARTIATION COAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUUACUUU	ABBERNITIA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUAAAAGG	TACALICATA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAGAAUUC	ATTENDING GGAGGAAACHCC CU UCAAGGACAUCGUCCGGG CUACAUGU	AUGNOCCA COACCAAACUCC CU UCAAGGACAUCGUCOGG CAGUUCUC	CALIAITIAA GGARGAAACUCC CU UCAAGGACAUCGUCGGG CACCAGUU	THANTOTICE CONCORDANTICE CU UCAAGGACAUCGUCGGG UGUCACAU	MANUCUCA GENERALISCO CII IICAAGGACAUCGUCGGG UAAUCUCA	CONCESSION CONCESSION OF THE PARCENCE COURAGE COURAGE	COACHOOS SCANOSARCING CTI IICAAGGACAUCGUCGGG UACAGUGC	ADMINOCH GENOCEPERCOS CT. HORAGGACALICGICCEGG UCAGAUAA	ARCOCORG GENERALING CO.	CUAGGUAA GGAGGAAACUCC CU UCAAGGACAUCUUCCGGG UCOMACGC	AUGGUAAG GGAGGAAACUCC CU UCAAGGACAUCGUCUGGG UAGGUAAC	GAAGACAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGCAAAA	AUGUUAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGAAUGG	UNUCCUNG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGCAUUG	INCIDENCE GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGAAAUC	AAAAAAITA GGAGGAAACUCC CU UCAAGGACAUCGUCGGG UUGAGAUA	TIACALICIGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CAACAAGU	ARRENICAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUAGAUG	HEECEGUAA GGAGGAAACUCE CU UCAAGGACAUCGUCCGGG CCCCAUGU	ATTIGUES GGAGGAAACUCC CU UCAAGGACAUCGUCGGG UCCCCUAA	CIGGACTICA GGAGGAAACUCC CU UCAAGGACAUGGUCCGGG GAAUUGUC	HILITANSA GRANGAAACUCC CU UCAAGGACAUCGUCCGGG CCACGAAU	USDECTION OF THE PROPERTY OF T	ADACONO CONSCIENTING OU HONNOCONONICONOCIONAS DELINIMOS	UUAAUUUA GGAGGAAACUCC CO OCTROSTOCIOCOCO GGAAAIIA	AUAUAACA GGAGGAAACUCC CU UCAAGGAAACOCGGCGGG GCAAGGGG	CUAGCUUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUAUUGU	UNCUCUAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUACUUUA
853	854		200	920	6 6	828	658	200	198	298	200	800	865	998	867	898	869	870	17.0	27.0	073	27.0	278	920	010	0.70	0/0	87.8	880	881	882	883
ACTANICAN C HANGGADA		Augshan e chasecen	AAAGUAAG G CCAUACUC	CCUUUNA G UAAUUUU	GAAUUCUA G UACAUGUA	ACAUGUAG G UAAAUCAU	GAGAACUG G UGGUUAAU	AACUGGUG G UUAAUG	AUGUGACA G UGAGAUUA	UGAGAUUA G UCAUAUCA	CAUUUAAG G CACUGUAG	GCACUGUA G UGAAUUAU	UNAUCUGA G CUAGAGUU	GAGCUAGA G UUACCUAG	GUUACCUA G CUUACCAU	THEREGAS G UNGUCUNC	CONTROL OF COURSE ON IN	Canada Constitution	CAMOCAGE G CONCORDS	GROUDCCA G DOACAGO	UNDCOCHA C CACCOCCO	ACOUGING & CCCAOCON	CAUCUACA G COGNECCO	ACAUGGG G OUNGGGGG	UDAGGGA G CUGACAGO	GACAMOUC & OGGGOCCO	AUTOGOGG G OCCOCANA	ACCUAAUA G CCUACUAU	CAUAAACA G UAAAUUAA	UAUUUUGC G UGUUAUAU	ACAAUAAA G UAAGCUAG	TANACHAR C CHACAGAA
	955	906	971	1003	1033	1043	1001	1094	1108	1117	1163	1111	1184	1190	1198	1257		2001	1621	1314	1339	1416	1436	1456	1465	1476	1480	1506	1545	1566	1603	200

2599	0097	2601	2602	2603	2604	2605	2606	2607	2608	2609	2610	2611	2612	2613	2614	2615	2616	2617	2618	2619	2620	2621	2622	2623	2624	2625	2626	2627	2628	2629
GGAGUUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGACUCUG	UAUGAAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUACGGGU	UAGGUAGE GGAGGAAACUCE CU UCAAGGACAUCGUCCGGG UUGGEAGC	ACUGUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUUAGGU	AUAACUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCUUUUA	CUGGCAGC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AAAUAUGA	CAGGAAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAAGUUU	CAUGAUAC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AGCAGGAC	ACUUUCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGAUACC	GACUUUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUGAUAC	USGACUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCAUGAU	AGGCUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUAUAGCU	UNGAGGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCUUAUA	AAUAGAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUAGCUU	CUGCAGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAGAGGUU	UUUCCUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCAUGGG	UNGUIUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUCUGCA	AUTGUIUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGUCUGC	GAAGUGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUUAUAC	AAACUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UACUCAGG	ANGAMACU GGAGGAMACUCC CU UCANGGACAUCGUCCGGG UUCUACUC	AUCUUGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUUCACA	GUCUUDAD GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGACCUU	GUIUUAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUAAUCUU	ACAAGAUC GGAGGAAACUCC CU UCAAGGACAUGGUCCGGG AACAGAUG	UACAAGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAACAGAU	AUAAAGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUUCAUG	AAUAAAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUUUUCAU	UUGUGAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGUUGAG	CUCUUCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCAGAAA	ACUAAACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCAUCUU
1060	1001	1062	1063	1064	1065	1066	1067	1068	1069	1070	1011	1072	1073	1074	1075	1076	1077	1078	1079	1080	1081	1082	1083	1084	1085	1086	1087	1088	1089	1090
CAGAGUCA G AAAACUCC	ACCCGUAA G ACUUCAUA	GCUGCCAA G GCUACCUA	ACCUARAS G ASGACAGU	UAAAAGAA G ACAGUUAU	UCAUAUTU G GCUGCCAG	AAACUUCA G ACUUCCUG	guccuecu e enaucaue	GGUAUCAU G GAGAAAGU	GUAUCAUG G AGAAAGUC	AUCAUGGA G AAAGUCCA	AGCUAUAA G AAGAGCCU	UAUNAGAA G AGCCUCAA	AAGCUACA G AAUCUAUU	AACCUCUA G AUCUGCAG	CCCAUGCA G ACAGGAAA	UGCAGACA G GAAAACAA	GCAGACAG G AAAACAAU	GUAUAACA G ACCACUUC	CCUGAGUA G AAGAGUUU	GAGUAGAA G AGUUUCUU	UGUGAAAA G GUCAAGAU	AAGGUCAA G AUUAAGAC	AAGAUUAA G ACUAAAAC	CAUCUGUU G GAUCUUGU	AUCUGUUG G AUCUUGUA	CAUGAAAA G GGCUUUAU	AUGAAAAG G GCUUUAUU	CUCAACAU G GCUCACAA	UUUCUGAA G AUGAAGAG	AAGAUGAA G AGUUUAGU
6	36	84	96	66	117	160	176	184	185	187	219	222	268	360	405	409	410	430	446	646	466	472	478	515	516	535	536	602	989	642

2661	2662	2663	2664	2665	2666	2667	2668	2669	2670	2671	2672	2673	2674	
ANUAUAAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAAUAAUU	AGAUGGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACAAGUU	CURACCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGUUCAA	CCURACCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUGUUCA	CCCURACC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG CCAUGUUC	CCCCUMAC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG CCCAUGUU	CAGCUCCC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG UAACCCCC	UCAGCUCC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG CUAACCCC	GUCAGCUC GGAGGAAACUCC CU UCAAGGACAUGGUCGGG CCUAACCC	UGUCAGCU GGAGGAAACUCC CU UCAAGGACAUCGUCGGG CCCUAACC	UGCGGACC GGAGGAACUCC CU UCAAGGACAUCGUCGGG ACGAAUUG	UUGCGGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACGAAUU	CAUTUTICU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAGCUUAC	AACAUUUU GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG UCUAGCUU	The second secon
1122	1123	1124	1125	1126	1127	1128	1129	1130	1131	1132	1133	1134	1135	
AAUUAUUA G AUUAUAUU	AACUUGUU G GCCCAUCU	UUGAACAU G GGGGUUAG	UGAACAUG G GGGUUAGG	GAACAUGG G GGUUAGGG	AACAUGGG G GUUAGGGG	GGGGGUUA G GGGAGCUG	GGGGUUAG G GGAGCUGA	GGGUUAGG G GAGCUGAC	GGUUAGGG G AGCUGACA	CAAUUCGU G GGUCCGCA	AAUUCGUG G GUCCGCAA	GUAAGCUA G AGAAAAUG	AAGCUAGA G AAAAUGUU	
1390	1415	1452	1453	1454	1455	1460	1461	1462	1463	1478	1479	1611	1613	l

Input Sequence = PLIN. Cut Site = G/.
Stern Length = 8. Core Sequence = GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG
PLN (Homo sapiens pivospholamban (PLN) mRNA: 1635 bp)

Table 30: Human Phospholamban (PLN) Antisense and Target Sequence

Pos	Target	Seq ID	Antisense	AS Seq ID
1	CAGAGUCAGAAAACUCCCCAGCUAA	2447	TTAGCTGGGGAGTTTTCTGACTCTG	3051
2	AGAGUCAGAAAACUCCCCAGCUAAA	2448	TTTAGCTGGGGAGTTTTCTGACTCT	3052
3	GAGUCAGAAAACUCCCCAGCUAAAC	2449	GTTTAGCTGGGGAGTTTTCTGACTC	3053
4	AGUCAGAAAACUCCCCAGCUAAACA	2450	TGTTTAGCTGGGGAGTTTTCTGACT	3054
5	GUCAGAAAACUCCCCAGCUAAACAC	2451	GTGTTTAGCTGGGGAGTTTTCTGAC	3055
6	UCAGAAAACUCCCCAGCUAAACACC	2452	GGTGTTTAGCTGGGGAGTTTTCTGA	3056
7	CAGAAAACUCCCCAGCUAAACACCC	2453	GGGTGTTTAGCTGGGGAGTTTTCTG	3057
8	AGAAAACUCCCCAGCUAAACACCCG	2454	CGGGTGTTTAGCTGGGGAGTTTTCT	305B
9	GAAAACUCCCCAGCUAAACACCCGU	2455	ACGGGTGTTTAGCTGGGGAGTTTTC	3059
10	AAAACUCCCCAGCUAAACACCCGUA	2456	TACGGGTGTTTAGCTGGGGAGTTTT	3060
11	AAACUCCCCAGCUAAACACCCGUAA	2457	TTACGGGTGTTTAGCTGGGGAGTTT	3061
12	AACUCCCCAGCUAAACACCCGUAAG	2458	CTTACGGGTGTTTAGCTGGGGAGTT	3062
13	ACUCCCCAGCUAAACACCCGUAAGA	2459	TCTTACGGGTGTTTAGCTGGGGAGT	3063
14	CUCCCCAGCUAAACACCCGUAAGAC	2460	GTCTTACGGGTGTTTAGCTGGGGAG	3064
15	UCCCCAGCUAAACACCCGUAAGACU	2461	AGTCTTACGGGTGTTTAGCTGGGGA	3065
16	CCCCAGCUAAACACCCGUAAGACUU	2462	AAGTCTTACGGGTGTTTAGCTGGGG	3066
17	CCCAGCUAAACACCCGUAAGACUUC	2463	GAAGTCTTACGGGTGTTTAGCTGGG	3067
18	CCAGCUAAACACCCGUAAGACUUCA	2464	TGAAGTCTTACGGGTGTTTAGCTGG	3068
19	CAGCUAAACACCCGUAAGACUUCAU	2465	ATGAAGTCTTACGGGTGTTTAGCTG	3069
20	AGCUAAACACCCGUAAGACUUCAUA	2466	TATGAAGTCTTACGGGTGTTTAGCT	3070
21	GCUAAACACCCGUAAGACUUCAUAC	2467	GTATGAAGTCTTACGGGTGTTTAGC	3071
22	CUAAACACCCGUAAGACUUCAUACA	2468	TGTATGAAGTCTTACGGGTGTTTAG	3072
23	UAAACACCCGUAAGACUUCAUACAA	2469	TTGTATGAAGTCTTACGGGTGTTTA	3073
24	AAACACCCGUAAGACUUCAUACAAC	2470	GTTGTATGAAGTCTTACGGGTGTTT	3074
25	AACACCCGUAAGACUUCAUACAACA	2471	TGTTGTATGAAGTCTTACGGGTGTT	3075
26	ACACCCGUAAGACUUCAUACAACAC	2472	GTGTTGTATGAAGTCTTACGGGTGT	3076
27	CACCCGUAAGACUUCAUACAACACA	2473	TGTGTTGTATGAAGTCTTACGGGTG	3077
28	ACCCGUAAGACUUCAUACAACACAA	2474	TTGTGTTGTATGAAGTCTTACGGGT	3078
29	CCCGUAAGACUUCAUACAACACAAU	2475	ATTGTGTTGTATGAAGTCTTACGGG	3079
63	UGUGAUGAUCACAGCUGCCAAGGCU	2476	AGCCTTGGCAGCTGTGATCATCACA	3080
64	GUGAUGAUCACAGCUGCCAAGGCUA	2477	TAGCCTTGGCAGCTGTGATCATCAC	3081
65	UGAUGAUCACAGCUGCCAAGGCUAC	2478	GTAGCCTTGGCAGCTGTGATCATCA	3082
66	GAUGAUCACAGCUGCCAAGGCUACC	2479	GGTAGCCTTGGCAGCTGTGATCATC	3083
67	AUGAUCACAGCUGCCAAGGCUACCU	2480	AGGTAGCCTTGGCAGCTGTGATCAT	3084
68	UGAUCACAGCUGCCAAGGCUACCUA	2481	TAGGTAGCCTTGGCAGCTGTGATCA	3085
69	GAUCACAGCUGCCAAGGCUACCUAA	2482	TTAGGTAGCCTTGGCAGCTGTGATC	3086
70	AUCACAGCUGCCAAGGCUACCUAAA	2483	TTTAGGTAGCCTTGGCAGCTGTGAT	3087
71	UCACAGCUGCCAAGGCUACCUAAAA	2484	TTTTAGGTAGCCTTGGCAGCTGTGA	3088
72	CACAGCUGCCAAGGCUACCUAAAAG	2485	CTTTTAGGTAGCCTTGGCAGCTGTG	3089
73	ACAGCUGCCAAGGCUACCUAAAAGA	2486	TCTTTTAGGTAGCCTTGGCAGCTGT	3090
74	CAGCUGCCAAGGCUACCUAAAAGAA	2487	TTCTTTTAGGTAGCCTTGGCAGCTG	3091
75	AGCUGCCAAGGCUACCUAAAAGAAG	2488	CTTCTTTTAGGTAGCCTTGGCAGCT	3092
76	GCUGCCAAGGCUACCUAAAAGAAGA	2489	TCTTCTTTTAGGTAGCCTTGGCAGC	3093
77	CUGCCAAGGCUACCUAAAAGAAGAC	2490	GTCTTCTTTTAGGTAGCCTTGGCAG	3094

78	UGCCAAGGCUACCUAAAAGAAGACA	2491	TGTCTTCTTTTAGGTAGCCTTGGCA	3095
79	GCCAAGGCUACCUAAAAGAAGACAG	2492	CTGTCTTCTTTTAGGTAGCCTTGGC	3096
80	CCAAGGCUACCUAAAAGAAGACAGU	2493	ACTGTCTTCTTTTAGGTAGCCTTGG	3097
81	CAAGGCUACCUAAAAGAAGACAGUU	2494	AACTGTCTTCTTTTAGGTAGCCTTG	3098
98	AGACAGUUAUCUCAUAUUUGGCUGC	2495	GCAGCCAAATATGAGATAACTGTCT	3099
99	GACAGUUAUCUCAUAUUUGGCUGCC	2496	GGCAGCCAAATATGAGATAACTGTC	3100
100	ACAGUUAUCUCAUAUUUGGCUGCCA	2497	TGGCAGCCAAATATGAGATAACTGT	3101
101	CAGIIIAUCUCAUAUUUGGCUGCCAG	2498	CTGGCAGCCAAATATGAGATAACTG	3102
102	AGUUAUCUCAUAUUUGGCUGCCAGC	2499	GCTGGCAGCCAAATATGAGATAACT	3103
102	GUUAUCUCAUAUUUGGCUGCCAGCU	2500	AGCTGCAGCCAAATATGAGATAAC	3104
103	IIIJAUCUCAUAUJUUGGCUGCCAGCUU	2501	AAGCTGGCAGCCAAATATGAGATAA	3105
104	UAUCUCAUAUUUGGCUGCCAGCUUU	2502	AAAGCTGGCAGCCAAATATGAGATA	3106
	AUCUCAUAUUUGGCUGCCAGCUUUU	2502	AAAAGCTGGCAGCCAAATATGAGAT	3107
106	UCUCAUAUUUGGCUGCCAGCUUUUU	2504	AAAAAGCTGGCAGCCAAATATGAGA	3108
107	CUCAUAUUUGGCUGCCAGCUUUUUA	2505	TAAAAAGCTGGCAGCCAAATATGAG	3109
108	UCAUAUUUGGCUGCCAGCUUUUUAU	2505	ATAAAAGCTGGCAGCCAAATATGA	3110
109		2508	GATAAAAAGCTGGCAGCCAAATATG	3111
110	CAUAUUUGGCUGCCAGCUUUUUAUC	2507	AGATAAAAAGCTGGCAGCCAAATAT	3112
111	AUAUUUGGCUGCCAGCUUUUUAUCU	2509	AGATAAAAAGCTGGCAGCCAAATA	3113
112	UAUUUGGCUGCCAGCUUUUUAUCUU		AAGATAAAAAGCTGGCAGCCAAAT	3114
113	AUUUGGCUGCCAGCUUUUUAUCUUU	2510	GAAAGATAAAAAGCTGGCAGCCAAA	3115
114	UUUGGCUGCCAGCUUUUUAUCUUUC	2511	AGAAGATAAAAAGCTGGCAGCCAAA	3116
115	UUGGCUGCCAGCUUUUUAUCUUUCU	2512	GAGAAGATAAAAAGCTGGCAGCCAA	3117
116	UGGCUGCCAGCUUUUUAUCUUUCUC	2513	AGAGAAAGATAAAAAGCTGGCAGCCA AGAGAAAGATAAAAAGCTGGCAGCC	3117
117	GGCUGCCAGCUUUUUAUCUUUCUCU	2514	GAGAGAAGATAAAAAGCTGGCAGCC	3119
118	GCUGCCAGCUUUUUAUCUUUCUCUC	2515	CGAGAGAAAGATAAAAAGCTGGCAGC	3119
119	CUGCCAGCUUUUUAUCUUUCUCUCG	2516		3120
120	UGCCAGCUUUUUAUCUUUCUCUCGA	2517	TCGAGAGAAAGATAAAAAGCTGGCA	3121
121	GCCAGCUUUUUAUCUUUCUCUCGAC	2518	GTCGAGAGAAAGATAAAAAGCTGGC	3122
122	CCAGCUUUUUAUCUUUCUCUCGACC	2519	GGTCGAGAGAAAGATAAAAAGCTGG	3123
123	CAGCUUUUUAUCUUUCUCUCGACCA	2520	TGGTCGAGAGAAAAAAAAGCTG	
124	AGCUUUUUAUCUUUCUCUCGACCAC	2521	GTGGTCGAGAGAAAAAAAAGCT	3125
125	GCUUUUUAUCUUUCUCUCGACCACU	2522	AGTGGTCGAGAGAAAGATAAAAAGC	
126	CUUUUUAUCUUUCUCGACCACUU	2523	AAGTGGTCGAGAGAAAGATAAAAAG	3127
132	AUCUUUCUCUCGACCACUUAAAACU	2524	AGTTTTAAGTGGTCGAGAGAAAGAT	3128
133	UCUUUCUCGACCACUUAAAACUU	2525	AAGTTTTAAGTGGTCGAGAGAAAGA	3129
134	CUUUCUCUCGACCACUUAAAACUUC	2526	GAAGTTTTAAGTGGTCGAGAGAAAG	3130
135	UUUCUCUCGACCACUUAAAACUUCA	2527	TGAAGTTTTAAGTGGTCGAGAGAAA	3131
136	UUCUCUCGACCACUUAAAACUUCAG	2528	CTGAAGTTTTAAGTGGTCGAGAGAA	3132
137	UCUCUCGACCACUUAAAACUUCAGA	2529	TCTGAAGTTTTAAGTGGTCGAGAGA	3133
138	CUCUCGACCACUUAAAACUUCAGAC	2530	GTCTGAAGTTTTAAGTGGTCGAGAG	3134
139	UCUCGACCACUUAAAACUUCAGACU	2531	AGTCTGAAGTTTTAAGTGGTCGAGA	3135
140	CUCGACCACUUAAAACUUCAGACUU	2532	AAGTCTGAAGTTTTAAGTGGTCGAG	3136
141	UCGACCACUUAAAACUUCAGACUUC	2533	GAAGTCTGAAGTTTTAAGTGGTCGA	3137
142	CGACCACUUAAAACUUCAGACUUCC	2534	GGAAGTCTGAAGTTTTAAGTGGTCG	3138
143	GACCACUUAAAACUUCAGACUUCCU	2535	AGGAAGTCTGAAGTTTTAAGTGGTC	3139
144	ACCACUUAAAACUUCAGACUUCCUG	2536	CAGGAAGTCTGAAGTTTTAAGTGGT	3140
145	CCACUUAAAACUUCAGACUUCCUGU	2537	ACAGGAAGTCTGAAGTTTTAAGTGG	3141

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147	ACUUAAAACUUCAGACUUCCUGUCC	2538	GGACAGGAAGTCTGAAGTTTTAAGT	3142
148	CUUAAAACUUCAGACUUCCUGUCCU	2539	AGGACAGGAAGTCTGAAGTTTTAAG	3143
149	INIAAAACINICAGACINICCUGUCCUG	2540	CAGGACAGGAAGTCTGAAGTTTTAA	3144
150	HAAACUUCAGACUUCCUGUCCUGC	2541	GCAGGACAGGAAGTCTGAAGTTTTA	3145
151	AAAACUUCAGACUUCCUGUCCUGCU	2542	AGCAGGACAGGAAGTCTGAAGTTTT	3146
152	AAACUUCAGACUUCCUGUCCUGCUG	2543	CAGCAGGACAGGAAGTCTGAAGTTT	3147
153	AACUUCAGACUUCCUGUCCUGCUGG	2544	CCAGCAGGACAGGAAGTCTGAAGTT	3148
153	ACUTICAGACUTICCUGUCCUGCUGGU	2545	ACCAGCAGGACAGGAAGTCTGAAGT	3149
	CUUCAGACUUCCUGUCCUGCUGGUA	2546	TACCAGCAGGACAGGAAGTCTGAAG	3150
155 156	ITICAGACUUCCUGUCCUGCUGGUAU	2547	ATACCAGCAGGACAGGAAGTCTGAA	3151
	UCAGACUTICCUGUCCUGCUGUAUC	2548	GATACCAGCAGGACAGGAAGTCTGA	3152
157	CAGACUUCCUGUCCUGCUGGUAUCA	2549	TGATACCAGCAGGACAGGAAGTCTG	3153
158	AGACUUCCUGUCCUGCUGGUAUCAU	2549	ATGATACCAGCAGGACAGGAAGTCT	3154
159		2551	CATGATACCAGCAGGACAGGAAGTC	3155
160	GACUUCCUGUCCUGCUGGUAUCAUG	2551	CATGATACCAGCAGGACAGGAAGT	3156
161	ACUUCCUGUCCUGCUGGUAUCAUGG	2552	TCCATGATACCAGCAGGACAGGAAGT	3157
162	CUUCCUGUCCUGCUGGUAUCAUGGA		CTCCATGATACCAGCAGGACAGGAAG	3158
163	UUCCUGUCCUGCUGGUAUCAUGGAG	2554		3159
164	UCCUGUCCUGCUGGUAUCAUGGAGA	2555	TCTCCATGATACCAGCAGGACAGGA	
165	CCUGUCCUGCUGGUAUCAUGGAGAA	2556	TTCTCCATGATACCAGCAGGACAGG	3160 3161
166	CUGUCCUGCUGGUAUCAUGGAGAAA	2557	TTTCTCCATGATACCAGCAGGACAG	
167	UGUCCUGCUGGUAUCAUGGAGAAAG	2558	CTTTCTCCATGATACCAGCAGGACA	3162
168	GUCCUGCUGGUAUCAUGGAGAAAGU	2559	ACTTTCTCCATGATACCAGCAGGAC	3163
169	UCCUGCUGGUAUCAUGGAGAAAGUC	2560	GACTTTCTCCATGATACCAGCAGGA	3164
170	CCUGCUGGUAUCAUGGAGAAAGUCC	2561	GGACTTTCTCCATGATACCAGCAGG	3165
180	UCAUGGAGAAAGUCCAAUACCUCAC	2562	GTGAGGTATTGGACTTTCTCCATGA	3166
181	CAUGGAGAAAGUCCAAUACCUCACU	2563	AGTGAGGTATTGGACTTTCTCCATG	3167
182	AUGGAGAAAGUCCAAUACCUCACUC	2564	GAGTGAGGTATTGGACTTTCTCCAT	3168
183	UGGAGAAAGUCCAAUACCUCACUCG	2565	CGAGTGAGGTATTGGACTTTCTCCA	
184	GGAGAAAGUCCAAUACCUCACUCGC	2566	GCGAGTGAGGTATTGGACTTTCTCC	3170
185	GAGAAAGUCCAAUACCUCACUCGCU	2567	AGCGAGTGAGGTATTGGACTTTCTC	3171
186	AGAAAGUCCAAUACCUCACUCGCUC	2568	GAGCGAGTGAGGTATTGGACTTTCT	3172
187	GAAAGUCCAAUACCUCACUCGCUCA	2569	TGAGCGAGTGAGGTATTGGACTTTC	3173
188	AAAGUCCAAÜACCUCACUCGCUCAG	2570	CTGAGCGAGTGAGGTATTGGACTTT	3174
189	AAGUCCAAUACCUCACUCGCUCAGC	2571	GCTGAGCGAGTGAGGTATTGGACTT	3175
190	AGUCCAAUACCUCACUCGCUCAGCU	2572	AGCTGAGCGAGTGAGGTATTGGACT	3176
191	GUCCAAUACCUCACUCGCUCAGCUA	2573	TAGCTGAGCGAGTGAGGTATTGGAC	3177
192	UCCAAUACCUCACUCGCUCAGCUAU	2574	ATAGCTGAGCGAGTGAGGTATTGGA	3178
193	CCAAUACCUCACUCGCUCAGCUAUA	2575	TATAGCTGAGCGAGTGAGGTATTGG	3179
194	CAAUACCUCACUCGCUCAGCUAUAA	2576	TTATAGCTGAGCGAGTGAGGTATTG	3180
195	AAUACCUCACUCGCUCAGCUAUAAG	2577	CTTATAGCTGAGCGAGTGAGGTATT	3181
196	AUACCUCACUCGCUCAGCUAUAAGA	2578	TCTTATAGCTGAGCGAGTGAGGTAT	3182
197	UACCUCACUCGCUCAGCUAUAAGAA	2579	TTCTTATAGCTGAGCGAGTGAGGTA	3183
198	ACCUCACUCGCUCAGCUAUAAGAAG	2580	CTTCTTATAGCTGAGCGAGTGAGGT	3184
199	CCUCACUCGCUCAGCUAUAAGAAGA	2581	TCTTCTTATAGCTGAGCGAGTGAGG	3185
200	CUCACUCGCUCAGCUAUAAGAAGAG	2582	CTCTTCTTATAGCTGAGCGAGTGAG	3186
201	UCACUCGCUCAGCUAUAAGAAGAGC	2583	GCTCTTCTTATAGCTGAGCGAGTGA	3187
202	CACUCGCUCAGCUAUAAGAAGAGCC	2584	GGCTCTTCTTATAGCTGAGCGAGTG	3188

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203	ACUCGCUCAGCUAUAAGAAGAGCCU	2585	AGGCTCTTCTTATAGCTGAGCGAGT	3189
204	CUCGCUCAGCUAUAAGAAGAGCCUC	2586	GAGGCTCTTCTTATAGCTGAGCGAG	3190
205	UCGCUCAGCUAUAAGAAGAGCCUCA	2587	TGAGGCTCTTCTTATAGCTGAGCGA	3191
206	CGCUCAGCUAUAAGAAGAGCCUCAA	2588	TTGAGGCTCTTCTTATAGCTGAGCG	3192
207	GCUCAGCUAUAAGAAGAGCCUCAAC	2589	GTTGAGGCTCTTCTTATAGCTGAGC	3193
208	CUCAGCUAUAAGAAGAGCCUCAACC	2590	GGTTGAGGCTCTTCTTATAGCTGAG	3194
209	UCAGCUAUAAGAAGAGCCUCAACCA	2591	TGGTTGAGGCTCTTCTTATAGCTGA	3195
210	CAGCUAUAAGAAGAGCCUCAACCAU	2592	ATGGTTGAGGCTCTTCTTATAGCTG	3196
211	AGCUAUAAGAAGAGCCUCAACCAUU	2593	AATGGTTGAGGCTCTTCTTATAGCT	3197
212	GCUAUAAGAAGAGCCUCAACCAUUG	2594	CAATGGTTGAGGCTCTTCTTATAGC	3198
213	CUAUAAGAAGAGCCUCAACCAUUGA	2595	TCAATGGTTGAGGCTCTTCTTATAG	3199
214	UAUAAGAAGAGCCUCAACCAUUGAA	2596	TTCAATGGTTGAGGCTCTTCTTATA	3200
215	AUAAGAAGAGCCUCAACCAUUGAAA	2597	TTTCAATGGTTGAGGCTCTTCTTAT	3201
216	HAAGAAGAGCCUCAACCAUUGAAAU	2598	ATTTCAATGGTTGAGGCTCTTCTTA	3202
217	AAGAAGAGCCUCAACCAUUGAAAUG	2599	CATTTCAATGGTTGAGGCTCTTCTT	3203
218	AGAAGAGCCUCAACCAUUGAAAUGC	2600	GCATTTCAATGGTTGAGGCTCTTCT	3204
219	GAAGAGCCUCAACCAUUGAAAUGCC	2601	GGCATTTCAATGGTTGAGGCTCTTC	3205
220	AAGAGCCUCAACCAUUGAAAUGCCU	2602	AGGCATTTCAATGGTTGAGGCTCTT	3206
221	AGAGCCUCAACCAUUGAAAUGCCUC	2603	GAGGCATTTCAATGGTTGAGGCTCT	3207
222	GAGCCUCAACCAUUGAAAUGCCUCA	2604	TGAGGCATTTCAATGGTTGAGGCTC	3208
223	AGCCIICAACCAUUGAAAUGCCUCAA	2605	TTGAGGCATTTCAATGGTTGAGGCT	3209
224	GCCUCAACCAUUGAAAUGCCUCAAC	2606	GTTGAGGCATTTCAATGGTTGAGGC	3210
225	CCUCAACCAUUGAAAUGCCUCAACA	2607	TGTTGAGGCATTTCAATGGTTGAGG	3211
226	CUCAACCAUUGAAAUGCCUCAACAA	2608	TTGTTGAGGCATTTCAATGGTTGAG	3212
227	UCAACCAUUGAAAUGCCUCAACAAG	2609	CTTGTTGAGGCATTTCAATGGTTGA	3213
228	CAACCAUUGAAAUGCCUCAACAAGC	2610	GCTTGTTGAGGCATTTCAATGGTTG	3214
229	AACCAUUGAAAUGCCUCAACAAGCA	2611	TGCTTGTTGAGGCATTTCAATGGTT	3215
230	ACCAUUGAAAUGCCUCAACAAGCAC	2612	GTGCTTGTTGAGGCATTTCAATGGT	3216
231	CCAUUGAAAUGCCUCAACAAGCACG	2613	CGTGCTTGTTGAGGCATTTCAATGG	3217
232	CAUUGAAAUGCCUCAACAAGCACGU	2614	ACGTGCTTGTTGAGGCATTTCAATG	3218
233	AUUGAAAUGCCUCAACAAGCACGUC	2615	GACGTGCTTGTTGAGGCATTTCAAT	3219
234	UUGAAAUGCCUCAACAAGCACGUCA	2616	TGACGTGCTTGTTGAGGCATTTCAA	3220
235	UGAAAUGCCUCAACAAGCACGUCAA	2617	TTGACGTGCTTGTTGAGGCATTTCA	3221
236	GAAAUGCCUCAACAAGCACGUCAAA	2618	TTTGACGTGCTTGTTGAGGCATTTC	3222
237	AAAUGCCUCAACAAGCACGUCAAAA	2619	TTTTGACGTGCTTGTTGAGGCATTT	3223
238	AAUGCCUCAACAAGCACGUCAAAAG	2620	CTTTTGACGTGCTTGTTGAGGCATT	3224
239	AUGCCUCAACAAGCACGUCAAAAGC	2621	GCTTTTGACGTGCTTGTTGAGGCAT	3225
240	UGCCUCAACAAGCACGUCAAAAGCU	2622	AGCTTTTGACGTGCTTGTTGAGGCA	3226
241	GCCUCAACAAGCACGUCAAAAGCUA	2623	TAGCTTTTGACGTGCTTGTTGAGGC	3227
242	CCUCAACAAGCACGUCAAAAGCUAC	2624	GTAGCTTTTGACGTGCTTGTTGAGG	3228
243	CUCAACAAGCACGUCAAAAGCUACA	2625	TGTAGCTTTTGACGTGCTTGTTGAG	3229
244	UCAACAAGCACGUCAAAAGCUACAG	2626	CTGTAGCTTTTGACGTGCTTGTTGA	3230
245	CAACAAGCACGUCAAAAGCUACAGA	2627	TCTGTAGCTTTTGACGTGCTTGTTG	3231
246	AACAAGCACGUCAAAAGCUACAGAA	2628	TTCTGTAGCTTTTGACGTGCTTGTT	3232
247	ACAAGCACGUCAAAAGCUACAGAAU	2629	ATTCTGTAGCTTTTGACGTGCTTGT	3233
248	CAAGCACGUCAAAAGCUACAGAAUC	2630	GATTCTGTAGCTTTTGACGTGCTTG	3234
249	AAGCACGUCAAAAGCUACAGAAUCU	2631	AGATTCTGTAGCTTTTGACGTGCTT	3235
219	- I COACCOCIATE CONTOCCO			

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250	AGCACGUCAAAAGCUACAGAAUCUA	2632	TAGATTCTGTAGCTTTTGACGTGCT	3236
251	GCACGUCAAAAGCUACAGAAUCUAU	2633	ATAGATTCTGTAGCTTTTGACGTGC	3237
252	CACGUCAAAAGCUACAGAAUCUAUU	2634	AATAGATTCTGTAGCTTTTGACGTG	3238
253	ACGUCAAAAGCUACAGAAUCUAUUU	2635	AAATAGATTCTGTAGCTTTTGACGT	3239
254	CGUCAAAAGCUACAGAAUCUAUUUA	2636	TAAATAGATTCTGTAGCTTTTGACG	3240
255	GUCAAAAGCUACAGAAUCUAUUUAU	2637	ATAAATAGATTCTGTAGCTTTTGAC	3241
256	UCAAAAGCUACAGAAUCUAUUUAUC	2638	GATAAATAGATTCTGTAGCTTTTGA	3242
257	CAAAAGCUACAGAAUCUAUUUAUCA	2639	TGATAAATAGATTCTGTAGCTTTTG	3243
258	AAAAGCUACAGAAUCUAUUUAUCAA	2640	TTGATAAATAGATTCTGTAGCTTTT	3244
259	AAAGCUACAGAAUCUAUUUAUCAAU	2641	ATTGATAAATAGATTCTGTAGCTTT	3245
260	AAGCUA CAGAAUCUAUUUAUCAAUU	2642	AATTGATAAATAGATTCTGTAGCTT	3246
261	AGCUACAGAAUCUAUUUAUCAAUUU	2643	AAATTGATAAATAGATTCTGTAGCT	3247
262	GCUACAGAAUCUAUUUAUCAAUUUC	2644	GAAATTGATAAATAGATTCTGTAGC	3248
263	CUACAGAAUCUAUUUAUCAAUUUCU	2645	AGAAATTGATAAATAGATTCTGTAG	3249
264	UACAGAAUCUAUUUAUCAAUUUCUG	2646	CAGAAATTGATAAATAGATTCTGTA	3250
265	ACAGAAUCUAUUUAUCAAUUUCUGU	2647	ACAGAAATTGATAAATAGATTCTGT	3251
266	CAGAAUCUAUUUAUCAAUUUCUGUC	2648	GACAGAAATTGATAAATAGATTCTG	3252
267	AGAAUCUAUUUAUCAAUUUCUGUCU	2649	AGACAGAATTGATAAATAGATTCT	3253
268	GAAUCUAUUUAUCAAUUUCUGUCUC	2650	GAGACAGAAATTGATAAATAGATTC	3254
269	AAUCUAUUUAUCAAUUUCUGUCUCA	2651	TGAGACAGAAATTGATAAATAGATT	3255
270	AUCUAUUUAUCAAUUUCUGUCUCAU	2652	ATGAGACAGAAATTGATAAATAGAT	3256
271	UCUAUUUAUCAAUUUCUGUCUCAUC	2653	GATGAGACAGAAATTGATAAATAGA	3257
272	CUAUUUAUCAAUUUCUGUCUCAUCU	2654	AGATGAGACAGAAATTGATAAATAG	3258
273	UAUUUAUCAAUUUCUGUCUCAUCUU	2655	AAGATGAGACAGAAATTGATAAATA	3259
274	AUUUAUCAAUUUCUGUCUCAUCUUA	2656	TAAGATGAGACAGAAATTGATAAAT	3260
275	UUUAUCAAUUUCUGUCUCAUCUUAA	2657	TTAAGATGAGACAGAAATTGATAAA	3261
276	UUAUCAAUUUCUGUCUCAUCUUAAU	2658	ATTAAGATGAGACAGAAATTGATAA	3262
277	UAUCAAUUUCUGUCUCAUCUUAAUA	2659	TATTAAGATGAGACAGAAATTGATA	3263
278	AUCAAUUUCUGUCUCAUCUUAAUAU	2660	ATATTAAGATGAGACAGAAATTGAT	3264
279	UCAAUUUCUGUCUCAUCUUAAUAUG	2661	CATATTAAGATGAGACAGAAATTGA	3265
280	CAAUUUCUGUCUCAUCUUAAUAUGU	2662	ACATATTAAGATGAGACAGAAATTG	3266
281	AAUUUCUGUCUCAUCUUAAUAUGUC	2663	GACATATTAAGATGAGACAGAAATT	3267
282	AUUUCUGUCUCAUCUUAAUAUGUCU	2664	AGACATATTAAGATGAGACAGAAAT	3268
283	UUUCUGUCUCAUCUUAAUAUGUCUC	2665	GAGACATATTAAGATGAGACAGAAA	3269
284	UUCUGUCUCAUCUUAAUAUGUCUCU	2666	AGAGACATATTAAGATGAGACAGAA	3270
285	UCUGUCUCAUCUUAAUAUGUCUCUU	2667	AAGAGACATATTAAGATGAGACAGA	3271
286	CUGUCUCAUCUUAAUAUGUCUCUUG	2668	CAAGAGACATATTAAGATGAGACAG	3272
287	UGUCUCAUCUUAAUAUGUCUCUUGC	2669	GCAAGAGACATATTAAGATGAGACA	3273
288	GUCUCAUCUUAAUAUGUCUCUUGCU	2670	AGCAAGAGACATATTAAGATGAGAC	3274
289	UCUCAUCUUAAUAUGUCUCUUGCUG	2671	CAGCAAGAGACATATTAAGATGAGA	3275
290	CUCAUCUUAAUAUGUCUCUUGCUGA	2672	TCAGCAAGAGACATATTAAGATGAG ATCAGCAAGAGACATATTAAGATGA	3276
291	UCAUCUUAAUAUGUCUCUUGCUGAU	2673	ATCAGCAAGAGACATATTAAGATGA GATCAGCAAGAGACATATTAAGATG	3277
292	CAUCUUAAUAUGUCUCUUGCUGAUC	2674	GATCAGCAAGAGACATATTAAGATG AGATCAGCAAGAGACATATTAAGAT	3278
293	AUCUUAAUAUGUCUCUUGCUGAUCU	2675	AGATCAGCAAGAGACATATTAAGAT CAGATCAGCAAGAGACATATTAAGA	3279
294	UCUUAAUAUGUCUCUUGCUGAUCUG	2676		3280
295	CUUAAUAUGUCUCUUGCUGAUCUGU	2677	ACAGATCAGCAAGAGACATATTAAG TACAGATCAGCAAGAGACATATTAA	3281
296	UUAAUAUGUCUCUUGCUGAUCUGUA	2678	TACAGATCAGCAAGAGACATATTAA	3202

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297	UAAUAUGUCUCUUGCUGAUCUGUAU	2679	ATACAGATCAGCAAGAGACATATTA	3283
298	AAUAUGUCUCUUGCUGAUCUGUAUC	2680	GATACAGATCAGCAAGAGACATATT	3284
299	AUAUGUCUCUUGCUGAUCUGUAUCA	2681	TGATACAGATCAGCAAGAGACATAT	3285
300	UAUGUCUCUUGCUGAUCUGUAUCAU	2682	ATGATACAGATCAGCAAGAGACATA	3286
301	AUGUCUCUUGCUGAUCUGUAUCAUC	2683	GATGATACAGATCAGCAAGAGACAT	3287
302	UGUCUCUUGCUGAUCUGUAUCAUCG	2684	CGATGATACAGATCAGCAAGAGACA	3288
303	GUCUCUUGCUGAUCUGUAUCAUCGU	2685	ACGATGATACAGATCAGCAAGAGAC	3289
304	UCUCUUGCUGAUCUGUAUCAUCGUG	2686	CACGATGATACAGATCAGCAAGAGA	3290
305	CUCUUGCUGAUCUGUAUCAUCGUGA	2687	TCACGATGATACAGATCAGCAAGAG	3291
306	UCUUGCUGAUCUGUAUCAUCGUGAU	2688	ATCACGATGATACAGATCAGCAAGA	3292
307	CUUGCUGAUCUGUAUCAUCGUGAUG	2689	CATCACGATGATACAGATCAGCAAG	3293
308	UUGCUGAUCUGUAUCAUCGUGAUGC	2690	GCATCACGATGATACAGATCAGCAA	3294
309	UGCUGAUCUGUAUCAUCGUGAUGCU	2691	AGCATCACGATGATACAGATCAGCA	3295
310	GCUGAUCUGUAUCAUCGUGAUGCUU	2692	AAGCATCACGATGATACAGATCAGC	3296
311	CUGAUCUGUAUCAUCGUGAUGCUUC	2693	GAAGCATCACGATGATACAGATCAG	3297
312	UGAUCUGUAUCAUCGUGAUGCUUCU	2694	AGAAGCATCACGATGATACAGATCA	3298
313	GAUCUGUAUCAUCGUGAUGCUUCUC	2695	GAGAAGCATCACGATGATACAGATC	3299
314	AUCUGUAUCAUCGUGAUGCUUCUCU	2696	AGAGAAGCATCACGATGATACAGAT	3300
315	UCUGUAUCAUCGUGAUGCUUCUCUG	2697	CAGAGAAGCATCACGATGATACAGA	3301
316	CUGUAUCAUCGUGAUGCUUCUCUGA	2698	TCAGAGAAGCATCACGATGATACAG	3302
317	UGUAUCAUCGUGAUGCUUCUCUGAA	2699	, TTCAGAGAAGCATCACGATGATACA	3303
318	GUAUCAUCGUGAUGCUUCUCUGAAG	2700	CTTCAGAGAAGCATCACGATGATAC	3304
319	UAUCAUCGUGAUGCUUCUCUGAAGU	2701	ACTTCAGAGAAGCATCACGATGATA	3305
320	ADCADCGUGAUGCUUCUCUGAAGUU	2702	AACTTCAGAGAAGCATCACGATGAT	3306
321	UCAUCGUGAUGCUUCUCUGAAGUUC	2703	GAACTTCAGAGAAGCATCACGATGA	3307
322	CAUCGUGAUGCUUCUCUGAAGUUCU	2704	AGAACTTCAGAGAAGCATCACGATG	3308
323	AUCGUGAUGCUUCUCUGAAGUUCUG	2705	CAGAACTTCAGAGAAGCATCACGAT	3309
324	DEGUGAUGEUUCUCUGAAGUUCUGE	2706	GCAGAACTTCAGAGAAGCATCACGA	3310
325	CGUGAUGCUUCUCUGAAGUUCUGCU	2707	AGCAGAACTTCAGAGAAGCATCACG	3311
326	GUGAUGCUUCUCUGAAGUUCUGCUA	2708	TAGCAGAACTTCAGAGAAGCATCAC	3312
327	UGAUGCUUCUCUGAAGUUCUGCUAC	2709	GTAGCAGAACTTCAGAGAAGCATCA	3313
328	GAUGCUUCUGAAGUUCUGCUACA	2710	TGTAGCAGAACTTCAGAGAAGCATC	3314
329 ·	AUGCUUCUCUGAAGUUCUGCUACAA	2711	TTGTAGCAGAACTTCAGAGAAGCAT	3315
330	UGCUUCUCUGAAGUUCUGCUACAAC	2712	GTTGTAGCAGAACTTCAGAGAAGCA	3316
331	GCUUCUCUGAAGUUCUGCUACAACC	2713	GGTTGTAGCAGAACTTCAGAGAAGC	3317
332	CUUCUCUGAAGUUCUGCUACAACCU	2714	AGGTTGTAGCAGAACTTCAGAGAAG	3318
333	UUCUCUGAAGUUCUGCUACAACCUC	2715	GAGGTTGTAGCAGAACTTCAGAGAA	3319
334	DCUCUGAAGUUCUGCUACAACCUCU	2716	AGAGGTTGTAGCAGAACTTCAGAGA	3320
335	CUCUGAAGUUCUGCUACAACCUCUA	2717	TAGAGGTTGTAGCAGAACTTCAGAG	3321
336	UCUGAAGUUCUGCUACAACCUCUAG	2718	CTAGAGGTTGTAGCAGAACTTCAGA	3322
337	CUGAAGUUCUGCUACAACCUCUAGA	2719	TCTAGAGGTTGTAGCAGAACTTCAG	3323
338	UGAAGUUCUGCUACAACCUCUAGAU	2720	ATCTAGAGGTTGTAGCAGAACTTCA	3324
339	GAAGUUCUGCUACAACCUCUAGAUC	2721	GATCTAGAGGTTGTAGCAGAACTTC	3325
340	AAGUUCUGCUACAA CCUCUAGAUCU	2722	AGATCTAGAGGTTGTAGCAGAACTT	3326
341	AGUUCUGCUACAACCUCUAGAUCUG	2723	CAGATCTAGAGGTTGTAGCAGAACT	3327
342	GUUCUGCUACAACCUCUAGAUCUGC	2724	GCAGATCTAGAGGTTGTAGCAGAAC	3328
343	UUCUGCUACAACCUCUAGAUCUGCA	2725	TGCAGATCTAGAGGTTGTAGCAGAA	3329

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344	UCUGCUACAACCUCUAGAUCUGCAG	2726	CTGCAGATCTAGAGGTTGTAGCAGA	3330
345	CUGCUACAACCUCUAGAUCUGCAGC	2727	GCTGCAGATCTAGAGGTTGTAGCAG	3331
346	UGCUACAACCUCUAGAUCUGCAGCU	2728	AGCTGCAGATCTAGAGGTTGTAGCA	3332
347	GCUACAACCUCUAGAUCUGCAGCUU	2729	AAGCTGCAGATCTAGAGGTTGTAGC	3333
348	CUACAACCUCUAGAUCUGCAGCUUG	2730	CAAGCTGCAGATCTAGAGGTTGTAG	3334
349	UACAACCUCUAGAUCUGCAGCUUGC	2731	GCAAGCTGCAGATCTAGAGGTTGTA	3335
350	ACAACCUCUAGAUCUGCAGCUUGCC	2732	GGCAAGCTGCAGATCTAGAGGTTGT	3336
351	CAACCUCUAGAUCUGCAGCUUGCCA	2733	TGGCAAGCTGCAGATCTAGAGGTTG	3337
352	AACCUCUAGAUCUGCAGCUUGCCAC	2734	GTGGCAAGCTGCAGATCTAGAGGTT	3338
353	ACCUCUAGAUCUGCAGCUUGCCACA	2735	TGTGGCAAGCTGCAGATCTAGAGGT	3339
354	CCUCUAGAUCUGCAGCUUGCCACAU	2736	ATGTGGCAAGCTGCAGATCTAGAGG	3340
355	CUCUAGAUCUGCAGCUUGCCACAUC	2737	GATGTGGCAAGCTGCAGATCTAGAG	3341
356	UCUAGAUCUGCAGCUUGCCACAUCA	2738	TGATGTGGCAAGCTGCAGATCTAGA	3342
357	CUAGAUCUGCAGCUUGCCACAUCAG	2739	CTGATGTGGCAAGCTGCAGATCTAG	3343
358	UAGAUCUGCAGCUUGCCACAUCAGC	2740	GCTGATGTGGCAAGCTGCAGATCTA	3344
368	GCUUGCCACAUCAGCUUAAAAUCUG	2741	CAGATTTTAAGCTGATGTGGCAAGC	3345
369	CUUGCCACAUCAGCUUAAAAUCUGU	2742	ACAGATTTTAAGCTGATGTGGCAAG	3346
370	UUGCCACAUCAGCUUAAAAUCUGUC	2743	GACAGATTTTAAGCTGATGTGGCAA	3347
371	UGCCACAUCAGCUUAAAAUCUGUCA	2744	TGACAGATTTTAAGCTGATGTGGCA	3348
372	GCCACAUCAGCUUAAAAUCUGUCAU	2745	ATGACAGATTTTAAGCTGATGTGGC	3349
373	CCACAUCAGCUUAAAAUCUGUCAUC	2746	GATGACAGATTTTAAGCTGATGTGG	3350
374	CACAUCAGCUUAAAAUCUGUCAUCC	2747	GGATGACAGATTTTAAGCTGATGTG	3351
375	ACAUCAGCUUAAAAUCUGUCAUCCC	2748	GGGATGACAGATTTTAAGCTGATGT	3352
376	CAUCAGCUUAAAAUCUGUCAUCCCA	2749	TGGGATGACAGATTTTAAGCTGATG	3353
377	AUCAGCUUAAAAUCUGUCAUCCCAU	2750	ATGGGATGACAGATTTTAAGCTGAT	3354
378	UCAGCUUAAAAUCUGUCAUCCCAUG.	2751	CATGGGATGACAGATTTTAAGCTGA	3355
379	CAGCUUAAAAUCUGUCAUCCCAUGC	2752	GCATGGGATGACAGATTTTAAGCTG	3356
380	AGCUUAAAAUCUGUCAUCCCAUGCA	2753	TGCATGGGATGACAGATTTTAAGCT	3357
381.	GCUUAAAAUCUGUCAUCCCAUGCAG	2754	CTGCATGGGATGACAGATTTTAAGC	-3358
382	CUUAAAAUCUGUCAUCCCAUGCAGA	2755	TCTGCATGGGATGACAGATTTTAAG	3359
383	UUAAAAUCUGUCAUCCCAUGCAGAC	2756	GTCTGCATGGGATGACAGATTTTAA	3360
384	UAAAAUCÜGUCAUCCCAUGCAGACA	2757	TGTCTGCATGGGATGACAGATTTTA	3361
391	UGUCAUCCCAUGCAGACAGGAAAAC	2758	GTTTTCCTGTCTGCATGGGATGACA	3362
392	GUCAUCCCAUGCAGACAGGAAAACA	2759	TGTTTCCTGTCTGCATGGGATGAC	3363
393	UCAUCCCAUGCAGACAGGAAAACAA	2760	TTGTTTTCCTGTCTGCATGGGATGA	3364
394	CAUCCCAUGCAGACAGGAAAACAAU	2761	ATTGTTTTCCTGTCTGCATGGGATG	3365
395	AUCCCAUGCAGACAGGAAAACAAUA	2762	TATTGTTTTCCTGTCTGCATGGGAT	3366
396	UCCCAUGCAGACAGGAAAACAAUAU	2763	ATATTGTTTTCCTGTCTGCATGGGA	3367
397	CCCAUGCAGACAGGAAAACAAUAUU	2764	AATATTGTTTTCCTGTCTGCATGGG	3368
398	CCAUGCAGACAGGAAAACAAUAUUG	2765	CAATATTGTTTTCCTGTCTGCATGG	3369
399	CAUGCAGACAGGAAAACAAUAUUGU	2766	ACAATATTGTTTTCCTGTCTGCATG	3370
400	AUGCAGACAGGAAAACAAUAUUGUA	2767	TACAATATTGTTTTCCTGTCTGCAT	3371
401	UGCAGACAGGAAAACAAUAUUGUAU	2768	ATACAATATTGTTTTCCTGTCTGCA	3372
426	AACAGACCACUUCCUGAGUAGAAGA	2769	TCTTCTACTCAGGAAGTGGTCTGTT	3373
427	ACAGACCACUUCCUGAGUAGAAGAG	2770	CTCTTCTACTCAGGAAGTGGTCTGT	3374
428	CAGACCACUUCCUGAGUAGAAGAGU	2771	ACTCTTCTACTCAGGAAGTGGTCTG	3375
430	GACCACUUCCUGAGUAGAAGAGUUU	2772	AAACTCTTCTACTCAGGAAGTGGTC	3376

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431	ACCACUUCCUGAGUAGAAGAGUUUC	2773	GAAACTCTTCTACTCAGGAAGTGGT	3377
432	CCACUUCCUGAGUAGAAGAGUUUCU	2774	AGAAACTCTTCTACTCAGGAAGTGG	3378
445	AGAAGAGUUUCUUUGUGAAAAGGUC	2775	GACCTTTTCACAAAGAAACTCTTCT	3379
446	GAAGAGUUUCUUUGUGAAAAGGUCA	2776	TGACCTTTTCACAAAGAAACTCTTC	3380
447	AAGAGUUUCUUUGUGAAAAGGUCAA	2777	TTGACCTTTTCACAAAGAAACTCTT	3381
448	AGAGUUUCUUUGUGAAAAGGUCAAG	2778	CTTGACCTTTTCACAAAGAAACTCT	3382
449	GAGUUUCUUUGUGAAAAGGUCAAGA	2779	TCTTGACCTTTTCACAAAGAAACTC	3383
450	AGUUUCUUUGUGAAAAGGUCAAGAU	2780	ATCTTGACCTTTTCACAAAGAAACT	3384
451	GUUUCUUUGUGAAAAGGUCAAGAUU	2781	AATCTTGACCTTTTCACAAAGAAAC	3385
452	UUUCUUUGUGAAAAGGUCAAGAUUA	2782	TAATCTTGACCTTTTCACAAAGAAA	3386
453	UUCUUUGUGAAAAGGUCAAGAUUAA	2783	TTAATCTTGACCTTTTCACAAAGAA	3387
504	AUUCAUCUGUUGGAUCUUGUAAACA	2784	TGTTTACAAGATCCAACAGATGAAT	3388
505	HIICAUCUGUUGGAUCUUGUAAACAU	2785	ATGTTTACAAGATCCAACAGATGAA	3389
506	UCAUCUGUUGGAUCUUGUAAACAUG	2786	CATGTTTACAAGATCCAACAGATGA	3390
507	CAUCUGUUGGAUCUUGUAAACAUGA	2787	TCATGTTTACAAGATCCAACAGATG	3391
508	AUCUGUUGGAUCUUGUAAACAUGAA	2788	TTCATGTTTACAAGATCCAACAGAT	3392
509	HCUGUHGGAUCUUGUAAACAUGAAA	2789	TTTCATGTTTACAAGATCCAACAGA	3393
510	CUGUUGGAUCUUGUAAACAUGAAAA	2790	TTTTCATGTTTACAAGATCCAACAG	3394
511	UGUUGGAUCUUGUAAACAUGAAAAG	2791	CTTTTCATGTTTACAAGATCCAACA	3395
512	GUUGGAUCUUGUAAACAUGAAAAGG	2792	CCTTTTCATGTTTACAAGATCCAAC	3396
513	UUGGAUCUUGUAAACAUGAAAAGGG	2793	CCCTTTTCATGTTTACAAGATCCAA	3397
514	UGGAUCUUGUAAACAUGAAAAGGGC	2794	GCCCTTTTCATGTTTACAAGATCCA	3398
515	GGAUCUUGUAAACAUGAAAAGGGCU	2795	AGCCCTTTTCATGTTTACAAGATCC	3399
516	GAUCUUGUAAACAUGAAAAGGGCUU	2796	AAGCCCTTTTCATGTTTACAAGATC	3400
517	AUCUUGUAAACAUGAAAAGGGCUUU	2797	AAAGCCCTTTTCATGTTTACAAGAT	3401
518	UCUUGUAAACAUGAAAAGGGCUUUA	2798	TAAAGCCCTTTTCATGTTTACAAGA	34-02
519	CUUGUAAACAUGAAAAGGGCUUUAU	2799	ATAAAGCCCTTTTCATGTTTACAAG	3403
520	UUGUAAACAUGAAAAGGGCUUUAUU	2800	AATAAAGCCCTTTTCATGTTTACAA	3404
521	UGUAAACAUGAAAAGGGCUUUAUUU	2801	AAATAAAGCCCTTTTCATGTTTACA	3405
522	GUAAACAUGAAAAGGGCUUUAUUUU	2802	AAAATAAAGCCCTTTTCATGTTTAC	3406
531	AAAAGGGCUUUAUUUUCAAAAAUUA	2803	TAATTTTTGAAAATAAAGCCCTTTT	3407
532	AAAGGCUUUAUUUUCAAAAAUUAA	2804	TTAATTTTTGAAAATAAAGCCCTTT	3408
533	AAGGCUUUAUUUUCAAAAAUUAAC	2805	GTTAATTTTTGAAAATAAAGCCCTT	3409
534	AGGGCUUUAUUUUCAAAAAUUAACU	2806	AGTTAATTTTTGAAAATAAAGCCCT	3410
535	GGGCUUUAUUUUCAAAAAUUAACUU	2807	AAGTTAATTTTTGAAAATAAAGCCC	3411
570	GUAUAAAAUGCAACUGUUGAUUUCC	2808	GGAAATCAACAGTTGCATTTTATAC	3412
571	UAUAAAAUGCAACUGUUGAUUUCCU	2809	AGGAAATCAACAGTTGCATTTTATA	3413
572	AUAAAAUGCAACUGUUGAUUUCCUC	2810	GAGGAAATCAACAGTTGCATTTTAT	3414
573	UAAAAUGCAACUGUUGAUUUCCUCA	2811	TGAGGAAATCAACAGTTGCATTTTA	3415
574	AAAAUGCAACUGUUGAUUUCCUCAA	2812	TTGAGGAAATCAACAGTTGCATTTT	3416
586	UUGAUUUCCUCAACAUGGCUCACAA	2813	TTGTGAGCCATGTTGAGGAAATCAA	3417
587	UGAUUUCCUCAACAUGGCUCACAAA	2814	TTTGTGAGCCATGTTGAGGAAATCA	3418
588	GAUUUCCUCAACAUGGCUCACAAAU	2815	ATTTGTGAGCCATGTTGAGGAAATC	3419
589	AUUUCCUCAACAUGGCUCACAAAUU	2816	AATTTGTGAGCCATGTTGAGGAAAT	3420
590	UUUCCUCAACAUGGCUCACAAAUUU	2817	AAATTTGTGAGCCATGTTGAGGAAA	3421
591	UTICCUCAACAUGGCUCACAAAUUUC	2818	GAAATTTGTGAGCCATGTTGAGGAA	3422
592	UCCUCAACAUGGCUCACAAAUUUCU	2819	AGAAATTTGTGAGCCATGTTGAGGA	3423

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	The second of th	2820	TAGAAATTTGTGAGCCATGTTGAGG	3424
593	CCUCAACAUGGCUCACAAAUUUCUA		ATAGAAATTTGTGAGCCATGTTGAG	3425
594	CUCAACAUGGCUCACAAAUUUCUAU	2821	GATAGAAATTTGTGAGCCATGTTGA	3426
595	UCAACAUGGCUCACAAAUUUCUAUC		GGATAGAAATTTGTGAGCCATGTTG	3427
596	CAACAUGGCUCACAAAUUUCUAUCC	2823	GGGATAGAAATTTGTGAGCCATGTT	3428
597	AACAUGGCUCACAAAUUUCUAUCCC	2824		3429
598	ACAUGGCUCACAAAUUUCUAUCCCA	2825	TGGGATAGAAATTTGTGAGCCATGT	
599	CAUGGCUCACAAAUUUCUAUCCCAA	2826	TTGGGATAGAAATTTGTGAGCCATG	3430
600	AUGGCUCACAAAUUUCUAUCCCAAA	2827	TTTGGGATAGAAATTTGTGAGCCAT	3431
601	UGGCUCACAAAUUUCUAUCCCAAAU	2828	ATTTGGGATAGAAATTTGTGAGCCA	3432
602	GGCUCACAAAUUUCUAUCCCAAAUC	2829	GATTTGGGATAGAAATTTGTGAGCC	3433
603	GCUCACAAAUUUCUAUCCCAAAUCU	2830	AGATTTGGGATAGAAATTTGTGAGC	3434
604	CUCACAAUUUCUAUCCCAAAUCUU	2831	AAGATTTGGGATAGAAATTTGTGAG	3435
605	UCACAAAUUUCUAUCCCAAAUCUUU	2832	AAAGATTTGGGATAGAAATTTGTGA	3436
606	CACAAAUUUCUAUCCCAAAUCUUUU	2833	AAAAGATTTGGGATAGAAATTTGTG	3437
607	ACAAAUUUCUAUCCCAAAUCUUUUC	2834	GAAAAGATTTGGGATAGAAATTTGT	3438
608	CAAAUUUCUAUCCCAAAUCUUUUCU	2835	AGAAAGATTTGGGATAGAAATTTG	3439
609	AAAUUUCUAUCCCAAAU CUUUUCUG	2836	CAGAAAAGATTTGGGATAGAAATTT	3440
610	AAUUUCUAUCCCAAAUCUUUUCUGA	2837	TCAGAAAAGATTTGGGATAGAAATT	3441
611	AUUUCUAUCCCAAAUCUUUUCUGAA	2838	TTCAGAAAAGATTTGGGATAGAAAT	3442
612	UUUCUAUCCCAAAUCUUUUCUGAAG	2839	CTTCAGAAAAGATTTGGGATAGAAA	3443
613	UUCUAUCCCAAAUCUUUUCUGAAGA	2840	TCTTCAGAAAAGATTTGGGATAGAA	3444
644	GUUUAGUUUUAAAACUGCACUGCCA	2841	TGGCAGTGCAGTTTTAAAACTAAAC	3445
645	UUUAGUUUUAAAACUGCACUGCCAA	2842	TTGGCAGTGCAGTTTTAAAACTAAA	3446
646	UUAGUUUUAAAACUGCACUGCCAAC	2843	GTTGGCAGTGCAGTTTTAAAACTAA	3447
647	UAGUUUUAAAACUGCACUGCCAACA	2844	TGTTGGCAGTGCAGTTTTAAAACTA	3448
648	AGUUUUAAAACUGCACUGCCAACAA	2845	TTGTTGGCAGTGCAGTTTTAAAACT	3449
649	GUUUUAAAACUGCACUGCCAACAAG	2846	CTTGTTGGCAGTGCAGTTTTAAAAC	3450
650	UUUUAAAACUGCACUGCCAACAAGU	2847	ACTTGTTGGCAGTGCAGTTTTAAAA	3451
651	UUUAAAACUGCACUGCCAACAAGUU	2848	AACTTGTTGGCAGTGCAGTTTTAAA	3452
652	UUAAAACUGCACUGCCAACAAGUUC	2849	GAACTTGTTGGCAGTGCAGTTTTAA	3453
653	UAAAACUGCACUGCCAACAAGUUCA	2850	TGAACTTGTTGGCAGTGCAGTTTTA	3454
654	AAAACUGCACUGCCAACAAGUUCAC	2851	GTGAACTTGTTGGCAGTGCAGTTTT	3455
655	AAACUGCACUGCCAACAAGUUCACU	2852	AGTGAACTTGTTGGCAGTGCAGTTT	3456
656	AACUGCACUGCCAACAAGUUCACUU	2853	AAGTGAACTTGTTGGCAGTGCAGTT	3457
657	ACUGCACUGCCAACAAGUUCACUUC	2854	GAAGTGAACTTGTTGGCAGTGCAGT	3458
658	CUGCACUGCCAACAAGUUCACUUCA	2855	TGAAGTGAACTTGTTGGCAGTGCAG	3459
659	UGCACUGCCAACAAGUUCACUUCAU	2856	ATGAAGTGAACTTGTTGGCAGTGCA	3460
660	GCACUGCCAACAAGUUCACUUCAUA	2857	TATGAAGTGAACTTGTTGGCAGTGC	3461
661	CACUGCCAACAAGUUCACUUCAUAU	2858	ATATGAAGTGAACTTGTTGGCAGTG	3462
662	ACUGCCAACAAGUUCACUUCAUAUA	2859	TATATGAAGTGAACTTGTTGGCAGT	3463
663	CUGCCAACAAGUUCACUUCAUAUAU	2860	ATATATGAAGTGAACTTGTTGGCAG	3464
755	UAAGUAUUUUUCAGGUCUUCACCAA	2861	TTGGTGAAGACCTGAAAAATACTTA	3465
756	AAGUAUUUUUCAGGUCUUCACCAAG	2862	CTTGGTGAAGACCTGAAAAATACTT	3466
757	AGUAUUUUUCAGGUCUUCACCAAGU	2863	ACTTGGTGAAGACCTGAAAAATACT	3467
760	AUUUUUCAGGUCUUCACCAAGUAUC	2864	GATACTTGGTGAAGACCTGAAAAAT	3468
761	UUUUUCAGGUCUUCACCAAGUAUCA	2865	TGATACTTGGTGAAGACCTGAAAAA	3469
762	UUUUCAGGUCUUCACCAAGUAUCAA	2866	TTGATACTTGGTGAAGACCTGAAAA	3470

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			TTTGATACTTGGTGAAGACCTGAAA	3471
763	UUUCAGGUCUUCACCAAGUAUCAAA	2867	CTTTGATACTTGGTGAAGACCTGAA	3472
764	UUCAGGUCUUCACCAAGUAUCAAAG	2868		3473
765	UCAGGUCUUCACCAAGUAUCAAAGU	2869	ACTTTGATACTTGGTGAAGACCTGA	3474
766	CAGGUCUUCACCAAGUAUCAAAGUA	2870	TACTTTGATACTTGGTGAAGACCTG	3474
813	AUUCAAAAUAGUCCACUGACUCCUC	2871	GAGGAGTCAGTGGACTATTTTGAAT	
814	UUCAAAAUAGUCCACUGACUCCUCA	2872	TGAGGAGTCAGTGGACTATTTTGAA	3476
815	UCAAAAUAGUCCACUGACUCCUCAC	2873	GTGAGGAGTCAGTGGACTATTTTGA	3478
816	CAAAAUAGUCCACUGACUCCUCACA	2874	TGTGAGGAGTCAGTGGACTATTTTG	
817	AAAAUAGUCCACUGACUCCUCACAU	2875	ATGTGAGGAGTCAGTGGACTATTTT	3479
818	AAAUAGUCCACUGACUCCUCACAUC	2876	GATGTGAGGAGTCAGTGGACTATTT	3480
819	AAUAGUCCACUGACUCCUCACAUCU	2877	AGATGTGAGGAGTCAGTGGACTATT	3481
820	AUAGUCCACUGACUCCUCACAUCUG	2878	CAGATGTGAGGAGTCAGTGGACTAT	3482
821	UAGUCCACUGACUCCUCACAUCUGU	2879	ACAGATGTGAGGAGTCAGTGGACTA	3483
822	AGUCCACUGACUCCUCACAUCUGUU	2880	AACAGATGTGAGGAGTCAGTGGACT	3484
823	GUCCACUGACUCCUCACAUCUGUUA	2881	TAACAGATGTGAGGAGTCAGTGGAC	3485
824	UCCACUGACUCCUCACAUCUGUUAU	2882	ATAACAGATGTGAGGAGTCAGTGGA	3486
825	CCACUGACUCCUCACAUCUGUUAUC	2883	GATAACAGATGTGAGGAGTCAGTGG	3487
911	UUUUUCUAUGCCACAUUAACAUCUU	2884	AAGATGTTAATGTGGCATAGAAAAA	3488
912	UUUUCUAUGCCACAUUAACAUCUUU	2885	AAAGATGTTAATGTGGCATAGAAAA	3489
913	UUUCUAUGCCACAUUAACAUCUUUU	2886	AAAAGATGTTAATGTGGCATAGAAA	3490
919	UGCCACAUUAACAUCUUUUAAAGUU	2887	AACTTTAAAAGATGTTAATGTGGCA	3491
920	GCCACAUUAACAUCUUUUAAAGUUG	2888	CAACTTTAAAAGATGTTAATGTGGC	3492
948	AGAAUCAAGUAUGGAAAAGUAAGGC	2889	GCCTTACTTTTCCATACTTGATTCT	3493
949	GAAUCAAGUAUGGAAAAGUAAGGCC	2890	GGCCTTACTTTTCCATACTTGATTC	3494
950	AAUCAAGUAUGGAAAAGUAAGGCCA	2891	TGGCCTTACTTTTCCATACTTGATT	3495
959	UGGAAAAGUAAGGCCAUACUCUUAC	2892	GTAAGAGTATGGCCTTACTTTCCA	3496
960	GGAAAAGUAAGGCCAUACUCUUACA	2893	TGTAAGAGTATGGCCTTACTTTTCC	3497
1067	CAUAUGAUCAACAGAUGAGAACUGG	2894	CCAGTTCTCATCTGTTGATCATATG	3498
1069	UAUGAUCAACAGAUGAGAACUGGUG	2895	CACCAGTTCTCATCTGTTGATCATA	3499
1070	AUGAUCAACAGAUGAGAACUGGUGG	2896	CCACCAGTTCTCATCTGTTGATCAT	3500
1071	UGAUCAACAGAUGAGAACUGGUGGU	2897	ACCACCAGTTCTCATCTGTTGATCA	3501
1072	GAUCAACAGAUGAGAACUGGUGGUU	2898	AACCACCAGTTCTCATCTGTTGATC	3502
1073	AUCAACAGAUGAGAACUGGUGGUUA	2899	TAACCACCAGTTCTCATCTGTTGAT	3503
1074	UCAACAGAUGAGAACUGGUGGUUAA	2900	TTAACCACCAGTTCTCATCTGTTGA	3504
1075	CAACAGAUGAGAACUGGUGGUUAAU	2901	ATTAACCACCAGTTCTCATCTGTTG	3505
1078	CAGAUGAGAACUGGUGGUUAAUAUG	2902	CATATTAACCACCAGTTCTCATCTG	3506
1080	GAUGAGAACUGGUGGUUAAUAUGUG	2903	CACATATTAACCACCAGTTCTCATC	3507
1081	AUGAGAACUGGUGGUUAAUAUGUGA	2904	TCACATATTAACCACCAGTTCTCAT	3508
1082	UGAGAACUGGUGGUUAAUAUGUGAC	2905	GTCACATATTAACCACCAGTTCTCA	3509
1083	GAGAACUGGUGGUUAAUAUGUGACA	2906	TGTCACATATTAACCACCAGTTCTC	3510
1086	AACUGGUGGUUAAUAUGUGACAGUG	2907	CACTGTCACATATTAACCACCAGTT	3511
1087	ACUGGUGGUUAAUAUGUGACAGUGA	2908	TCACTGTCACATATTAACCACCAGT	3512
1088	CUGGUGGUUAAUAUGUGACAGUGAG	2909	CTCACTGTCACATATTAACCACCAG	3513
1089	UGGUGGUUAAUAUGUGACAGUGAGA	2910	TCTCACTGTCACATATTAACCACCA	3514
1141	CAGAAUCUAAUCUUCAUUUAAGGCA	2911	TGCCTTAAATGAAGATTAGATTCTG	3515
1150	AUCUUCAUUUAAGGCACUGUAGUGA	2912	TCACTACAGTGCCTTAAATGAAGAT	3516
1151	UCUUCAUUUAAGGCACUGUAGUGAA	2913	TTCACTACAGTGCCTTAAATGAAGA	3517
1151	DC00CA000AAGGCACOCOACGCAA			

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1153	UUCAUUUAAGGCACUGUAGUGAAUU	2914	AATTCACTACAGTGCCTTAAATGAA	3518
1161	AGGCACUGUAGUGAAUUAUCUGAGC	2915	GCTCAGATAATTCACTACAGTGCCT	3519
1162	GGCACUGUAGUGAAUUAUCUGAGCU	2916	AGCTCAGATAATTCACTACAGTGCC	3520
1211	UAUCUUUGGAAUCAUGAAACCUUAA	2917	TTAAGGTTTCATGATTCCAAAGATA	3521
1212	AUCUUUGGAAUCAUGAAACCUUAAG	2918	CTTAAGGTTTCATGATTCCAAAGAT	3522
1213	UCUUUGGAAUCAUGAAACCUUAAGA	2919	TCTTAAGGTTTCATGATTCCAAAGA	3523
1213	CUUUGGAAUCAUGAAACCUUAAGAC	2920	GTCTTAAGGTTTCATGATTCCAAAG	3524
1214	UUUGGAAUCAUGAAACCUUAAGACU	2921	AGTCTTAAGGTTTCATGATTCCAAA	3525
1215	UUGGAAUCAUGAAACCUUAAGACUU	2922	AAGTCTTAAGGTTTCATGATTCCAA	3526
1217	UGGAAUCAUGAAACCUUAAGACUUC	2923	GAAGTCTTAAGGTTTCATGATTCCA	3527
1217	GGAAUCAUGAAACCUUAAGACUUCA	2924	TGAAGTCTTAAGGTTTCATGATTCC	3528
1218	CAUGAAACCUUAAGACUUCAGAAUG	2925	CATTCTGAAGTCTTAAGGTTTCATG	3529
1223	CCUUAAGACUUCAGAAUGAUUUUUGC	2926	GCAAAATCATTCTGAAGTCTTAAGG	3530
1231	CUUAAGACUUCAGAAUGAUUUUGCA	2927	TGCAAAATCATTCTGAAGTCTTAAG	3531
1231	UUAAGACUUCAGAAUGAUUUUGCAG	2928	CTGCAAAATCATTCTGAAGTCTTAA	3532
1232	UAAGACUUCAGAAUGAUUUUGCAGG	2929	CCTGCAAAATCATTCTGAAGTCTTA	3533
1233	AAGACUUCAGAAUGAUUUUGCAGGU	2930	ACCTGCAAAATCATTCTGAAGTCTT	3534
1234	AGACUUCAGAAUGAUUUUUGCAGGUU	2931	AACCTGCAAAATCATTCTGAAGTCT	3535
1235	GACUUCAGAAUGAUUUUGCAGGUUG	2932	CAACCTGCAAAATCATTCTGAAGTC	3536
1237	ACUUCAGAAUGAUUUUGCAGGUUGU	2933	ACAACCTGCAAAATCATTCTGAAGT	3537
1237	CUUCAGAAUGAUUUUGCAGGUUGUC	2934	GACAACCTGCAAAATCATTCTGAAG	3538
1239	UUCAGAAUGAUUUUGCAGGUUGUCU	2935	AGACAACCTGCAAAATCATTCTGAA	3539
1240	UCAGAAUGAUUUUGCAGGUUGUCUU	2936	AAGACAACCTGCAAAATCATTCTGA	3540
1241	CAGAAUGAUUUUGCAGGUUGUCUUC	2937	GAÁGACAACCTGCAAAATCATTCTG	3541
1242	AGAAUGAUUUUGCAGGUUGUCUUCC	2938	GGAAGACAACCTGCAAAATCATTCT	3542
1243	GAAUGAUUUUGCAGGUUGUCUUCCA	2939	TGGAAGACAACCTGCAAAATCATTC	3543
1244	AAUGAUUUUGCAGGUUGUCUUCCAU	2940	ATGGAAGACAACCTGCAAAATCATT	3544
1245	AUGAUUUUGCAGGUUGUCUUCCAUU	2941	AATGGAAGACAACCTGCAAAATCAT	3545
1246	UGAUUUUGCAGGUUGUCUUCCAUUC	2942	GAATGGAAGACAACCTGCAAAATCA	3546
1247	GAUUUUGCAGGUUGUCUUCCAUUCC	2943	GGAATGGAAGACAACCTGCAAAATC	3547
1248	AUJUUGCAGGUUGUCUUCCAUUCCA	2944	TGGAATGGAAGACAACCTGCAAAAT	3548
1249	UUUUGCAGGUUGUCUUCCAUUCCAG	2945	CTGGAATGGAAGACAACCTGCAAAA	3549
1250	UUUGCAGGUUGUCUUCCAUUCCAGC	2946	GCTGGAATGGAAGACAACCTGCAAA	3550
1251	UUGCAGGUUGUCUUCCAUUCCAGCC	2947	GGCTGGAATGGAAGACAACCTGCAA	3551
1252	UGCAGGUUGUCUUCCAUUCCAGCCU	2948	AGGCTGGAATGGAAGACAACCTGCA	3552
1253	GCAGGUUGUCUUCCAUUCCAGCCUA	2949	TAGGCTGGAATGGAAGACAACCTGC	3553
1254	CAGGUUGUCUUCCAUUCCAGCCUAA	2950	TTAGGCTGGAATGGAAGACAACCTG	3554
1255	AGGUUGUCUUCCAUUCCAGCCUAAC	2951	GTTAGGCTGGAATGGAAGACAACCT	3555
1256	GGUUGUCUUCCAUUCCAGCCUAACA	2952	TGTTAGGCTGGAATGGAAGACAACC	3556
1257	GUUGUCUUCCAUUCCAGCCUAACAU	2953	ATGTTAGGCTGGAATGGAAGACAAC	3557
1258	UUGUCUUCCAUUCCAGCCUAACAUC	2954	GATGTTAGGCTGGAATGGAAGACAA	3558
1259	UGUCUUCCAUUCCAGCCUAACAUCC	2955	GGATGTTAGGCTGGAATGGAAGACA	3559
1260	GUCUUCCAUUCCAGCCUAACAUCCA	2956	TGGATGTTAGGCTGGAATGGAAGAC	3560
1261	UCUUCCAUUCCAGCCUAACAUCCAA	2957	TTGGATGTTAGGCTGGAATGGAAGA	3561
1262	CUUCCAUUCCAGCCUAACAUCCAAU	2958	ATTGGATGTTAGGCTGGAATGGAAG	3562
1263	UUCCAUUCCAGCCUAACAUCCAAUG	2959	CATTGGATGTTAGGCTGGAATGGAA	3563
1264	UCCAUUCCAGCCUAACAUCCAAUGC	2960	GCATTGGATGTTAGGCTGGAATGGA	3564

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1266	1565 1566 1567
2961 CCTGCATTGGATGTTAGGCTGGATT 274	567
1274 CCUMACAUCCANGCAAGGAAA 2964 TTCCTTGCCTGCATTGGATGTTAGG 3 1275 CUMACAUCCANGCAGGAAGGAAA 2965 TTCCTTGCCTGCATTGGATGTTAG 1276 UMACAUCCANGCAGGCAAGGAAAA 2965 TTTCCTTGCCTGCATTGGATGTTAG 1276 UAACAUCCANGCAGGCAAGGAAAAU 2967 ATTTCCTTGCCTGCATTGGATGTT 3 1278 ACAUCCAAUGCAGGCAAGGAAAUA 2968 TATTTTCCTTGCCTGCATTGGATGT 3 1279 CAUCCAAUGCAGGCAAGGAAAUAA 2968 TATTTTCCTTGCCTGCATTGGATG 3 1279 CAUCCAAUGCAGGCAAGGAAAUAAA 2970 TTTATTTCCTTGCCTGCATTGGATG 3 1281 UCCAAUGCAGGCAAGGAAAUAAAA 2971 TTTATTTTCCTTGCCTGCATTGGAT 1281 UCCAAUGCAGGCAAGGAAAUAAAA 2971 TTTATTTTCCTTGCCTGCATTGGAT 1282 CAAUGCAGGCAAGGAAAUAAAAA 2971 TTTATTTTCCTTGCCTGCATTGGA 1282 CAAUGCAGGCAAGGAAAUAAAAA 2972 CTTTATTTTCCTTGCCTGCATTGGA 1282 CAAUGCAGGCAAGGAAAUAAAAACA 2973 ATCTTTTATTTTCCTTGCCTGCATT 1285 AUGCAGGCAAGGAAAUAAAAACA 2975 AATCTTTATTTTCCTTGCCTGCAT 1285 UGCAGGCAAGGAAAUAAAAGAUU 2976 AATCTTTTATTTCCTTGCCTGCAT 1287 CAGGGCAAGGAAAUAAAAGAUU 2976 AATCTTTATTTTCCTTGCCTGCCT 1287 CAGGGCAAGGAAAUAAAAAAAAA 2978 ATTTTCTTTGCTTGCCTGCCT 1301 UMAAAGAUUUCCAGUGACAGAAAAA 2978 ATTTTCTTTTTTTTTTTTTTTTTTCCTTGCCTGCATT 1393 UUUUGAAUGAACUUGUUGGCC 2980 GCCAACAAGTTCATTTCAAAATAT 1394 AUAUUUUGAAUUGAACUUGUUGGCC 2981 GGCCAACAAGTTCATTTCAAAATAT 1395 AUUUUGAAAUGAACUUGUUGGCC 2981 GGCCAACAAGTTCATTCAAAATAT 1397 UUUUGAAAUGAACUUGUUGGCCC 2981 GGCCAACAAGTTCATTCAAAATAT 1397 UUUUGAAAUGAACUUGUUGGCCC 2981 GGCCAACAAGTTCATTCAAAATAT 1397 UUUUGAAAUGAACUUGUUGGCCC 2981 GGCCAACAAGTTCATTCAAAATAT 1397 UUUUGAAAUGAACUUGUUGGCCCAU 2981 GGCCAACAAGTTCATTTCAAAATAT 1397 UUUUGAAAUGAACUUGUUGGCCCAU 2981 GGCCAACAAGTTCATTCAAAATAT 1397 UUUUGAAAUGAACUUGUUGGCCCAU 2981 GGCCAACAAGTTCATTCAAAATAT 1397 UUUUGAAAUGAACUUGUUGGCCCAU 2981 GGCCAACAAGTTCATTCAAAATAT 1397 UUUUGAAAUGAACUUGUUGGCCCAU 2981 GGCCAACAAGTTCATTTCAAAATT 1397 UUUUGAAAUGAACUUGUUGGCCCAU 2981 GGCCAACAAGTTCATTCAAAATT 1397 UUUUGAAAUGAACUUGUUGGCCCAU 2981	
1275 CUMACAUCCANBECAGGAAGAAA 2965 TTTCCTTGCCTGCATTGGATGTAG 3 1276	568
1276	
2967 ARCHUCCAUGGCAGGCANGANAN 2967 ATTTTCCTTGCCTGCATTGGATGT 3 1278 ACCUUCAUGGCAGGCANGGANAN 2968 TATTTTCCTTGCCTGCATTGGATGT 3 1279 ACCUUCAUGCAGGCANGGAAAUGA 2968 TATTTTCCTTGCCTGCATTGGATG 3 1279 AUCCAUGCAGGCANGGAAAUGAA 2969 TTATTTCCTTGCCTGCATTGGATG 3 1281 UCCAUGCAGGCAAGGAAAUGAA 2967 TTATTTTCCTTGCCTGCATTGGATG 3 1281 UCCAUGCAGGCAAGGAAAUGAAA 2971 TTTATTTTCCTTGCCTGCATTGGAT 3 1282 CANUGCAGGCAAGGAAAUGAAAG 2972 CTTTTATTTTCCTTGCCTGCATTGG 3 1283 CANUGCAGGCAAGGAAAUGAAAGA 2973 ATCTTTTATTTTCCTTGCCTGCATTG 3 1284 AUGCAGGCAAGGAAAUGAAAGA 2975 AATCTTTTATTTCCTTGCTGCATT 3 1285 AUGCAGGCAAGGAAAUGAAAGAUU 2975 AATCTTTTATTTCCTTGCTGCATT 3 1286 UGCAGGCAAGGAAAUGAAAGAUU 2976 AAATCTTTTATTTCCTTGCCTGCATT 3 1287 GAGGCAAGAGAAUGAAAGAUU 2976 AAATCTTTTATTTCTTGCTGCTGCTGT 3 1287 GAGGCAAGAGAAUGAAAGAUU 2978 AATCTTTTATTTCTTGCTGCTGCCTG 3 1287 GAAGAGUUUCCAGUGACAGAAAAU 2979 ATTTTCTGTCACTGCTGCT 3 1391 UUUUGAAAUGAACUUGUUGGCC 2980 GCCAACAAGTTCATTCAAAATAT 3 3 UUUUGAAAUGAACUUGUUGGCCC 2981 GGCCAACAAGTTCATTTCAAAATAT 3 3 UUUUGAAAUGAACUUGUUGGCCC 2981 GGCCAACAAGTTCATTTCAAAATAT 3 3 UUUUGAAAUGAACUUGUUGGCCC 2982 GGCCAACAAGTTCATTTCAAAATAT 3 3 UUUUGAAAUGAACUUGUUGGCCC 2984 ATGGGCCAACAAGTTCATTTCAAAATAT 3 3 UUUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGGCCAACAAGTTCATTTCAAAATAT 3 3 UUUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGGCCAACAAGAGTCATTTCAAAATAT 3 3 UUUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGGCCAACAAGAGTCATTTCATACAA A UUUUGAAUGAACUUGGCCCAU 2984 ATGGGGC	569
1278	570
2969 TRATTTCCTTGCCTGCATTGCATG 1280 AUCCAAUGCAGGAAAAUAAA 2969 TRATTTCCTTGCCTGCATTGCATG 1281 UCCAAUGCAGGCAAGGAAAUAAA 2970 TTATTTTCCTTGCCTGCATTGCATG 1281 UCCAAUGCAGGCAAGGAAAAUAAAA 2971 TTTATTTTCCTTGCCTGCATTGGAT 1282 CCAAUGCAGGCAAGGAAAAUAAAAGA 2973 TTTTATTTTCCTTGCCTGCATTGG 1283 CAAUGCAGGCAAGGAAAAUAAAAGA 2973 TCTTTTATTTTCCTTGCCTGCATTG 1284 AUGCAGGCAAGGAAAAUAAAAGAU 2974 ATCTTTTATTTTCCTTGCCTGCATT 1285 AUGCAGGCAAGGAAAAUAAAAGAU 2976 AATCTTTTATTTTCCTTGCCTGCAT 1286 UGCAGGCAAGGAAAAUAAAAGAUU 2976 AATCTTTTATTTTCCTTGCCTGCAT 1287 GCAGGCAAGGAAAUAAAAGAUU 2976 AATCTTTTATTTTCCTTGCCTGCA 1287 GCAGGCAAGGAAAUAAAAAGAUU 2978 ATTTTCTTGTCATGCATGCA 1301 UAAAAGAUUUCCAGUGACAGAAAAA 2978 ATTTTCTGTCACTGGAAATCTTTTA 1302 AUAAUGUUCCAGUGACAGAAAAA 2978 ATTTTCTGTCACTGGAAATCTTTTA 1303 UAUAUUUGAAAUGAACUUGUUGGC 2980 GCCAACAAGTTCATTCAAAATAT 1394 AUAUUUUGAAAUGAACUUGUUGGCC 2981 GSCCAACAAGTTCATTTCAAAATAT 1395 AUUUUGAAAUGAACUUGUUGGCCC 2981 GSGCCAACAAGTTCATTTCAAAATAT 1397 UUUUGAAAUGAACUUGUUGGCCCA 2981 GGGCCAACAAGTTCATTTCAAAATAT 1398 UUUGAAAUGAACUUGUUGGCCCA 2981 GGGCCAACAAGTTCATTTCAAAATAT 1399 UUUGAAAUGAACUUGUUGGCCCA 2981 GGGCCAACAAGTTCATTTCAAAATAT 1399 UUUGAAAUGAACUUGUUGGCCCA 2981 GGGCCAACAAGTTCATTTCAAAATAT 1391 UUUGAAAUGAACUUGUUGGCCCA 2981 GGGCCAACAAGTTCATTTCAAAATA 1399 UUUGAAAUGAACUUGUUGGCCCA 2981 GGGCCAACAAGTTCATTTCAAAATA 1391 UUUGAAAUGAACUUGUUGGCCCA 2981 GGGCCAACAAGTTCATTTCAAAATA 1391 UUUGAAAUGAACUUGUUGGCCCA 2981 GGGCCAACAAGTTCATTTCAAAATA 1391 UUUGAAAUGAACUUGUUGGCCCA 2981 GGGCCAACAAGTTCATTTCAAATAT 1391 UUUGAAAUGAACUUGUUGGCCCA 2981 GGGCCAACAAGTTCATTTCAAAATA 1391 UUUGAAAUGAACUUGUUGGCCCAU 2981 GATGGGCCAACAAGTTCATTTCAAATAT	571
1286	572
1281 UCCANUGCAGGCAAGGAAANAAA 2971 TITTATTTCCTTGCCTGCATTGGA 1282 CCANUGCAGGCAAGGAAANAAA 2972 CTTTTATTTCCTTGCCTGCATTGG 1283 CANUGCAGGCAAGGAAANAANAAG 2973 TCTTTTATTTCCTTGCCTGCATTGG 1284 ANUGCAGGCAAGGAANAUNAAAGAU 2974 ATCTTTTATTTCCTTGCCTGCATTG 1285 AUGCAGGCAAGGAAANAANAAGAUU 2975 AATCTTTTATTTCCTTGCCTGCAT 1286 UGCAGGCAAGGAAANAANAAGAUU 2976 AATCTTTTATTTTCCTTGCCTGCA 1287 GCAGGCAAGGAANAANAAAGAUUUC 2977 GAANCTTTTATTTTCCTTGCCTGCA 1301 UAAAAGAUUUCCAGUGACAGAAAAAU 2978 TTTTCTGTCACTGGAAATCTTTTA 1302 AAAAGAUUUCCAGUGACAGAAAAAU 2978 ATTTTCTGTCACTGGAAATCTTTT 1391 UAUAUGAANUGAACUUGUUGGCC 2981 GCCAACAAGTTCATTCAAAATATA 1394 AUAUUUGAAAUGAACUUGUUGGCC 2981 GGCCAACAAGTTCATTTCAAAATAT 1395 UAUUUGAAAUGAACUUGUUGGCCC 2982 GGCCAACAAGTTCATTTCAAAATAT 1396 AUUUUGAAAUGAACUUGUUGGCCC 2983 TGGGCCAACAAGTTCATTTCAAAATAT 1397 UUUUGAAAUGAACUUGUUGGCCC 2984 ATGGGCCAACAAGTTCATTTCAAAATAT 1397 UUUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTTCAAAAT 1397 UUUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGGCCAACAAGTTCATTTCAAAATA 1398 UUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTTCAAAATA 1398 UUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTTCAAAATA 1398 UUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTTCAAAAA	573
1282 CCANUCCAGCANGGAAANUANAMG 2972 CTTTATTTCCTTGCCTCGCATTGG 1283 CANUCCAGCAGGAAANUANAMGA 2973 TCTTTATTTCCTTGCCTCGCATTGG 1284 ANDCCAGCCAGGGAAANUANAMGA 2974 ATCTTTATTTCCTTGCCTGCATT 1285 ANDCCAGCCAGGAAANUANAGAANU 2975 AATCTTTATTTCCTTGCCTGCAT 1286 UGCAGCCAGGAAANUANAAGANU 2976 AATCTTTTATTTCCTTGCCTGCAT 1286 UGCAGCCAGGAAANUANAAGANUU 2976 AATCTTTTATTTCCTTGCCTGCCA 1287 GCAGCCAGGAAANUANAAGANUU 2977 GAAATCTTTTATTTTCCTTGCCTGC 1301 UAAAAGANUUCCAGUGACAGAAANA 2978 TTTTCTGTCACTGGAAATCTTTT 1302 AAAAGANUUCCAGUGACAGAAANA 2978 ATTTTCTGTCACTGGAAATCTTTT 1302 UAUAINUUGAAAUGAACUUGUUGGC 2980 GCCAACAAGTTCATTTCAAAATT 1394 ANAUTUGAAAUGAACUUGUUGGCC 2981 GCCCAACAAGTTCATTCAAAATT 1395 UAUUUGAAAUGAACUUGUUGGCCC 2982 GGCCGAACAAGTTCATTCAAAATT 1396 AUUUUGAAAUGAACUUGUUGGCCC 2983 TGGGCCAACAAGTTCATTTCAAAATT 1397 UUUUGAAAUGAACUUGUUGGCCCA 2983 TGGGCCAACAAGTTCATTTCAAAATT 1397 UUUUGAAAUGAACUUGUUGGCCCA 2984 ATGGGCCAACAAGTTCATTTCAAAATT 1398 UUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTTCAAAAT 1398 UUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTCAAAAT 1398 UUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTCAAAAT 1398 UUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGGCCAACAAGTTCATTCAAAAT 1398 UUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTCAAAA 1398 UUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGGCCAACAAGTTCATTCAAAA 1398 UUUGAAAUGAACUUGUUGGCCCAU 2985 ATGGGGCCAACAAGTTCATTCAAAA 1398 UUUGAAAUGAACUUGUUGGCCCAU 2985 ATGGGCCAACAAGTCATTCATTCAAAA 1398 ATGGGGCCAACAAGTCATTCATTCAAAC 1398 ATGGGGCCAACAAGTCATTCATTCAAAA 1398 ATGGGGCCAACAAGTCATTCATTCAAA 1398 ATGGGGCCAACAAGTCATTCATTCAAAA 1398 ATGGGGCCAACAAGTCATTCATTCAAACA	574
1283	575
1284	576
1285	3577
1286	3578
1287 GCAGCCAGGAAAUAAAAGAUUCC 2977 GAAATCTTTATTTCCTTGCCTCC 1201	3579
1301	3580
1302	3581
1393 MANADURGAAMGACUUGUUGGC 2980 GCCAACAAGTTCATTCAAAATAT 1394 AMADURGAAMGAACUUGUUGGC 2981 GGCCAACAAGTTCATTCAAAATAT 1395 MADURGAAMGAACUUGUUGGCC 2982 GGCCAACAAGTTCATTCAAAATAT 1396 AUUUUGAAAMGAACUUGUUGGCCCA 2983 TGGGCCAACAAGTTCATTCAAAATAT 1397 UUUUGAAMGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTCAAAAT 1398 UUUGAAAGGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTCAAAA 1398 UUUGAAAGGAACUUGUUGGCCCAU 2985 GATGGGCCAACAAGTTCATTCAAA	3582
1394 AUJUUUGAAAUGAACUUGUUGGCC 2981 GGCCAACAAGTTCATTCAAAATAT 1395 UAUJUUGAAAUGAACUUGUUGGCC 2983 GGGCAACAAGTTCATTCAAAATAT 1396 AUJUUGAAAUGAACUUGUUGGCCCA 2983 TGGGCCAACAAGTTCATTCAAAATAT 1397 UUJUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTCAAAA 1398 UUJUGAAAUGAACUUGUUGGCCCAU 2985 GATGGGCCAACAAGTTCATTCAAAA 1398 UUJUGAAAUGAACUUGUUGGCCCAUC 2985 GATGGGCCAACAAGTTCATTCAAAA 1398 UUJUGAAAUGAACUUGUUGGCCCAUC 2985 GATGGGCCAACAAGTTCATTCAAAA 1398 UUJUGAAAUGAACUUGUUGGCCCAUC 2985 GATGGGCCAACAAGTTCATTCAAA 1	3583
1395 MUJUUGAANGAACUUGUUGGCCC 2982 GGGCCAACAAGTTCATTCAAAATA	3584
1396 AUUUUGAAAUGAACUUGUUGGCCCAU 2983 TGGGCCAACAAGTTCATTTCAAAAT 1397 UUUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTTCAAAA 1398 UUUGAAAUGAACUUGUUGGCCCAUC 2985 GATGGGCCAACAAGTTCATTTCAAAA 1	3585
1397 UUUUGAAAUGAACUUGUUGGCCCAU 2984 ATGGGCCAACAAGTTCATTCAAAA 1398 UUUGAAAUGAACUUGUUGGCCCAUC 2985 GATGGGCCAACAAGTTCATTTCAAAA :	3586
1398 UUUGAAAUGAACUUGUUGGCCCAUC 2985 GATGGGCCAACAAGTTCATTTCAAA	3587
1398 OCOGNACONOCCCCCCCC	3588
	3589
1399 UUGAAAUGAACUUGUUGGCCCAUCU 2986 AGATGGGCCAACAAGTTCATTTCAA	3590
1400 UGAAAUGAACUUGUUGGCCCAUCUA 2987 TAGATGGGCCAACAAGTTCATTTCA	3591
1401 GAAAUGAACUUGUUGGCCCAUCUAU 2988 ATAGATGGGCCAACAAGTTCATTTC :	3592
1402 AAAUGAACUUGUUGGCCCAUCUAUU 2989 AATAGATGGGCCAACAAGTTCATTT :	3593
1403 AAUGAACUUGUUGGCCCAUCUAUUA 2990 TAATAGATGGGCCAACAAGTTCATT :	3594
1404 AUGAACUUGUUGGCCCAUCUAUUAC 2991 GTAATAGATGGGCCAACAAGTTCAT	3595
1405 UGAACUUGUUGGCCCAUCUAUUACA 2992 TGTAATAGATGGGCCAACAAGTTCA	3596
1406 GAACUUGUUGGCCCAUCUAUUACAU 2993 ATGTAATAGATGGGCCAACAAGTTC	3597
1407 AACUUGUUGGCCCAUCUAUUACAUC 2994 GATGTAATAGATGGGCCAACAAGTT :	3598
1408 ACUUGUUGGCCCAUCUAUUACAUCU 2995 AGATGTAATAGATGGGCCAACAAGT :	3599
1409 CUUGUUGGCCCAUCUAUUACAUCUA 2996 TAGATGTAATAGATGGGCCAACAAG	3600
1410 UUGUUGGCCCAUCUAUUACAUCUAC 2997 GTAGATGTAATAGATGGGCCAACAA	3601
1411 UGUUGGCCCAUCUAUUACAUCUACA 2998 TGTAGATGTAATAGATGGGCCAACA	3602
1412 GUUGGCCCAUCUAUUACAUCUACAG 2999 CTGTAGATGTAATAGATGGGCCAAC :	3603
1413 UUGGCCCAUCUAUUACAUCUACAGC 3000 GCTGTAGATGTAATAGATGGGCCAA	3604
1414 UGGCCCAUCUAUUACAUCUACAGCU 3001 AGCTGTAGATGTAATAGATGGGCCA	3605
1415 GGCCCAUCUAUUACAUCUACAGCUG 3002 CAGCTGTAGATGTAATAGATGGGCC	3606
1416 GCCCAUCUAUUACAUCUACAGCUGA 3003 TCAGCTGTAGATGTAATAGATGGGC	3607
1422 CUNUUNCAUCUACAGCUGACCCUUG 3004 CAAGGGTCAGCTGTAGATGTAATAG	3608
1423 UAUUACAUCUACAGCUGACCCUUGA 3005 TCAAGGGTCAGCTGTAGATGTAATA	3609
1425 UUACAUCUACAGCUGACCCUUGAAC 3007 GTTCAAGGGTCAGCTGTAGATGTAA	3610

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Table 30

			•	
1426	UACAUCUACAGCUGACCCUUGAACA	3008	TGTTCAAGGGTCAGCTGTAGATGTA	3612
1427	ACAUCUACAGCUGACCCUUGAACAU	3009	ATGTTCAAGGGTCAGCTGTAGATGT	3613
1428	CAUCUACAGCUGACCCUUGAACAUG	3010	CATGTTCAAGGGTCAGCTGTAGATG	3614
1429	AUCUACAGCUGACCCUUGAACAUGG	3011	CCATGTTCAAGGGTCAGCTGTAGAT	3615
1442	CCUUGAACAUGGGGGUUAGGGGAGC	3012	GCTCCCCTAACCCCCATGTTCAAGG	3616
1443	CUUGAACAUGGGGGUUAGGGGAGCU	3013	AGCTCCCCTAACCCCCATGTTCAAG	3617
1444	UUGAACAUGGGGGUUAGGGGAGCUG	3014	CAGCTCCCCTAACCCCCATGTTCAA	3618
1445	UGAACAUGGGGGUUAGGGGAGCUGA	3015	TCAGCTCCCCTAACCCCCATGTTCA	3619
1446	GAACAUGGGGGUUAGGGGAGCUGAC	3016	GTCAGCTCCCCTAACCCCCATGTTC	3620
1447	AACAUGGGGUUAGGGGAGCUGACA	3017	TGTCAGCTCCCCTAACCCCCATGTT	3621
1448	ACAUGGGGGUUAGGGGAGCUGACAA	3018	TTGTCAGCTCCCCTAACCCCCATGT	3622
1449	CAUGGGGUUAGGGGAGCUGACAAU	3019	ATTGTCAGCTCCCCTAACCCCCATG	3623
1450	AUGGGGUUAGGGGAGCUGACAAUU	3020	AATTGTCAGCTCCCCTAACCCCCAT	3624
1451	UGGGGGUUAGGGGAGCUGACAAUUC	3021	GAATTGTCAGCTCCCCTAACCCCCA	3625
1452	GGGGGUUAGGGGAGCUGACAAUUCG	3022	CGAATTGTCAGCTCCCCTAACCCCC	3626
1453	GGGGUUAGGGGAGCUGACAAUUCGU	3023	ACGAATTGTCAGCTCCCCTAACCCC	3627
1454	GGGUUAGGGGAGCUGACAAUUCGUG	3024	CACGAATTGTCAGCTCCCCTAACCC	3628
1455	GGUUAGGGGAGCUGACAAUUCGUGG	3025	CCACGAATTGTCAGCTCCCCTAACC	3629
1456	GUUAGGGAGCUGACAAUUCGUGGG	3026	CCCACGAATTGTCAGCTCCCCTAAC	3630
1457	UUAGGGGAGCUGACAAUUCGUGGGU	3027	ACCCACGAATTGTCAGCTCCCCTAA	3631
1458	UAGGGGAGCUGACAAUUCGUGGGUC	3028	GACCCACGAATTGTCAGCTCCCCTA	3632
. 1459	AGGGGAGCUGACAAUUCGUGGGUCC	3029	GGACCCACGAATTGTCAGCTCCCCT	3633
1460	GGGGAGCUGACAAUUCGUGGGUCCG	3030	CGGACCCACGAATTGTCAGCTCCCC	3634
1462	GGAGCUGACAAUUCGUGGGUCCGCA	3031	TGCGGACCCACGAATTGTCAGCTCC	3635
1463	GAGCUGACAAUUCGUGGGUCCGCAA	3032	TTGCGGACCCACGAATTGTCAGCTC	3636
1464	AGCUGACAAUUCGUGGGUCCGCAAA	3033	TTTGCGGACCCACGAATTGTCAGCT	3637
1465	GCUGACAAUUCGUGGGUCCGCAAAA	3034	TTTTGCGGACCCACGAATTGTCAGC	3638
1466	CUGACAAUUCGUGGGUCCGCAAAAU	3035	ATTTTGCGGACCCACGAATTGTCAG	3639
1467	UGACAAUUCGUGGGUCCGCAAAAUC	3036	GATTTTGCGGACCCACGAATTGTCA	3640
1468	GACAAUUCGUGGGUCCGCAAAAUCU	3037	AGATTTTGCGGACCCACGAATTGTC	3641
1469	ACAAUUCGUGGGUCCGCAAAAUCUU	3038	AAGATTTTGCGGACCCACGAATTGT	3642
1470	CAAUUCGUGGGUCCGCAAAAUCUUA	3039	TAAGATTTTGCGGACCCACGAATTG	3643
1471	AAUUCGUGGGUCCGCAAAAUCUUAA	3040	TTAAGATTTTGCGGACCCACGAATT	3644
1472	AUUCGUGGGUCCGCAAAAUCUUAAC	3041	GTTAAGATTTTGCGGACCCACGAAT	3645
1473	UUCGUGGGUCCGCAAAAUCUUAACU	3042	AGTTAAGATTTTGCGGACCCACGAA	3646
1474	UCGUGGGUCCGCAAAUCUUAACUA	3043	TAGTTAAGATTTTGCGGACCCACGA	3647
1475	CGUGGGUCCGCAAAAUCUUAACUAC	3044	GTAGTTAAGATTTTGCGGACCCACG	3648
1476	GUGGGUCCGCAAAAUCUUAACUACC	3045	GGTAGTTAAGATTTTGCGGACCCAC	3649
1477	UGGGUCCGCAAAAUCUUAACUACCU	3046	AGGTAGTTAAGATTTTGCGGACCCA	3650
1478	GGGICCGCAAAAUCUUAACUACCUA	3047	TAGGTAGTTAAGATTTTGCGGACCC	3651
1479	GGUCCGCAAAAUCUUAACUACCUAA	3048	TTAGGTAGTTAAGATTTTGCGGACC	3652
1480	GUCCGCAAAAUCUUAACUACCUAAU	3049	ATTAGGTAGTTAAGATTTTGCGGAC	3653
	UCCGCAAAAUCUUAACUACCUAAUA	3050	TATTAGGTAGTTAAGATTTTGCGGA	3654
1481	UCCGCAAAAUCUUAACUACCUAAUA	3050	TATTAGGIAGITAAGATTITGCGGA	3004

Input Sequence = PLN Oligo Length = 25

PLN (Homo sapiens phospholamban (PLN) mRNA.; 1635 bp)

Table 31: Anti-Her2 Ribozyme and Substrate Sequence

		Seq ID	Nos
1	NCH Ribozyme Sequence	NCH Substrate Sequence	
	asqscsuscca cUGAuGaggccguuaggccGaa Igugcuc B	GAGCACC A UGGAGCU	D
	gsasgsgsgcg cUGAuGaggccguuaggccGaa Igaggag B	cuccucc u cacceuc	c
	usceasusque cUGAuGaggeeguuaggeeGaa Iugeegg B	CCGGCAC A GACAUGA	A
	cscsasgsgug cUGAuGaggccguuaggccGaa Iucucgg B	CCGAGAC C CACCUGG	G
	ascsasgsgcu cUGAuGaggccguuaggccGaa Icauugg B	CCAAUGC C AGCCUGU	n
	cscsususuca cUGAuGaggccguuaggccGaa Iaucucu B	AGAGAUC U UGAAAGG	9
	csgsusgsucc cUGAuGaggccguuaggccGaa Iguagca B	UGCUACC A GGACACG	9
	ususgsasagu cUGAuGaggccgunaggccGaa Iaggcag B	CUGCCUC C ACUUCAA	4
	gsususgsaag cUGAuGaggccgunaggccGaa Igaggca B	UGCCUCC A CUUCAAC	رد
	usgsgsusuga cUGAuGaggccguuaggccGaa Iuggagg B	CCUCCAC U UCAACCA	А
	usgsususgua cUGAuGaggccguuaggccGaa Iugacca B	UGGUCAC C UACAACA	4
	uscausgaugu cUGAuGaggccguuaggccGaa Iuaggug B	CACCUAC A ACACAGA	e.
	gsusgsuscug cUGAuGaggccguuaggccGaa Iuuguag B	CUACAAC A CAGACAC	D,
	usgsgsgscau cUGAuGaggccguuaggccGaa Iacucaa B	UUGAGUC C AUGCCCA	¥.
	asgsgsusagu cUGAuGaggccguuaggccGaa Iuaggga B	UCCCUAC A ACUACCU	2
	asgsascscau cUGAuGaggccguuaggccGaa Icacacu B	AGUGUGC U AUGGUCU	P:
	csuscscscaa cUGAuGaggccguuaggccGaa Iaucuuc B	GAAGAUC U UUGGGAG	J.
	gegsusasacc cUGAuGaggccguuaggccGaa Iugaucu B	AGAUCAC A GGUUACC	R
	gscscsasugc cUGAuGaggccguuaggccGaa Iagaugu B	ACAUCUC A GCAUGGC	30
	asgsgsusucu cUGAuGaggccguuaggccGaa Iaagacg B	CGUCUUC C AGAACCU	20
	asasgsasgcu cUGAuGaggccguuaggccGaa Iucccag B	CUGGGAC C AGCUCUU	DC DC
	gscsasceucc cUGAuGaggccguuaggccGaa Igccccg B	CGGGGCC A GGAGUGC	30
	gscsasusgua cUGAuGaggccguuaggccGaa Iagaggu B	ACCUCUC C DACAUGO	30
1	gsgscsasugu cUGAuGaggccguuaggccGaa Igagagg B	CCUCUCC U ACAUGCC	8
	asgsususgau cUGAuGaggccguuaggccGaa Iggcaag B	CUUGCCC C AUCAACU	DC.

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UJGCCCC A UCAACUG	CUBCACC C ACUCCUG	UGCACCC A CUCCUGU	CGAUGCC C AACCAGG	AAGGUGC U UGGAUCU	UUGGCAC A GUCUACA	GUGACAC A GCUUAUG	GAUUGCC A AGGGGAU	CUCGUAC A CAGGGAC	UNCEGEC U GECUCGE	GCUCGGC U GCUGGAC	CGGCUGC U GGACAUU	GGCUGC U GGACAU	ceecuec u geacauu	GGCUGC U GGACAU	CGGCUGC U GGACAUU	GGCUGC U GGACAU	CGGCUGC U GGACAUU	GGCUGC U GGACAU	GCUGGAC A UUGACGA	ACGAGAC A GAGUACC	UGGGGCC A AACCUUA	GCCAAAC C UUACGAU	CCAAAC C UUACGA	GCCAAAC C UUACGAU	CCAAAC C UUACGA	GCCAAAC C UUACGAU	CCANAC C UDACGA	GCCAAAC C UUACGAU	CCAAAC C UUACGA	CCAAACC U UACGAUG
	csasqsgsagu cUGAuGaggccgunaggccGaa Igugcag B	ascsasgeda cUGAuGaggccguuaggccGaa Iggugca B	cacanagegun cUGAuGaqqccquuaggccGaa Igcaucg B	accessinance citthugacaccounagecesas Icaccuu B	usganasagac cudhugaqccquuaqqccGaa Iugccaa B	CRASUSASSAC CUGAUGAGCCGuuaggccGaa Ingucac B	asusososocu cUGAuGaggocogunaggocogaa Igcaauc B	qsuscscscug cUGAuGaggccguuaggccGaa Iuacgag B	cscsqsasqcc cUGAuGaggccguuaggccGaa Icccgaa B	gsuscscaage cUGAuGaggeegunaggeeGaa Icegage B	asasusgsucc cUGAuGaggccguuaggccGaa Icagccg B	asusgsuscc cUGAuGaggccguuaggccGaa Icagcc B	asasusgsucc cUGAuGaggcguuagccGaa Icagccg B	asusqsuscc cUGAuGaggcguuagccGaa Icagcc B	asasusgsucc cUGAUGaggccguuaggccGaa Icagccg B	asusgsuscc cUGAUGaggccguuaggccGaa Icagcc B	asasusqsucc cUGAUGaggcguuagccGaa Icagccg B	asusqsuscc cUGAUGaggcguuagccGaa Icagcc B	uscagauscaa cUGAuGaggccguuaggccGaa Iuccagc B	gsgsusascuc cUGAuGaggccguuaggccGaa Iucucgu B	usasasgsguu cUGAuGaggccguuaggccGaa Igcccca B	aguscsgsuaa cUGAuGaggccguuaggccGaa Iuuuggc B	uscsgsusaa cUGAuGaggccguuaggccGaa Iuuugg B	asuscegsuaa cUGAuGaggcguuagccGaa Iuuuggc B	uscaqsusaa cUGAuGaggcguuagccGaa Iuuugg B	asuscegsuaa cUGAUGaggccguuaggccGaa Iuuuggc B	ngceosusaa cUGAUGaqqccquuaqqccGaa Iuuugg B	asuscesuna cUGAUGaggcguuagccGaa Iuuuggc B	uscsgsusaa cUGAUGaggcguuagccGaa Iuuugg B	csasuscsgua cUGAuGaggccguuaggccGaa Iguuugg B
2056	2068	2069	2295	2361	2323	2520	2665	2702	2771	2780	2783	2783	2783	2783	2783	2783	2783	2783	2788	2799	2935	2939	2939	2939	2939	2939	2939	2939	2939	2940
17239	17240	17241	17272	2727.2	17044	17245	17246	17247	17248	18261	17249	18265	18267	18269	18271	18273	18275	18277	18262	17250	18263	17251	18266	18268	18270	18272	10274	18276	18278	18264

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asgsasasunc cUGhuGaggccgunaggccGaa Iacacca B
asusasceauc cuchucaggecguaggeccaa tayecay b
csusqsusaqa cUGAuGaggccguuaggccGaa Igcuggg B
asgscscsauc cUGAuGaggccguuaggccGaa Iucucag B
cscsasgsagu cliGAuGaggccguuaggccGaa Icaccag B
uscsusceac cUGAuGaggccgunaggccGaa Icacccc B
asasgsgscug cUGAuGaggccguuaggccGaa Icugaag B
usasasusaga cUGAuGaggccguuaggccGaa Iuugucg B
gsasasgsuca cUGAuGaggccguuaggccGaa Iccuucc B
Hammerhead Ribozyme Sequence
gscsgsgscac cUGAuGaggccgunaggccGaa Aggccgc B
gsgsnsgsgcg cUGAuGaggccgunaggccGaa Agcaugu B
cscsuscsaaa cUGAuGaggccguuaggccGaa Agcuggg B
usgsuscscuc cUGAuGaggccguuaggccGaa Aagagcu B
gsgsasuscaa cUGAuGaggccguuaggccGaa Accccuc B
gsgscsasca cUGAuGaguccgugaggacGaa Acagugc B
usgsusgsung cUGAuGaggccguuaggccGaa Aggugac B
gsusasgsung cUGAuGaggccgunaggccGaa Agggaca B
csasgsascca cUGAuGaggccguuaggccGaa Agcacac B
gscsuscscca cUGAuGaggccgunaggccGaa Agaucuu B
gsgscsusccc cUGAuGaggccgunaggccGaa Aagaucu B
cscscscsauc cUGAuGaggccguuaggccGaa Aagcucu B
cscsasusgen ctGAuGaggeeguuaggeeGaa Agaugua B
qsususcsugg cUGAuGaggccguuaggccGaa Agacgcu B
qsqsususcug cUGAuGaggccguuaggccGaa Aagacgc B
gsgsususccg clighudaggccgunaggccdaa Aagagcu B
usgscsasguu cUGAuGaggccguuaggccGaa Acacacu B
csasusqsuaq cUGAuGaggccguuaggccGaa Agagguc B

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cucuccu a causece	GCCCCAU C AACUGCA	ACCCACU C CUGUGUG	AGGUGCU U GGAUCUG	ACAGCUU A UGCCCUA	UGCGGCU C GUACACA	ecneeco c cecoeco	UGGACAU U GACGAGA	GAUGACU U UUGGGGC	UGACUUU U GGGGCCA	AAACCUU A CGAUGGG	CGGGAGU U GGUGUCU	GAGGACU U GGGCCCA	CAGCCCU C UACAGCG	GCCCUCU A CAGCGGU	AUGGGGU C GUCAAAG	ccacccu c cuccusc	CAGCCUU C GACAACC	CCUCUAU U ACUGGGA
Аддадад В	модада В	g n666n6 _b	Agcaccu B	Aagcugu B	Agccgca B	Agccage B	Augueca B	Agucauc B	Aaaguca B	Aagguuu B	Acuccog B	Aguccuc B	Agggcug B	Agagggc B	Acccau B	Agggugg B	Aaggcug B	Auagagg B
gsgsgscsaug clighuGaggccguuaggccGaa Aggagag	usgscsasguu cUGAuGaggccguuaggccGaa Auggggc	csascsascag cUGAuGaggccgunaggccGaa Agugggu	csasgsasucc cUGAuGaggccguuaggccGaa Agcaccu	usasgsgsgca cUGAuGaggccgunaggccGaa Aagcugu	usgsusgsuac cUGAuGaggccgunaggccGaa Agccgca B	asgscsasgcc cUGAuGaggccgunaggccGaa Agccagc B	uscsuscegue cUGAuGaggecguuaggecGaa Augueca B	gecececaa cUGAuGaggccguuaggccGaa Agucauc B	usgsgscsccc cUGAuGaggccgunaggccGaa Aaaguca B	cscscsasucg cUGAuGaggccgunaggccGaa Aagguuu	asgsascsacc cUGAuGaggccguuaggccGaa Acucccg	usgsgsgsccc cUGAuGaggccguuaggccGaa Aguccuc B	csgscsusgua cUGAuGaggccgunaggccGaa Agggcug B	ascecegecug cUGAuGaggccguuaggccGaa Agagggc	csusususgac cUGAuGaggccguuaggccGaa Accccau	gscsasgsgag cUGAuGaggccguuaggccGaa Agggugg	gegsususguc cUGAmGaggccguuaggccGaa Aaggcug	uscscscsagu cUGAuGaggccguuaggccGaa Auagagg B
gsgsgscsaug	usgacsasguu	csascsascag	csasgsasucc	usasgagaga	negenegenac	asgscsasgcc	onecensosanc	gscscscsaa	cossessen	cscscsasncd	asgsascsacc	posessesses	csgscsusgna	ascecegecue	csususgac	gscsasgsgag	onSenensEsE	uscscscsagu
2003	2058	2012	2352	2575	2697	2776	2790	2926	2928	2942	3089	3155	3499	3501	3714	3802	3825	3838
17194	17205	17206	17195	17196	17197	18257	18258	17207	18259	18260	17198	17208	17209	17210	17211	17199	17200	17201

Lowercase = Uppercase:

2.-O-methyl Modifications

1. Uppercase U under Ribozyme Sequence = 2'-C-Allyl U

Al oldher Uppercases = Ribonucleotides
Inosine
3'-3' Inverted abasic deoxyribose

B __

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Table 32: RNA Cleavage by NCH-XYLO Ribozyme (Reaction: 50 mM TRIS-Cl pH 7.5, 10 mM Mg²⁺, 37°C, 500 nM FINAL [Rz], Trace Substrate)

DATA SUMMARY

NCH-Xylo Ribozyme (RPI No.)	TARGET TRIPLET NCX-3'	5′-	k obs (min. ⁻¹) guua + A15.1 = xylo
14827	5'-GCA-3'		1.649
14828	5'-ACA-3'		0.293
14829	5'-UCA-3'		0.272
14830	5'-CCA-3'		0.214

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Table 33

Table 33: Examples of NCH-Xylo Ribozyme and Substrate Sequences

RPI Nos.	Ribozyme Sequence	Seq. ID. Nos.	Substrate Sequence	Seq. ID. Nos.
14827	14827 5'-ucu cca u cDGA uGa ggcc guua ggcc Gaa I cuc ccuB-3'		5'-AGGGA GCA AUGGAGA-3'	
14828	5'-ucu cca u cOGA uGa ggcc guua ggcc Gaa I uuc ccuB-3'		5'-AGGGA ACA AUGGAGA-3'	
14829	5'-ucu cca u cUGA uGa ggcc guua ggcc Gaa I auc ccuB-3'		5'-AGGGA UCA AUGGAGA-3'	
14830	5'-ucu cca u cUGA uGa ggcc guua ggcc Gaa I guc ccuB-3'		5'-AGGGA CCA AUGGAGA-3'	

Uppercase = Ribonucleotides Lowercase = 2'-O-methyl nucleotides

Lowercase = Z-O-metnyl nucle

I = Xylo -Inosine

B = 3'-3' inverted abasic U = 2'-C-allyl-U

Table 34

Table 34: Anti-HER2 NCH Ribozyme and Target Sequences

nt. Position	NCH Substrate Sequence	Seq. ID Nos.	NCH Ribozyme Sequence	Seq. ID Nos.
14	AGGUAAC C CUGGCCC		GGGCCAG CUGAUGAG X CGAA IUUACCU	
15	GGUAACC C UGGCCCC		GGGGCCA CUGAUGAG X CGAA IGUUACC	
16	GUAACCC U GGCCCCU		AGGGGCC CUGAUGAG X CGAA IGGUUAC	
20	CCCUGGC C CCUUUGG		CCAAAGG CUGAUGAG X CGAA ICCAGGG	
21	CCUGGCC C CUUUGGU		ACCAAAG CUGAUGAG X CGAA IGCCAGG	
22	CUGGCCC C UUUGGUC		GACCAAA CUGAUGAG X CGAA IGGCCAG	
23	UGGCCCC U UUGGUCG		CGACCAA CUGAUGAG X CGAA IGGGCCA	
35	UCGGGGC C CCGGGCA		UGCCCGG CUGAUGAG X CGAA ICCCCGA	
36	CGGGGCC C CGGGCAG		CUGCCCG CUGAUGAG X CGAA IGCCCCG	
37	GGGGCCC C GGGCAGC		GCUGCCC CUGAUGAG X CGAA IGGCCCC	
42	CCCGGGC A GCCGCGC		GCGCGGC CUGAUGAG X CGAA ICCCGGG	
45	GGGCAGC C GCGCGCC		GGCGCGC CUGAUGAG X CGAA ICUGCCC	
52	CGCGCGC C CCUUCCC		GGGAAGG CUGAUGAG X CGAA ICGCGCG	
53	GCGCGCC C CUUCCCA		UGGGAAG CUGAUGAG X CGAA IGCGCGC	
54	CGCGCCC C UUCCCAC		GUGGGAA CUGAUGAG X CGAA IGGCGCG	
55	GCGCCCC U UCCCACG		CGUGGGA CUGAUGAG X CGAA IGGGCGC	
58	CCCCUUC C CACGGGG		CCCCGUG CUGAUGAG X CGAA IAAGGGG	
59	CCCUUCC C ACGGGGC		GCCCCGU CUGAUGAG X CGAA IGAAGGG	
60	CCUUCCC A CGGGGCC		GGCCCCG CUGAUGAG X CGAA IGGAAGG	
67	ACGGGGC C CUUUACU		AGUAAAG CUGAUGAG X CGAA ICCCCGU	
68	CGGGGCC C UUUACUG		CAGUAAA CUGAUGAG X CGAA IGCCCCG	
69	GGGGCCC U UUACUGC		GCAGUAA CUGAUGAG X CGAA IGGCCCC	
74	CCUUUAC U GCGCCGC		GCGGCGC CUGAUGAG X CGAA IUAAAGG	
79	ACUGCGC C GCGCGCC		GGCGCGC CUGAUGAG X CGAA ICGCAGU	
86	CGCGCGC C CGGCCCC		GGGGCCG CUGAUGAG X CGAA ICGCGCG	
87	GCGCGCC C GGCCCCC		GGGGGCC CUGAUGAG X CGAA IGCGCGC	
91	GCCCGGC C CCCACCC		GGGUGGG CUGAUGAG X CGAA ICCGGGC	
92	CCCGGCC C CCACCCC		GGGGUGG CUGAUGAG X CGAA IGCCGGG	
93	CCGGCCC C CACCCCU		AGGGGUG CUGAUGAG X CGAA IGGCCGG	
94	CGGCCCC C ACCCCUC		GAGGGGU CUGAUGAG X CGAA IGGGCCG	
95	GGCCCCC A CCCCUCG		CGAGGGG CUGAUGAG X CGAA IGGGGCC	
97	CCCCCAC C CCUCGCA		UGCGAGG CUGAUGAG X CGAA IUGGGGG	
98	CCCCACC C CUCGCAG		CUGCGAG CUGAUGAG X CGAA IGUGGGG	
99	CCCACCC C UCGCAGC		GCUGCGA CUGAUGAG X CGAA IGGUGGG	
100	CCACCCC U CGCAGCA		UGCUGCG CUGAUGAG X CGAA IGGGUGG	
104	CCCUCGC A GCACCCC		GGGGUGC CUGAUGAG X CGAA ICGAGGG	
107	UCGCAGC A CCCCGCG		CGCGGGG CUGAUGAG X CGAA ICUGCGA	
109	GCAGCAC C CCGCGCC		GGCGCGG CUGAUGAG X CGAA IUGCUGC	
110	CAGCACC C CGCGCCC		GGGCGCG CUGAUGAG X CGAA IGUGCUG	
111	AGCACCC C GCGCCCC		GGGGCGC CUGAUGAG X CGAA IGGUGCU	
116	CCCGCGC C CCGCGCC		GGCGCGG CUGAUGAG X CGAA ICGCGGG	
117	CCGCGCC C CGCGCCC		GGGCGCG CUGAUGAG X CGAA IGCGCGG	

Table 34

		AGGGCGC CUGAUGAG X CGAA IGGCGCG
118	CGCGCCC C GCGCCCU	
123	CCCGCGC C CUCCCAG	CUGGGAG CUGAUGAG X CGAA ICGCGGG
124	CCGCGCC C UCCCAGC	GCUGGGA CUGAUGAG X CGAA IGCGCGG
125	CGCGCCC U CCCAGCC	GGCUGGG CUGAUGAG X CGAA IGGCGCG
127	CGCCCUC C CAGCCGG	CCGGCUG CUGAUGAG X CGAA IAGGGCG
128	GCCCUCC C AGCCGGG	CCCGGCU CUGAUGAG X CGAA IGAGGGC
129	CCCUCCC A GCCGGGU	ACCCGGC CUGAUGAG X CGAA IGGAGGG
132	UCCCAGC C GGGUCCA	UGGACCC CUGAUGAG X CGAA ICUGGGA
138	CCGGGUC C AGCCGGA	UCCGGCU CUGAUGAG X CGAA IACCCGG
139	CGGGUCC A GCCGGAG	CUCCGGC CUGAUGAG X CGAA IGACCCG
142	GUCCAGC C GGAGCCA	UGGCUCC CUGAUGAG X CGAA ICUGGAC
148	CCGGAGC C AUGGGGC	GCCCCAU CUGAUGAG X CGAA ICUCCGG
149	CGGAGCC A UGGGGCC	GGCCCCA CUGAUGAG X CGAA IGCUCCG
156	AUGGGGC C GGAGCCG	CGGCUCC CUGAUGAG X CGAA ICCCCAU
162	CCGGAGC C GCAGUGA	UCACUGC CUGAUGAG X CGAA ICUCCGG
165	GAGCCGC A GUGAGCA	UGCUCAC CUGAUGAG X CGAA ICGGCUC
172	AGUGAGC A CCAUGGA	UCCAUGG CUGAUGAG X CGAA ICUCACU
174	UGAGCAC C AUGGAGC	GCUCCAU CUGAUGAG X CGAA IUGCUCA
175	GAGCACC A UGGAGCU	AGCUCCA CUGAUGAG X CGAA IGUGCUC
182	AUGGAGC U GGCGGCC	GGCCGCC CUGAUGAG X CGAA ICUCCAU
189	UGGCGGC C UUGUGCC	GGCACAA CUGAUGAG X CGAA ICCGCCA
190	GGCGGCC U UGUGCCG	CGGCACA CUGAUGAG X CGAA IGCCGCC
196	CUUGUGC C GCUGGGG	CCCCAGC CUGAUGAG X CGAA ICACAAG
199	GUGCCGC U GGGGGCU	AGCCCCC CUGAUGAG X CGAA ICGGCAC
206	UGGGGGC U CCUCCUC	GAGGAGG CUGAUGAG X CGAA ICCCCCA
208	GGGGCUC C UCCUCGC	GCGAGGA CUGAUGAG X CGAA IAGCCCC
209	GGGCUCC U CCUCGCC	GGCGAGG CUGAUGAG X CGAA IGAGCCC
211	GCUCCUC C UCGCCCU	AGGGCGA CUGAUGAG X CGAA IAGGAGC
212	CUCCUCC U CGCCCUC	GAGGGCG CUGAUGAG X CGAA IGAGGAG
216	UCCUCGC C CUCUUGC	GCAAGAG CUGAUGAG X CGAA ICGAGGA
217	CCUCGCC C UCUUGCC	GGCAAGA CUGAUGAG X CGAA IGCGAGG
218	CUCGCCC U CUUGCCC	GGGCAAG CUGAUGAG X CGAA IGGCGAG
220	CGCCCUC U UGCCCCC	GGGGGCA CUGAUGAG X CGAA IAGGGCG
224	CUCUUGC C CCCCGGA	UCCGGGG CUGAUGAG X CGAA ICAAGAG
225	UCUUGCC C CCCGGAG	CUCCGGG CUGAUGAG X CGAA IGCAAGA
226	CUUGCCC C CCGGAGC	GCUCCGG CUGAUGAG X CGAA IGGCAAG
227	UUGCCCC C CGGAGCC	GGCUCCG CUGAUGAG X CGAA IGGGCAA
228	UGCCCCC C GGAGCCG	CGGCUCC CUGAUGAG X CGAA IGGGGCA
234	CCGGAGC C GCGAGCA	UGCUCGC CUGAUGAG X CGAA ICUCCGG
241	CGCGAGC A CCCAAGU	ACUUGGG CUGAUGAG X CGAA ICUCGCG
243	CGAGCAC C CAAGUGU	ACACUUG CUGAUGAG X CGAA IUGCUCG
244	GAGCACC C AAGUGUG	CACACUU CUGAUGAG X CGAA IGUGCUC
245	AGCACCC A AGUGUGC	GCACACU CUGAUGAG X CGAA IGGUGCU
253	AGUGUGC A CCGGCAC	GUGCCGG CUGAUGAG X CGAA ICACACU
255	UGUGCAC C GGCACAG	CUGUGCC CUGAUGAG X CGAA IUGCACA
259	CACCGGC A CAGACAU	AUGUCUG CUGAUGAG X CGAA ICCGGUG
261	CCGGCAC A GACAUGA	UCAUGUC CUGAUGAG X CGAA IUGCCGG

Table 34

265	CACAGAC A UGAAGCU	AGCUUCA CUGAUGAG X CGAA IUCUGUG
272	AUGAAGC U GCGGCUC	GAGCCGC CUGAUGAG X CGAA ICUUCAU
278	CUGCGGC U CCCUGCC	GGCAGGG CUGAUGAG X CGAA ICCGCAG
280	GCGGCUC C CUGCCAG	CUGGCAG CUGAUGAG X CGAA IAGCCGC
281	CGGCUCC C UGCCAGU	ACUGGCA CUGAUGAG X CGAA IGAGCCG
282	GGCUCCC U GCCAGUC	GACUGGC CUGAUGAG X CGAA IGGAGCC
285	UCCCUGC C AGUCCCG	CGGGACU CUGAUGAG X CGAA ICAGGGA
286	CCCUGCC A GUCCCGA	UCGGGAC CUGAUGAG X CGAA IGCAGGG
290	GCCAGUC C CGAGACC	GGUCUCG CUGAUGAG X CGAA IACUGGC
291	CCAGUCC C GAGACCC	GGGUCUC CUGAUGAG X CGAA IGACUGG
297	CCGAGAC C CACCUGG	CCAGGUG CUGAUGAG X CGAA IUCUCGG
298	CGAGACC C ACCUGGA	UCCAGGU CUGAUGAG X CGAA IGUCUCG
299	GAGACCC A CCUGGAC	GUCCAGG CUGAUGAG X CGAA IGGUCUC
301	GACCCAC C UGGACAU	AUGUCCA CUGAUGAG X CGAA IUGGGUC
302	ACCCACC U GGACAUG	CAUGUCC CUGAUGAG X CGAA IGUGGGU
307	CCUGGAC A UGCUCCG	CGGAGCA CUGAUGAG X CGAA IUCCAGG
311	GACAUGC U CCGCCAC	GUGGCGG CUGAUGAG X CGAA ICAUGUC
313	CAUGCUC C GCCACCU	AGGUGGC CUGAUGAG X CGAA IAGCAUG
316	GCUCCGC C ACCUCUA	UAGAGGU CUGAUGAG X CGAA ICGGAGC
317	CUCCGCC A CCUCUAC	GUAGAGG CUGAUGAG X CGAA IGCGGAG
319	CCGCCAC C UCUACCA	UGGUAGA CUGAUGAG X CGAA IUGGCGG
320	CGCCACC U CUACCAG	CUGGUAG CUGAUGAG X CGAA IGUGGCG
322	CCACCUC U ACCAGGG	CCCUGGU CUGAUGAG X CGAA IAGGUGG
325	CCUCUAC C AGGGCUG	CAGCCCU CUGAUGAG X CGAA IUAGAGG
326	CUCUACC A GGGCUGC	GCAGCCC CUGAUGAG X CGAA IGUAGAG
331	CCAGGGC U GCCAGGU	ACCUGGC CUGAUGAG X CGAA ICCCUGG
334	GGGCUGC C AGGUGGU	ACCACCU CUGAUGAG X CGAA ICAGCCC
335	GGCUGCC A GGUGGUG	CACCACC CUGAUGAG X CGAA IGCAGCC
344	GUGGUGC A GGGAAAC	GUUUCCC CUGAUGAG X CGAA ICACCAC
352	GGGAAAC C UGGAACU	AGUUCCA CUGAUGAG X CGAA IUUUCCC
353	GGAAACC U GGAACUC	GAGUUCC CUGAUGAG X CGAA IGUUUCC
359	CUGGAAC U CACCUAC	GUAGGUG CUGAUGAG X CGAA IUUCCAG
361	GGAACUC A CCUACCU	AGGUAGG CUGAUGAG X CGAA IAGUUCC
363	AACUCAC C UACCUGC	GCAGGUA CUGAUGAG X CGAA IUGAGUU
364	ACUCACC U ACCUGCC	GGCAGGU CUGAUGAG X CGAA IGUGAGU
367	CACCUAC C UGCCCAC	GUGGGCA CUGAUGAG X CGAA IUAGGUG
368	ACCUACC U GCCCACC	GGUGGGC CUGAUGAG X CGAA IGUAGGU
371	UACCUGC C CACCAAU	AUUGGUG CUGAUGAG X CGAA ICAGGUA
372	ACCUGCC C ACCAAUG	CAUUGGU CUGAUGAG X CGAA IGCAGGU
373	CCUGCCC A CCAAUGC	GCAUUGG CUGAUGAG X CGAA IGGCAGG
375	UGCCCAC C AAUGCCA	UGGCAUU CUGAUGAG X CGAA IUGGGCA
376	GCCCACC A AUGCCAG	CUGGCAU CUGAUGAG X CGAA IGUGGGC
381	CCAAUGC C AGCCUGU	ACAGGCU CUGAUGAG X CGAA ICAUUGG
382	CAAUGCC A GCCUGUC	GACAGGC CUGAUGAG X CGAA IGCAUUG
385	UGCCAGC C UGUCCUU	AAGGACA CUGAUGAG X CGAA ICUGGCA
386	GCCAGCC U GUCCUUC	GAAGGAC CUGAUGAG X CGAA IGCUGGC
390	GCCUGUC C UUCCUGC	GCAGGAA CUGAUGAG X CGAA IACAGGC

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Table 34

394			
395 UCCUUCC U GOAGGAU	391	CCUGUCC U UCCUGCA	UGCAGGA CUGAUGAG X CGAA IGACAGG
398			
406	395	UCCUUCC U GCAGGAU	
407 GAUAUCC A GRACEUG 416 GAGGUC A GRACEUG 416 GAGGUC A GRACEUG 417 GACAGGU CUGANGAG X CGAA ICALUNC 421 GACAGGU CUGANGAG X CGAA ICACUUC 428 UACGUC CUGANGAG X CGAA ICACUUC 430 CGUGCUC A GACAGC 430 CGUGCUC A GACAGC 435 UCAUCGC U CACACC 436 UCAUCGC U CACACC 437 AUCGUC A CACACC 437 AUCGUC A CACACC 437 AUCGUC A CACACC 437 AUCGUC A CACACC 438 CACAGGU CUGANGAG X CGAA ICACGUA 437 AUCGUC A CACACC 439 CGUCAC A CACAGC 442 UCACAAC C AAGUGAC 442 UCACAAC C AAGUGAC 443 CACACC A AGUGAC 443 CGACACC A GUCACA 445 CGACACC A GUCACA 457 GACAGC C CACAGC 457 GACAGC C CACAGC 457 GACAGC C CACAGC 458 CACACC A AGUGAC 459 CGCACACC CGACAGC 459 GACAGC C CACAGCC 459 GACAGC C CACAGCC 459 GACAGC C CACAGCC 459 CACACC C CACAGCC 459 CACACC C CACAGCC 459 CACACCC 450 CACACCC	398	UUCCUGC A GGAUAUC	GAUAUCC CUGAUGAG X CGAA ICAGGAA
	406	GGAUAUC C AGGAGGU	
ACCIDENCE CARRIGORU AGCACGU CUGANUGAG X COGA ECCUBEC	407	GAUAUCC A GGAGGUG	CACCUCC CUGAUGAG X CGAA IGAUAUC
128	416	GAGGUGC A GGGCUAC	GUAGCCC CUGAUGAG X CGAA ICACCUC
1330	421	GCAGGGC U ACGUGCU	AGCACGU CUGAUGAG X CGAA ICCCUGC
135 UCADOGC U CACARCC GGUUGUG CUGAUGAG X CGAA ICGAUGA	428	UACGUGC U CAUCGCU	AGCGAUG CUGAUGAG X CGAA ICACGUA
AUCOCUC A CAACCAA	430	CGUGCUC A UCGCUCA	UGAGCGA CUGAUGAG X CGAA IAGCACG
439 CGCUCAC A ACCAAGU ACUDAGU CUGANUGAG X CGBA LUGAGCG 442 URACAACC AAGUGAG CUCACUU CUGANUGAG X CGBA LUGAGCG 443 CACAACC AAGUGAG CUCACUU CUGANUGAG X CGBA LUGAGCG 452 GUGAGGC C GAUGCAC 453 CGGGCC C AGUCCAC 454 CACACC AAGUGCA 455 AGGUCC C CAUUCAG 457 AGGUCC C CAUUCAG 458 CAGGUCC C CAUUCAG 458 CAGGUCC C CAUUCAG 459 AAGUCCC A CUGACAG 450 CAGGUCC C CAUUCAG 451 CAGGUCC C CAUUCAG 451 CAGGUCC C CAUUCAG 452 CAGGUCC C CAUUCAG 453 CAGGUCC C CAUUCAG 454 CACACC A CUGACAG 455 CAGGUCC C CAUUCAG 457 CAGGUCC C CAUUCAG 458 CAGGUCC C CAUUCAG 459 AAGUCCC A CUGACAG 450 CAGCUCC CUGANUGAG X CGBA LICACUGC 461 GUCCAC U GACAGAG 461 CACACC C A CUGACAG 461 CACACC C CAGCUCU 461 CACACC C CAGCUCU 462 CAGGCCC C CAGCUCU 463 CAGCACC C CAGCUCU 464 CACACC C CACCUCU 465 CAGCCC C CACCUCU 467 CAGCACC C CACCUCU 468 CACACC C CACCUCU 468 CACACC C CACCUCU 469 CAGCCC C CACCUCU 469 CACCC C CACCUCU 460 CAGCCC C CACCUCU 460 CAGCCC C CACCUCU 460 CACCC C CACCCC 460 CACCC C CACCCC 460 CACCC C CACCCC 460 CACCC C CACCCCC 460 CACCC C CACCCC 460 CACCC	435	UCAUCGC U CACAACC	GGUUGUG CUGAUGAG X CGAA ICGAUGA
442 UCACAAC C AAGUGAG 443 CACAACC A AGUGAGG 444 CACAACC A AGUGAGG 452 GUCAGUU CUGANGAG X CGAA IUUGUGA 457 GACAGCC A AGUGAGG 458 CAGAGCC CUGANGAG X CGAA IUUGUGA 458 CAGGUCC C ACUGCA 458 CAGGUCC C ACUGCA 458 CAGGUCC C ACUGCA 459 AGGUCC C ACUGCAG 459 AGGUCC C ACUGCAG 459 AGGUCC C ACUGCAG 461 GUCCAC U GCAAGG 461 GUCCAC U GCAAGG 461 CACCUGC C GACUGCA 461 CACCUGC C GACUGCAG 462 CACCUGC C GACUGCAG 463 CAGGUCC C ACUGCAG 464 CACCUGC C GACUGCAG 465 CAGGUC C GACUGCAG 466 CACCUGC C GACUGCAG 467 CACAGGC U GCAAGAG 467 CACCUGC C GACUGCAG 468 CACCUGC C GACUGCAG 469 GAGGCAC C ACUCCUGAGCAG 469 GAGGCAC C ACUCCUGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	437	AUCGCUC A CAACCAA	UUGGUUG CUGAUGAG X CGAA IAGCGAU
AND CACARCC A AGUIDAGG CCUCACU CUGAUGAG X CGAA IGUIDAGG	439	CGCUCAC A ACCAAGU	ACUUGGU CUGAUGAG X CGAA IUGAGCG
452 GUGAGGC A GGUCCCA	442	UCACAAC C AAGUGAG	CUCACUU CUGAUGAG X CGAA IUUGUGA
457 GAGGUC C CACUGCA	443	CACAACC A AGUGAGG	CCUCACU CUGAUGAG X CGAA IGUUGUG
1.5 1.5	452	GUGAGGC A GGUCCCA	UGGGACC CUGAUGAG X CGAA ICCUCAC
AGRICCC A CUGAGA	457	GCAGGUC C CACUGCA	UGCAGUG CUGAUGAG X CGAA IACCUGC
461 GUCCCAC U GCAGAGG CCUCUGC CUGAUGAG X CGAA IUGGGAC 464 CCACUGC A GAGGCUG CAGGCUC CUGAUGAG X CGAA IUGGGAC 467 CAGAGGC U GOGAUU AAUCCGC CUGAUGAG X CGAA ICAGURG 487 GCAGAGC U GOGAUU AAUCCGC CUGAUGAG X CGAA ICACUGG 489 GAGGCAC C CAGCUCU AGAGGCUG CUGAUGAG X CGAA ICACUGG 489 AGGCACC C AGCUCUU AAGAGCUG CUGAUGAG X CGAA IGUGCCU 490 AGGCACC C AGCUCUU AAGAGCU CUGAUGAG X CGAA IGUGCCU 491 GCCAGC U GUUUGAG CUCAUGAG X CGAA IGUGCCU 491 GCCAGC U UUUGAG CUCAUGAG C CUGAUGAG X CGAA IGUGCC 494 ACCCAGC U UUUGAG CUCAUGAG C CUGAUGAG X CGAA IGUGCC 555 UGAGGCAC U UUGAGGA UCCUCAA CUGAUGAG X CGAA IGUGCC 566 CCAGCUC U UUGAGGA UCCUCAA CUGAUGAG X CGAA IUGUCCA 567 UGAGGACA C AUGUGC GAGGCG C CUGAUGAG X CGAA IUGUCCA 568 GGACAC U AUGCCC AGGGCA CUGAUGAG X CGAA IUGUCCA 569 GAGCAC U GAUGAG CUCAUGAG X CGAA IUGUCCA 511 CULUGCC U UGGCCG CAGCCC CUGAUGAG X CGAA IUGUCCA 512 CULUGCC C UGGCCG CAGCCAG CUGAUGAG X CGAA IUGUCCA 513 ACUAUGC C UGGCCG CAGCCAG CUGAUGAG X CGAA IUGUCCA 514 CULUGCC C UGGCCG CAGCCAG CUGAUGAG X CGAA IUGUCCA 515 UAUGCCC U GGCCGUG CACGGCC CUGAUGAG X CGAA IUGUCCA 516 CACGCGC C GUGCAGA CUCAUGAG X CGAA IUGUCCA 517 CACCUGC C GUGCAGA CUCAUGAG X CGAA IUGUCCA 518 CACCGC C GUGCAGA CUCAUGAG X CGAA IUGUCCA 519 CACCGC C GUGCAGA CUCAUGAG X CGAA IUGUCCA 529 GCUAGAC A AUGGAGA UUCCCCA CUGAUGAG X CGAA IUCUCCA 539 GGAGACC C GCUGAA UUCAGC CUGAUGAG X CGAA IUCUCCA 539 GGAGACC C GCUGAA UUCAGC CUGAUGAG X CGAA IUCUCCA 541 GACCCC U GAACAAU AUUGUUC CUGAUGAG X CGAA IUCUCCA 552 CACAUGA AUACCAC GUGCAG CUGAUGAG X CGAA IUCUCCA 553 CACAGGC C UGAUGAG X CGAA IUCUCCA 554 GACCCC U GAACAAU AUUGUUC CUGAUGAG X CGAA IUCUCCA 555 CACAGGC C UGAUGAG X CGAA IUCUCCA 556 CACAGGC C UGAUGAG X CGAA IUCUCCA 557 CACAGCC C UGACAC GUGCACA CUGAUGAG X CGAA IUCUCCA 558 CACACCC C UGACCAC GUGCACA CUGAUGAG X CGAA IUCUCCA 556 UACCAC C CUGUCAC GUGCACA CUGAUGAG X CGAA IUCGCGC 557 CACAC	458	CAGGUCC C ACUGCAG	CUGCAGU CUGAUGAG X CGAA IGACCUG
AGE	459	AGGUCCC A CUGCAGA	UCUGCAG CUGAUGAG X CGAA IGGACCU
470 CAGAGGC U GCGGAUU AAUCCGC CUGAUGAG X CCAACCU 487 GCGAGGC A CCCAGCU AGACGGC CUGAUGAG X CCGAGCU AGACGGC CUGAUGAG X CCGAGCU 489 GAGGACC C AGCUCUU AGACGCC C GCGCUUU AAGAGGC CUGAUGAG X CGAA IGUGCCU 491 GGCACCC A GCUCUUU AAGAGGC CUGAUGAG X CGAA IGUGCCU 491 GCCACCC C GCUUUU AAGAGGC CUGAUGAG X CGAA IGUGCCC 494 ACCCAGC U CUUUGAG CUCAAAG CUGAUGAG X CGAA IGUGCCC 496 CCAGCCC U UUGACGA CUCAAAG CUGAUGAG X CGAA IGUGCCC 508 GGACAAC U UUGCCCU AGGGCAI CUGAUGAG X CGAA IGUGCCC 508 GGACAAC U AUGCCCU AGGGCAI CUGAUGAG X CGAA IGUCCUCA 508 GGACAAC U AUGCCCU AGGGCAI CUGAUGAG X CGAA IUGUCCC 513 ACUAUGC C CUGAGCG GCAICACU CUGAUGAG X CGAA IUGUCCC 515 UAUGCCC U GGCCGUG ACGGCCA CUGAUGAG X CGAA IUGUCCC 515 UAUGCCC CUGAGCG CACGCC CUGAUGAG X CGAA IUGUCCC 515 CUGAUGAC A GCCCUGA ACGGCCA CUGAUGAG X CGAA IUGUCCC 516 CCCCUGGC C GIRCCUAG CACGCC CUGAUGAG X CGAA ICCAGGGG 524 GCCGUGC U AGACAAU AUGUCCAU CUGAUGAG X CGAA IUCAGCG 529 GCUAGAC A AUGGAGA AUGUCCAU CUGAUGAG X CGAA IUCAGCG 538 UGAGAAC C GAGCAAU AUGUCCAU CUGAUGAG X CGAA IUCAGCC 539 GGAGAAC C GUGAUGAG X CGAA IUCAGCC 540 GCCGUG U AGACAAU AUGUCCAU CUGAUGAG X CGAA IUCAGCC 551 GCCGUG C GAGCAAC AUGUAGA C AUGUAGA X CGAA IUCAGCC 552 GCUAGAC A AUGGACA AUGUAGC CUGAUGAG X CGAA IUCAGCC 553 GGAGAAC C GGACAAU AUGUCCAU CUGAUGAG X CGAA IUCAGCC 554 GCCGCC C GGACCAA AUGUAGC CUGAUGAG X CGAA IUCAGCC 555 GUAGAC C GCCCUG C CACGCGC ACACGCC C GUGACAC GUGAGAC C CUGAUGAC X CGAA IUCACCC 555 ACAALAC C ACCCCUG C CAGGGCC CUGAUGAG X CGAA IUCACCC 555 AUACCAC C CUGUCAC GUGACAA C AUGCACC GUGACAA C AUGCACC GUGACAA C AUGCACC GUGACAA C CUGAUGAC C CUGAUGAG X CGAA IUCACAC 556 UACCACC C CUGUCAC GUGACAA C AUGCACC GUGACAA C AUGCACC GUGACAA C AUGCACC GUGACAA C CUGAUGAC 557 ALACACC C CUGUCAC GUGACAA C CUGAUGAC GUGACAA C CUGAUGAC GUGACAA C CUGAUGAC GUGACAAC CUGAUGAC GUGACAAC CUGAUGAC GUGACAAC CUGAUGAC GUGACAAC CUGAUGAC GUGACAAC CUGAUGAC GUGACAC CUGAUGAC GUGACACC CUGAUGAC GUGACAC CUGAUGAC GUGACAC CUGAUGACA CUGAUGAC CUGAUGAC C CUGAUGAC SGCCCCC CUGACAC GUGACACA CU	461	GUCCCAC U GCAGAGG	CCUCUGC CUGAUGAG X CGAA IUGGGAC
487 GCGAGGC A CCCAGCU	464	CCACUGC A GAGGCUG	CAGCCUC CUGAUGAG X CGAA ICAGUGG
AGAGCAC C CAGCUCU	470	CAGAGGC U GCGGAUU	AAUCCGC CUGAUGAG X CGAA ICCUCUG
AAGAGCC C AGCUCUU	487	GCGAGGC A CCCAGCU	AGCUGGG CUGAUGAG X CGAA ICCUCGC
491 GGCACCC A GCUCUUU AAAGAGC CUGAUGAG X CGAA ICGUGCC 494 ACCCAGCC U CUUUGAGA CUCACAAG CUGAUGAG X CGAA ICGUGCC 496 CAGCCC U CUUUGAGA CUCACAAG CUGAUGAGA X CGAA ICGUGCG 505 UGAGGAC A ACUAUGC GCACAC U AUGCCCI AGGGCAC CUGAUGAGA X CGAA ICCCCCA 513 ACUAUGC C CUGGCCG CGGCCAG CUGAUGAGA X CGAA ICCCCCA 514 CUAUGCC C CUGGCCG CGGCCAG CUGAUGAG X CGAA ICAUGCC 515 UAUGCCC C GUGCCG CGGCCAG CUGAUGAG X CGAA ICAUGCC 516 UAUGCCC C GUGCCG CGGCCAG CUGAUGAG X CGAA ICAUGCC 517 CCCUGGC C GUGCCAG CCGGCCC CUGAUGAG X CGAA ICAUGAG 519 CCCUGGC C GUGCCAG CCCGGCC CUGAUGAG X CGAA ICAUGCC 524 GCCGGC C GUGCCAG CUGAUGAG X CGAA ICACGGC 529 GCUAGAC A AUGCAAC 529 GCUAGAC A AUGCAAC 539 UGGAGAC C CGCUGAA CUCACAC CUGAUGAG X CGAA ICCCGGC 530 UGGAGAC C CGCUGAA CUCACAC CUGAUGAG X CGAA ICCCCGC 541 GCCCGC C GUGCAC GUCACAC CCCCCCC 552 GACCCGC C GACCAC CGCCCC CGCACAC CGCCCCC CGCACAC CGCCCCC CGCACAC CGCCCCC CGCACAC CGCCCCCCCCCC	489	GAGGCAC C CAGCUCU	AGAGCUG CUGAUGAG X CGAA IUGCCUC
494 ACCCAGC U CUJUIGAG 496 CCAGCUC U UUQAGGA 496 CCAGCUC U AGGGCAL 598 GGACAAC U AUGCCCU 598 GGACAAC U AUGCCCU 598 CCACCAC 513 ACUAUGC C UGGCCGG 598 CCACCAC 514 CUAUGCC C UGGCCGG 598 CCACCAC 515 UAUGCCC U GGCCGGG 598 CCACCAC 599 CCAGCAC 599 CCACCAC 599 CCAGCAC 599 CCAGCAC 599 CCACCAC 599 CCAGCAC 599 CCACCAC 599 CCAGCAC 599 CCACCAC 5	490	AGGCACC C AGCUCUU	AAGAGCU CUGAUGAG X CGAA IGUGCCU
496 CCAGCUC U UUGAGGA 595 UGAGGACA C ACUAUGC 596 GCARAGU CUGAUGAGA 597 UGAGGACA C ACUAUGC 598 GCARAGU CUGAUGAGA C CGAA TAGCUGG 513 ACUAUGC C CUGGCCC 513 ACUAUGC C CUGGCCC 514 CUAUGCC C UGGCCCC 515 UAUGCCC C UGGCCCC 516 CACCAGCC C UGGCCCC 517 CACCAGCC C UGGCCCC 518 CCUGGCC C UGGCCCC 519 CCCUGGC C GCGCCCC 519 CCCUGGC C GCGCCCC 519 CCCUGGC C GCGCCCC 519 CCCUGGC C GCGCCCC 524 GCCCUGC C GCGCCCC 524 GCCCUGC C GCGCCCC 525 GCUGACA C CUGCCCC 526 CCCUGCC C GCGCCCC 527 GCCCCCC C GCCCCCC 538 CGCCCCC C GCCCCCCC 539 CGCCCCC C GCCCCCCC 541 GCCCCCC C GCCCCCCC 542 GCCCCCC C GCCCCCCC 555 CACAUCC C CCCCCCCC 555 CACAUCC C CCCCCCC 555 CACAUCC C CCCCCCCC 556 UGCCCCC C CCCCCCCC 557 CACACCCC C CCCCCCCC 558 CACACCCC C CCCCCCCC 559 CACACCCC C CCCCCCCC 550 CACACCCC C CCCCCCCC 550 CACACCCC C CCCCCCCC 550 CACACCCC C CCCCCCCC 551 CACACCCC C CCCCCCCC 552 CACACCCC C CCCCCCCC 553 CACACCCC C CCCCCCCC 554 CACACCCC C CCCCCCCC 555 CACACCC C CCCCCCCC 556 UACCCCC C CCCCCCCC 557 CACACCC C CCCCCCCC 557 CACACCC C CCCCCCCC 557 CACACCC C CCCCCCCC 557 CACACCC C CCCCCCCCC 557 CACACCC C CCCCCCCC 557 CACACCC C CCCCCCCC 557 CACACCC C CCCCCCCCC 557 CACACCC C CCCCCCCCCC 557 CACACCC C CCCCCCCCC 557 CACACCC C CCCCCCCCCCCCCCCCCCCCCCCCCC	491	GGCACCC A GCUCUUU	AAAGAGC CUGAUGAG X CGAA IGGUGCC
SOS	494	ACCCAGC U CUUUGAG	CUCAAAG CUGAUGAG X CGAA ICUGGGU
SOB	496	CCAGCUC U UUGAGGA	UCCUCAA CUGAUGAG X CGAA IAGCUGG
STATE ACUAUGC C CURGOCCG COGGCCAG CUGAUGAG X CGAA ICAUAGU	505	UGAGGAC A ACUAUGC	
S14	508	GGACAAC U AUGCCCU	
S15	513		
CCCUGGC C GUGCIAG CUAGCAC CUGAUGAG X CGAA ICCAGGG	514		
S24 GCCGUGC U AGACAAU	515	UAUGCCC U GGCCGUG	
STATE STAT	519	CCCUGGC C GUGCUAG	
	524		
S39 GRADACC C GCURAAC GUUCAGC CUGAUGAG X CGAA IGUCUCC	529	GCUAGAC A AUGGAGA	
S42 GACCCCC U GAACAAU	538	UGGAGAC C CGCUGAA	
547 GCUGAAC A AUACCAC GUGGUAU CUGAUGAG X CGAA TUUUCAGC	539	GGAGACC C GCUGAAC	
S52 ACANAC C ACCCUG CAGGGGU CUGAUGAG X CGAA TUATUGU	542		
553 CAAUACC A CCCCUGU ACAGGG CUGAUGAG X CGAA IGUAUUG 555 AUACCAC C CUGUCA UGACAGG CUGAUGAG X CGAA IUGGUAU 556 UACCACC C CUGUCA UGACAGG CUGAUGAG X CGAA IUGGUAU 557 ACCACCC C UGUCACA UGUGACA CUGAUGAG X CGAA IGUGGUA 558 CCACCCC U GUCACAG UGUGACA CUGAUGAG X CGAA IGGGGG 558 CCACCCC U GUCACAG CUGUGAC CUGAUGAG X CGAA IGGCUGG	547		
S55 AUACCAC C CCUGUCA	552		
556			
557 ACCACCC C UGUCACA UGUGACA CUGAUGAG X CGAA IGGUGGU 558 CCACCCC U GUCACAG CUGUGAC CUGAUGAG X CGAA IGGGUGG	555		
558 CCACCCC U GUCACAG CUGUGAC CUGAUGAG X CGAA IGGGUGG	556		
	557		
562 CCCUGIC A CACGGGC GCCCCUG CUGAUGAG X CGAA TACAGGG	558	CCACCCC U GUCACAG	
John Coccess II Shouse Comments II care I ca	562	CCCUGUC A CAGGGGC	GCCCCUG CUGAUGAG X CGAA IACAGGG

Table 34

	THE PARTY OF THE P	AGGCCCC CUGAUGAG X CGAA IUGACAG
564	CUGUCAC A GGGGCCU	CUGGGGA CUGAUGAG X CGAA ICCCCUG
570	CAGOGGC C UCCCCAG	CCUGGGG CUGAUGAG X CGAA IGCCCCU
571	AGGGGCC U CCCCAGG	CUCCUGG CUGAUGAG X CGAA IAGGCCC
573	GGGCCUC C CCAGGAG	CCUCCUG CUGAUGAG X CGAA IGAGGCC
574	GGCCUCC C CAGGAGG	GCCUCCU CUGAUGAG X CGAA IGGAGGC
575	GCCUCCC C AGGAGGC	GGCCUCC CUGAUGAG X CGAA IGGGAGG
576	CCUCCCC A GGAGGCC	UCCCGCA CUGAUGAG X CGAA ICCUCCU
583	AGGAGGC C UGCGGGA	CUCCCGC CUGAUGAG X CGAA IGCCUCC
584	GGAGGCC U GCGGGAG CGGGAGC U GCAGCUU	AAGCUGC CUGAUGAG X CGAA ICUCCCG
593	GAGCUGC A GCUUCGA	UCGAAGC CUGAUGAG X CGAA ICAGCUC
596	CUGCAGC U UCGAAGC	GCUUCGA CUGAUGAG X CGAA ICUGCAG
599	UCGAAGC C UCACAGA	UCUGUGA CUGAUGAG X CGAA ICUUCGA
607	CGAAGCC U CACAGAG	CUCUGUG CUGAUGAG X CGAA IGCUUCG
608	AAGCCUC A CAGAGAU	AUCUCUG CUGAUGAG X CGAA IAGGCUU
610	GCCUCAC A GAGAUCU	AGAUCUC CUGAUGAG X CGAA IUGAGGC
612	AGAGAUC U UGAAAGG	CCUUUCA CUGAUGAG X CGAA IAUCUCU
619	AGGGGUC U UGAUCCA	UGGAUCA CUGAUGAG X CGAA IACCCCU
634	CUUGAUC C AGCGGAA	UUCCGCU CUGAUGAG X CGAA IAUCAAG
640	UUGAUCC A GCGGAAC	GUUCCGC CUGAUGAG X CGAA IGAUCAA
649	GCGGAAC C CCCAGCU	AGCUGGG CUGAUGAG X CGAA IUUCCGC
650	CGGAACC C CCAGCUC	GAGCUGG CUGAUGAG X CGAA IGUUCCG
651	GGAACCC C CAGCUCU	AGAGCUG CUGAUGAG X CGAA IGGUUCC
652	GAACCCC C AGCUCUG	CAGAGCU CUGAUGAG X CGAA IGGGUUC
653	AACCCCC A GCUCUGC	GCAGAGC CUGAUGAG X CGAA IGGGGUU
656	CCCCAGC U CUGCUAC	GUAGCAG CUGAUGAG X CGAA ICUGGGG
658	CCAGCUC U GCUACCA	UGGUAGC CUGAUGAG X CGAA IAGCUGG
661	GCUCUGC U ACCAGGA	UCCUGGU CUGAUGAG X CGAA ICAGAGC
664	CUGCUAC C AGGACAC	GUGUCCU CUGAUGAG X CGAA IUAGCAG
665	UGCUACC A GGACACG	CGUGUCC CUGAUGAG X CGAA IGUAGCA
670	CCAGGAC A CGAUUUU	AAAAUCG CUGAUGAG X CGAA IUCCUGG
688	GAAGGAC A UCUUCCA	UGGAAGA CUGAUGAG X CGAA IUCCUUC
691	GGACAUC U UCCACAA	UUGUGGA CUGAUGAG X CGAA IAUGUCC
694	CAUCUUC C ACAAGAA	UUCUUGU CUGAUGAG X CGAA IAAGAUG
695	AUCUUCC A CAAGAAC	GUUCUUG CUGAUGAG X CGAA IGAAGAU
697	CUUCCAC A AGAACAA	UUGUUCU CUGAUGAG X CGAA IUGGAAG
703	CAAGAAC A ACCAGCU	AGCUGGU CUGAUGAG X CGAA IUUCUUG
706	GAACAAC C AGCUGGC	GCCAGCU CUGAUGAG X CGAA IUUGUUC
707	AACAACC A GCUGGCU	AGCCAGC CUGAUGAG X CGAA IGUUGUU
710	AACCAGC U GGCUCUC	GAGAGCC CUGAUGAG X CGAA ICUGGUU
714	AGCUGGC U CUCACAC	GUGUGAG CUGAUGAG X CGAA ICCAGCU
716	CUGGCUC U CACACUG	CAGUGUG CUGAUGAG X CGAA IAGCCAG
718	GGCUCUC A CACUGAU	AUCAGUG CUGAUGAG X CGAA IAGAGCC
720	CUCUCAC A CUGAUAG	CUAUCAG CUGAUGAG X CGAA IUGAGAG
722	CUCACAC U GAUAGAC	GUCUAUC CUGAUGAG X CGAA IUGUGAG
730	GAUAGAC A CCAACCG	COGUUGG CUGAUGAG X CGAA IUCUAUC
732	UAGACAC C AACCGCU	AGCGGUU CUGAUGAG X CGAA IUGUCUA

Table 34

733	AGACACC A ACCGCUC	GAGCGGU CUGAUGAG X CGAA IGUGUCU
736	CACCAAC C GCUCUCG	CGAGAGC CUGAUGAG X CGAA IUUGGUG
739	CAACCGC U CUCGGGC	GCCCGAG CUGAUGAG X CGAA ICGGUUG
741	ACCGCUC U CGGGCCU	AGGCCCG CUGAUGAG X CGAA IAGCGGU
747	CUCGGGC C UGCCACC	GGUGGCA CUGAUGAG X CGAA ICCCGAG
748	UCGGGCC U GCCACCC	GGGUGGC CUGAUGAG X CGAA IGCCCGA
751	GGCCUGC C ACCCCUG	CAGGGGU CUGAUGAG X CGAA ICAGGCC
752	GCCUGCC A CCCCUGU	ACAGGGG CUGAUGAG X CGAA IGCAGGC
754	CUGCCAC C CCUGUUC	GAACAGG CUGAUGAG X CGAA IUGGCAG
755	UGCCACC C CUGUUCU	AGAACAG CUGAUGAG X CGAA IGUGGCA
756	GCCACCC C UGUUCUC	GAGAACA CUGAUGAG X CGAA IGGUGGC
757	CCACCCC U GUUCUCC	GGAGAAC CUGAUGAG X CGAA IGGGUGG
762	CCUGUUC U CCGAUGU	ACAUCGG CUGAUGAG X CGAA IAACAGG
764	UGUUCUC C GAUGUGU	ACACAUC CUGAUGAG X CGAA TAGAACA
778	UAAGGGC U CCCGCUG	CAGCGGG CUGAUGAG X CGAA ICCCUUA
	AGGGCUC C CGCUGCU	AGCAGCG CUGAUGAG X CGAA IAGCCCU
780	GGGCUCC C GCUGCUG	CAGCAGC CUGAUGAG X CGAA IGAGCCC
781	CUCCCGC U GCUGGGG	CCCCAGC CUGAUGAG X CGAA ICGGGAG
	CCGCUGC U GGGGAGA	UCUCCCC CUGAUGAG X CGAA ICAGCGG
787	AGAGUUC U GAGGAUU	AAUCCUC CUGAUGAG X CGAA IAACUCU
801	GAUUGUC A GAGCCUG	CAGGCUC CUGAUGAG X CGAA IACAAUC
812		CGCGUCA CUGAUGAG X CGAA ICUCUGA
817	UCAGAGC C UGACGCG	GCGCGUC CUGAUGAG X CGAA IGCUCUG
818	CAGAGCC U GACGCGC	CAGACAG CUGAUGAG X CGAA ICGCGUC
826	GACGCGC A CUGUCUG	CACAGAC CUGAUGAG X CGAA IUGCGCG
828	CGCGCAC U GUCUGUG	CCGGCAC CUGAUGAG X CGAA IACAGUG
832	CACUGUC U GUGCCGG	AGCCACC CUGAUGAG X CGAA ICACAGA
837	UCUGUGC C GGUGGCU	CGGGCAC CUGAUGAG X CGAA ICCACCG
844	CGGUGGC U GUGCCCG	UGCAGCG CUGAUGAG X CGAA ICACAGC
849	GCUGUGC C CGCUGCA	UUGCAGC CUGAUGAG X CGAA IGCACAG
850	CUGUGCC C GCUGCAA	CCCUUGC CUGAUGAG X CGAA ICGGGCA
853	UGCCCGC U GCAAGGG	GGCCCCU CUGAUGAG X CGAA ICAGCGG
856	COGCUGC A AGGGGCC	GGCCGU CUGAUGAG X CGAA ICCCCUU
863	AAGGGC C' ACUGCCC	UGGGCAG CUGAUGAG X CGAA IGCCCCU
864	AGGGGCC A CUGCCCA	AGUGGGC CUGAUGAG X CGAA IUGGCCC
866	GGGCCAC U GCCCACU	GUCAGUG CUGAUGAG X CGAA ICAGUGG
869	CCACUGC C CACUGAC	AGUCAGU CUGAUGAG X CGAA IGCAGUG
870	CACUGCC C ACUGACU	CAGUCAGU CUGAUGAG X CGAA IGCAGU
871	ACUGCCC A CUGACUG	AGCAGUC CUGAUGAG X CGAA IUGGGCA
873	UGCCCAC U GACUGCU	UGGCAGC CUGAUGAG X CGAA IUCAGUG
877	CACUGAC U GCUGCCA	UCAUGGC CUGAUGAG X CGAA ICAGUCA
880	UGACUGC U GCCAUGA	UCAUGGC CUGAUGAG X CGAA ICAGOCA UGCUCAU CUGAUGAG X CGAA ICAGCAG
883	CUGCUGC C AUGAGCA	
884	UGCUGCC A UGAGCAG	CUGCUCA CUGAUGAG X CGAA IGCAGCA
890	CAUGAGC A GUGUGCU	AGCACAC CUGAUGAG X CGAA ICUCAUG
897	AGUGUGC U GCCGGCU	AGCCGGC CUGAUGAG X CGAA ICACACU
900	GUGCUGC C GGCUGCA	UGCAGCC CUGAUGAG X CGAA ICAGCAC
904	UGCCGGC U GCACGGG	CCCGUGC CUGAUGAG X CGAA ICCGGCA

Table 34

907	CGGCUGC A CGGGCCC	GGGCCCG CUGAUGAG X CGAA ICAGCCG
913	CACGGGC C CCAAGCA	UGCUUGG CUGAUGAG X CGAA ICCCGUG
914	ACGGGCC C CAAGCAC	GUGCUUG CUGAUGAG X CGAA IGCCCGU
915	CGGGCCC C AAGCACU	AGUGCUU CUGAUGAG X CGAA IGGCCCG
916	GGGCCCC A AGCACUC	GAGUGCU CUGAUGAG X CGAA IGGGCCC
920	CCCAAGC A CUCUGAC	GUCAGAG CUGAUGAG X CGAA ICUUGGG
922	CAAGCAC U CUGACUG	CAGUCAG CUGAUGAG X CGAA IUGCUUG
924	AGCACUC U GACUGCC	GGCAGUC CUGAUGAG X CGAA IAGUGCU
928	CUCUGAC U GCCUGGC	GCCAGGC CUGAUGAG X CGAA IUCAGAG
931	UGACUGC C UGGCCUG	CAGGCCA CUGAUGAG X CGAA ICAGUCA
932	GACUGCC U GGCCUGC	GCAGGCC CUGAUGAG X CGAA IGCAGUC
936	GCCUGGC C UGCCUCC	GGAGGCA CUGAUGAG X CGAA ICCAGGC
937	CCUGGCC U GCCUCCA	UGGAGGC CUGAUGAG X CGAA IGCCAGG
940	GGCCUGC C UCCACUU	AAGUGGA CUGAUGAG X CGAA ICAGGCC
941	GCCUGCC U CCACUUC	GAAGUGG CUGAUGAG X CGAA IGCAGGC
943	CUGCCUC C ACUUCAA	UUGAAGU CUGAUGAG X CGAA IAGGCAG
944	UGCCUCC A CUUCAAC	GUUGAAG CUGAUGAG X CGAA IGAGGCA
946	CCUCCAC U UCAACCA	UGGUUGA CUGAUGAG X CGAA IUGGAGG
949	CCACUUC A ACCACAG	CUGUGGU CUGAUGAG X CGAA IAAGUGG
952	CUUCAAC C ACAGUGG	CCACUGU CUGAUGAG X CGAA IUUGAAG
953	UUCAACC A CAGUGGC	GCCACUG CUGAUGAG X CGAA IGUUGAA
955	CAACCAC A GUGGCAU	AUGCCAC CUGAUGAG X CGAA IUGGUUG
961	CAGUGGC A UCUGUGA	· UCACAGA CUGAUGAG X CGAA ICCACUG
964	UGGCAUC U GUGAGCU	AGCUCAC CUGAUGAG X CGAA IAUGCCA
971	UGUGAGC U GCACUGC	GCAGUGC CUGAUGAG X CGAA ICUCACA
974	GAGCUGC A CUGCCCA	UGGGCAG CUGAUGAG X CGAA ICAGCUC
976	GCUGCAC U GCCCAGC	GCUGGGC CUGAUGAG X CGAA IUGCAGC AGGGCUG CUGAUGAG X CGAA ICAGUGC
979	GCACUGC C CAGCCCU	CAGGGCU CUGAUGAG X CGAA ICAGUG
980	CACUGCC C AGCCCUG	CCAGGGC CUGAUGAG X CGAA IGCAGGU
981	ACUGCCC A GCCCUGG	UGACCAG CUGAUGAG X CGAA ICUGGGC
984	GCCCAGC C CUGGUCA	GUGACCA CUGAUGAG X CGAA IGCUGGG
985	CCCAGCC C UGGUCAC	GGUGACCA CUGAUGAG X CGAA IGCUGG
986	CCAGCCC U GGUCACC	UUGUAGG CUGAUGAG X CGAA IACCAGG
991	CCUGGUC A CCUACAA	UGUUGUA CUGAUGAG X CGAA IUGACCA
993	UGGUCAC C UACAACAC GGUCACC U ACAACAC	GUGUUGU CUGAUGAG X CGAA IGUGACC
994	CACCUAC A ACACAGA	UCUGUGU CUGAUGAG X CGAA IUAGGUG
1000	CUACAAC A CAGACAC	GUGUCUG CUGAUGAG X CGAA IUUGUAG
	ACAACAC A GACACGU	ACGUGUC CUGAUGAG X CGAA IUGUUGU
1002	CACAGAC A CGUUUGA	UCAAACG CUGAUGAG X CGAA IUCUGUG
1006	UUGAGUC C AUGCCCA	UGGGCAU CUGAUGAG X CGAA IACUCAA
1017	UGAGUC A UGCCCAA	UUGGGCA CUGAUGAG X CGAA IGACUCA
1018	UCCAUGC C CAAUCCC	GGGAUUG CUGAUGAG X CGAA ICAUGGA
1022	CCAUGCC C AAUCCCG	CGGGAUU CUGAUGAG X CGAA IGCAUGG
1023	CAUGCCC A AUCCCGA	UCGGGAU CUGAUGAG X CGAA IGGCAUG
1024	CCCAAUC C CGAGGGC	GCCCUCG CUGAUGAG X CGAA IAUUGGG
1028	CCAAUCC C GAGGGCC	GGCCCUC CUGAUGAG X CGAA IGAUUGG
1029	COMMOCC C GAGGGCC	

Table 34

1036	CGAGGGC C GGUAUAC	GUAUACC CUGAUGAG X CGAA ICCCUCG	
1044	GGUAUAC A UUCGGCG	CGCCGAA CUGAUGAG X CGAA IUAUACC	
1053	HCGGCGC C AGCUGUG	CACAGCU CUGAUGAG X CGAA ICGCCGA	
1054	CGGCGCC A GCUGUGU	ACACAGC CUGAUGAG X CGAA IGCGCCG	
1057	CGCCAGC U GUGUGAC	GUCACAC CUGAUGAG X CGAA ICUGGCG	
1065	GUGUGAC U GCCUGUC	GACAGGC CUGAUGAG X CGAA IUCACAC	
1068	UGACUGC C UGUCCCU	AGGGACA CUGAUGAG X CGAA ICAGUCA	
1069	GACUGCC U GUCCCUA	UAGGGAC CUGAUGAG X CGAA IGCAGUC	
1073	GCCUGUC C CUACAAC	GUUGUAG CUGALIGAG X CGAA IACAGGC	
1074	CCUGUCC C UACAACU	AGUUGUA CUGAUGAG X CGAA IGACAGG	
1075	CUGUCCC U ACAACUA	UAGUUGU CUGAUGAG X CGAA IGGACAG	
1078	UCCCUAC A ACUACCU	AGGUAGU CUGAUGAG X CGAA IUAGGGA	
1081	CUACAAC U ACCUUUC	GAAAGGU CUGAUGAG X CGAA IUUGUAG	
1084	CAACUAC C UUUCUAC	GUAGAAA CUGAUGAG X CGAA IUAGUUG	
1085	AACUACC U UUCUACG	CGUAGAA CUGAUGAG X CGAA IGUAGUU	
1089	ACCUUUC U ACGGACG	CGUCCGU CUGAUGAG X CGAA IAAAGGU	
1104	UGGGAUC C UGCACCC	GGGUGCA CUGAUGAG X CGAA IAUCCCA	
1105	GGGAUCC U GCACCCU	AGGGUGC CUGAUGAG X CGAA IGAUCCC	
1108	AUCCUGC A CCCUCGU	ACGAGGG CUGAUGAG X CGAA ICAGGAU	
1110	CCUGCAC C CUCGUCU	AGACGAG CUGAUGAG X CGAA IUGCAGG	
1111	CUGCACC C UCGUCUG	CAGACGA CUGAUGAG X CGAA IGUGCAG	
1112	UGCACCC U CGUCUGC	GCAGACG CUGAUGAG X CGAA IGGUGCA	
1117	CCUCGUC U GCCCCCU	AGGGGGC CUGAUGAG X CGAA IACGAGG	
1120	CGUCUGC C CCCUGCA	UGCAGGG CUGAUGAG X CGAA ICAGACG	
1121	GUCUGCC C CCUGCAC	GUGCAGG CUGAUGAG X CGAA IGCAGAC	
1122	UCUGCCC C CUGCACA	UGUGCAG CUGAUGAG X CGAA IGGCAGA	
1123	CUGCCCC C UGCACAA	UUGUGCA CUGAUGAG X CGAA IGGGCAG	
1124	UGCCCCC U GCACAAC	GUUGUGC CUGAUGAG X CGAA IGGGGCA	
1127	CCCCUGC A CAACCAA	UUGGUUG CUGAUGAG X CGAA ICAGGGG	
1129	CCUGCAC A ACCAAGA	UCUUGGU CUGAUGAG X CGAA IUGCAGG	
1132	GCACAAC C AAGAGGU	ACCUCUU CUGAUGAG X CGAA IUUGUGC	
1133	CACAACC A AGAGGUG	CACCUCU CUGAUGAG X CGAA IGUUGUG	
1143	AGGUGAC A GCAGAGG	CCUCUGC CUGAUGAG X CGAA IUCACCU	
1146	UGACAGC A GAGGAUG	CAUCCUC CUGAUGAG X CGAA ICUGUCA	
1158	AUGGAAC A CAGCGGU	ACCGCUG CUGAUGAG X CGAA IUUCCAU	
1160	GGAACAC A GCGGUGU	ACACCGC CUGAUGAG X CGAA IUGUUCC	
1177	GAAGUGC A GCAAGCC	GGCUUGC CUGAUGAG X CGAA ICACUUC	
1180	GUGCAGC A AGCCCUG	CAGGGCU CUGAUGAG X CGAA ICUGCAC	
1184	AGCAAGC C CUGUGCC	GGCACAG CUGAUGAG X CGAA ICUUGCU	
1185	GCAAGCC C UGUGCCC	GGGCACA CUGAUGAG X CGAA IGCUUGC	
1186	CAAGCCC U GUGCCCG	CGGGCAC CUGAUGAG X CGAA IGGCUUG	
1191	CCUGUGC C CGAGUGU	ACACUCG CUGAUGAG X CGAA ICACAGG	
1192	CUGUGCC C GAGUGUG	CACACUC CUGAUGAG X CGAA IGCACAG	
1201	AGUGUGC U AUGGUCU	AGACCAU CUGAUGAG X CGAA ICACACU	
1208	UAUGGUC U GGGCAUG	CAUGCCC CUGAUGAG X CGAA IACCAUA	
1213	UCUGGGC A UGGAGCA	UGCUCCA CUGAUGAG X CGAA ICCCAGA	
1220	AUGGAGC A CUUGCGA	UCGCAAG CUGAUGAG X CGAA ICUCCAU	

Table 34

1222	GGAGCAC U UGCGAGA	UCUCGCA CUGAUGAG X CGAA IUGCUCC
1239	UGAGGGC A GUUACCA	UGGUAAC CUGAUGAG X CGAA ICCCUCA
1245	CAGUUAC C AGUGCCA	UGGCACU CUGAUGAG X CGAA IUAACUG
1246	AGUUACC A GUGCCAA	UUGGCAC CUGAUGAG X CGAA IGUAACU
1251	CCAGUGC C AAUAUCC	GGAUAUU CUGAUGAG X CGAA ICACUGG
1252	CAGUGCC A AUAUCCA	UGGAUAU CUGAUGAG X CGAA IGCACUG
1258	CAAUAUC C AGGAGUU	AACUCCU CUGAUGAG X CGAA IAUAUUG
1259	AAUAUCC A GGAGUUU	AAACUCC CUGAUGAG X CGAA IGAUAUU
1269	AGUUUGC U GGCUGCA	UGCAGCC CUGAUGAG X CGAA ICAAACU
1273	UGCUGGC U GCAAGAA	UUCUUGC CUGAUGAG X CGAA ICCAGCA
1276	UGGCUGC A AGAAGAU	AUCUUCU CUGAUGAG X CGAA ICAGCCA
1285	GAAGAUC U UUGGGAG	CUCCCAA CUGAUGAG X CGAA IAUCUUC
1294	UGGGAGC C UGGCAUU	AAUGCCA CUGAUGAG X CGAA ICUCCCA
1295	GGGAGCC U GGCAUUU	AAAUGCC CUGAUGAG X CGAA IGCUCCC
1299	GCCUGGC A UUUCUGC	GCAGAAA CUGAUGAG X CGAA ICCAGGC
1304	GCAUUUC U GCCGGAG	CUCCGGC CUGAUGAG X CGAA IAAAUGC
1307	UUUCUGC C GGAGAGC	GCUCUCC CUGAUGAG X CGAA ICAGAAA
1315	GGAGAGC U UUGAUGG	CCAUCAA CUGAUGAG X CGAA ICUCUCC
1327	UGGGGAC C CAGCCUC	GAGGCUG CUGAUGAG X CGAA IUCCCCA
1328	GGGGACC C AGCCUCC	GGAGGCU CUGAUGAG X CGAA IGUCCCC
1329	GGGACCC A GCCUCCA	UGGAGGC CUGAUGAG X CGAA IGGUCCC
1332	ACCCAGC C UCCAACA	UGUUGGA CUGAUGAG X CGAA ICUGGGU
1333	CCCAGCC U CCAACAC	GUGUUGG CUGAUGAG X CGAA IGCUGGG
1335	CAGCCUC C AACACUG	CAGUGUU CUGAUGAG X CGAA IAGGCUG
1336	AGCCUCC A ACACUGC	GCAGUGU CUGAUGAG X CGAA IGAGGCU
1339	CUCCAAC A CUGCCCC	GGGGCAG CUGAUGAG X CGAA IUUGGAG
1341	CCAACAC U GCCCCGC	GCGGGGC CUGAUGAG X CGAA IUGUUGG
1344	ACACUGC C CCGCUCC	GGAGCGG CUGAUGAG X CGAA ICAGUGU
1345	CACUGCC C CGCUCCA	UGGAGCG CUGAUGAG X CGAA IGCAGUG
1346	ACUGCCC C GCUCCAG	CUGGAGC CUGAUGAG X CGAA IGGCAGU
1349	GCCCCGC U CCAGCCA	UGGCUGG CUGAUGAG X CGAA ICGGGGC
1351	CCCGCUC C AGCCAGA	UCUGGCU CUGAUGAG X CGAA IAGCGGG CUCUGGC CUGAUGAG X CGAA IGAGCGG
1352	CCGCUCC A GCCAGAG	CUCCUCU CUGAUGAG X CGAA ICUGGAG
1355	CUCCAGC C AGAGCAG	GCUGCUC CUGAUGAG X CGAA ICUGGA
1356	UCCAGCC A GAGCAGC	UUGGAGC CUGAUGAG X CGAA ICUCUGG
1361	CCAGAGC A GCUCCAA	CACUUGG CUGAUGAG X CGAA ICUGCUC
1364	GAGCAGC U CCAAGUG	AACACUU CUGAUGAG X CGAA IAGCUGC
1366	GCAGCUC C AAGUGUU	AAACACUU CUGAUGAG X CGAA TAGCUG
1367	CAGCUCC A AGUGUUU	CUUCCAG CUGAUGAG X CGAA IUCUCAA
1380	UUGAGAC U CUGGAAG GAGACUC U GGAAGAG	CUCUUCC CUGAUGAG X CGAA IAGUCUC
1382	AGAGAUC A CAGGUUA	UAACCUG CUGAUGAG X CGAA IAUCUCU
1393	AGAUCAC A GGUUACC	GGUAACC CUGAUGAG X CGAA IUGAUCU
1395	AGGUUAC C UAUACAU	AUGUAUA CUGAUGAG X CGAA IUAACCU
1402	GGUUACC U AUACAUC	GAUGUAU CUGAUGAG X CGAA IGUAACC
1403	CCUAUAC A UCUCAGO	GCUGAGA CUGAUGAG X CGAA IUAUAGG
	AUACAUC U CAGCAUG	CAUGCUG CUGAUGAG X CGAA IAUGUAU
1411	MUMCAUC U CMGCAUG	Chocos coaloate ii com

Table 34

		 GCCAUGC CUGAUGAG X CGAA IAGAUGU
1413	ACAUCUC A GCAUGGC	 CCGGCCA CUGAUGAG X CGAA ICUGAGA
1416	UCUCAGC A UGGCCGG	 GCUGUCC CUGAUGAG X CGAA ICCAUGC
1421	GCAUGGC C GGACAGC	
1426	GCCGGAC A GCCUGCC	GGCAGGC CUGAUGAG X CGAA IUCCGGC
1429	GGACAGC C UGCCUGA	 UCAGGCA CUGAUGAG X CGAA ICUGUCC
1430	GACAGCC U GCCUGAC	GUCAGGC CUGAUGAG X CGAA IGCUGUC
1433	AGCCUGC C UGACCUC	GAGGUCA CUGAUGAG X CGAA ICAGGCU
1434	GCCUGCC U GACCUCA	UGAGGUC CUGAUGAG X CGAA IGCAGGC
1438	GCCUGAC C UCAGCGU	ACGCUGA CUGAUGAG X CGAA IUCAGGC
1439	CCUGACC U CAGCGUC	GACGCUG CUGAUGAG X CGAA IGUCAGG
1441	UGACCUC A GCGUCUU	AAGACGC CUGAUGAG X CGAA IAGGUCA
1447	CAGCGUC U UCCAGAA	UUCUGGA CUGAUGAG X CGAA IACGCUG
1450	CGUCUUC C AGAACCU	AGGUUCU CUGAUGAG X CGAA IAAGACG
1451	GUCUUCC A GAACCUG	CAGGUUC CUGAUGAG X CGAA IGAAGAC
1456	CCAGAAC C UGCAAGU	ACUUGCA CUGAUGAG X CGAA IUUCUGG
1457	CAGAACC U GCAAGUA	UACUUGC CUGAUGAG X CGAA IGUUCUG
1460	AACCUGC A AGUAAUC	GAUUACU CUGAUGAG X CGAA ICAGGUU
1468	AGUAAUC C GGGGACG	CGUCCCC CUGAUGAG X CGAA IAUUACU
1481	CGAAUUC U GCACAAU	AUUGUGC CUGAUGAG X CGAA IAAUUCG
1484	AUUCUGC A CAAUGGC	GCCAUUG CUGAUGAG X CGAA ICAGAAU
1486	UCUGCAC A AUGGCGC	GCGCCAU CUGAUGAG X CGAA IUGCAGA
1494	AUGGCGC C UACUCGC	GCGAGUA CUGAUGAG X CGAA ICGCCAU
1495	UGGCGCC U ACUCGCU	AGCGAGU CUGAUGAG X CGAA IGCGCCA
1498	CGCCUAC U CGCUGAC	GUCAGCG CUGAUGAG X CGAA IUAGGCG
1502	UACUCGC U GACCCUG	CAGGGUC CUGAUGAG X CGAA ICGAGUA
1506	CGCUGAC C CUGCAAG	CUUGCAG CUGAUGAG X CGAA IUCAGCG
1507	GCUGACC C UGCAAGG	CCUUGCA CUGAUGAG X CGAA IGUCAGC
1508	CUGACCC U GCAAGGG	CCCUUGC CUGAUGAG X CGAA IGGUCAG
1511	ACCCUGC A AGGGCUG	CAGCCCU CUGAUGAG X CGAA ICAGGGU
1517	CAAGGC U GGGCAUC	GAUGCCC CUGAUGAG X CGAA ICCCUUG
1522	GCUGGGC A UCAGCUG	CAGCUGA CUGAUGAG X CGAA ICCCAGC
1525	GGGCAUC A GCUGGCU	AGCCAGC CUGAUGAG X CGAA IAUGCCC
1528	CAUCAGC U GGCUGGG	CCCAGCC CUGAUGAG X CGAA ICUGAUG
1532	AGCUGGC U GGGGCUG	CAGCCCC CUGAUGAG X CGAA ICCAGCU
1538	CUGGGGC U GCGCUCA	UGAGCGC CUGAUGAG X CGAA ICCCCAG
1543	GCUGCGC U CACUGAG	CUCAGUG CUGAUGAG X CGAA ICGCAGC
1545	UGCGCUC A CUGAGGG	CCCUCAG CUGAUGAG X CGAA IAGCGCA
1547	CGCUCAC U GAGGGAA	UUCCCUC CUGAUGAG X CGAA IUGAGCG
1556	AGGGAAC U GGGCAGU	ACUGCCC CUGAUGAG X CGAA IUUCCCU
1561	ACUGGGC A GUGGACU	AGUCCAC CUGAUGAG X CGAA ICCCAGU
1568	AGUGGAC U GGCCCUC	GAGGGCC CUGAUGAG X CGAA IUCCACU
1572	GACUGGC C CUCAUCC	GGAUGAG CUGAUGAG X CGAA ICCAGUC
1573	ACUGGCC C UCAUCCA	UGGAUGA CUGAUGAG X CGAA IGCCAGU
1574	CUGGCCC U CAUCCAC	GUGGAUG CUGAUGAG X CGAA IGGCCAG
1576	GGCCCUC A UCCACCA	UGGUGGA CUGAUGAG X CGAA IAGGGCC
1579	CCUCAUC C ACCAUAA	UUAUGGU CUGAUGAG X CGAA IAUGAGG
1580	CUCAUCC A CCAUAAC	GUUAUGG CUGAUGAG X CGAA IGAUGAG

Table 34

		THE PROPERTY OF THE PARTY OF TH
1582	CAUCCAC C AUAACAC	GUGUUAU CUGAUGAG X CGAA IUGGAUG
1583	AUCCACC A UAACACC	GGUGUUA CUGAUGAG X CGAA IGUGGAU
1588	CCAUAAC A CCCACCU	AGGUGGG CUGAUGAG X CGAA IUUAUGG
1590	AUAACAC C CACCUCU	AGAGGUG CUGAUGAG X CGAA IUGUUAU
1591	UAACACC C ACCUCUG	CAGAGGU CUGAUGAG X CGAA IGUGUUA
1592	AACACCC A CCUCUGC	GCAGAGG CUGAUGAG X CGAA IGGUGUU
1594	CACCCAC C UCUGCUU	AAGCAGA CUGAUGAG X CGAA IUGGGUG
1595	ACCCACC U CUGCUUC	GAAGCAG CUGAUGAG X CGAA IGUGGGU
1597	CCACCUC U GCUUCGU	ACGAAGC CUGAUGAG X CGAA IAGGUGG
1600	CCUCUGC U UCGUGCA	UGCACGA CUGAUGAG X CGAA ICAGAGG
1607	UUCGUGC A CACGGUG	CACCGUG CUGAUGAG X CGAA ICACGAA
1609	CGUGCAC A CGGUGCC	GGCACCG CUGAUGAG X CGAA IUGCACG
1616	ACGGUGC C CUGGGAC	GUCCCAG CUGAUGAG X CGAA ICACCGU
1617	CGGUGCC C UGGGACC	GGUCCCA CUGAUGAG X CGAA IGCACCG
1618	GGUGCCC U GGGACCA	UGGUCCC CUGAUGAG X CGAA IGGCACC
1624	CUGGGAC C AGCUCUU	AAGAGCU CUGAUGAG X CGAA IUCCCAG
1625	UGGGACC A GCUCUUU	AAAGAGC CUGAUGAG X CGAA IGUCCCA
1628	GACCAGC U CUUUCGG	CCGAAAG CUGAUGAG X CGAA ICUGGUC
1630	CCAGCUC U UUCGGAA	UUCCGAA CUGAUGAG X CGAA IAGCUGG
1639	UCGGAAC C CGCACCA	UGGUGCG CUGAUGAG X CGAA IUUCCGA
1640	CGGAACC C GCACCAA	UUGGUGC CUGAUGAG X CGAA IGUUCCG
1643	AACCCGC A CCAAGCU	AGCUUGG CUGAUGAG X CGAA ICGGGUU
1645	CCCGCAC C AAGCUCU	AGAGCUU CUGAUGAG X CGAA IUGCGGG
1646	CCGCACC A AGCUCUG	CAGAGCU CUGAUGAG X CGAA IGUGCGG
1650	ACCAAGC U CUGCUCC	GGAGCAG CUGAUGAG X CGAA ICUUGGU
1652	CAAGCUC U GCUCCAC	GUGGAGC CUGAUGAG X CGAA IAGCUUG
1655	GCUCUGC U CCACACU	AGUGUGG CUGAUGAG X CGAA ICAGAGC
1657	UCUGCUC C ACACUGC	GCAGUGU CUGAUGAG X CGAA IAGCAGA
1658	CUGCUCC A CACUGCC	GGCAGUG CUGAUGAG X CGAA IGAGCAG
1650	GCUCCAC A CUGCCAA	UUGGCAG CUGAUGAG X CGAA IUGGAGC
1662	UCCACAC U GCCAACC	GGUUGGC CUGAUGAG X CGAA IUGUGGA
1665	ACACUGC C AACCGGC	GCCGGUU CUGAUGAG X CGAA ICAGUGU
1666	CACUGCC A ACCGGCC	GGCCGGU CUGAUGAG X CGAA IGCAGUG
1669	UGCCAAC C GGCCAGA	UCUGGCC CUGAUGAG X CGAA IUUGGCA
1673	AACCGGC C AGAGGAC	GUCCUCU CUGAUGAG X CGAA ICCGGUU
1674	ACCGGCC A GAGGACG	CGUCCUC CUGAUGAG X CGAA IGCCGGU
1699	CGAGGGC C UGGCCUG	CAGGCCA CUGAUGAG X CGAA ICCCUCG
1700	GAGGGCC U GGCCUGC	GCAGGCC CUGAUGAG X CGAA IGCCCUC
1704	GCCUGGC C UGCCACC	GGUGGCA CUGAUGAG X CGAA ICCAGGC
1705	CCUGGCC U GCCACCA	UGGUGGC CUGAUGAG X CGAA IGCCAGG
1708	GGCCUGC C ACCAGCU	AGCUGGU CUGAUGAG X CGAA ICAGGCC
1709	GCCUGCC A CCAGCUG	CAGCUGG CUGAUGAG X CGAA IGCAGGC
1711	CUGCCAC C AGCUGUG	CACAGCU CUGAUGAG X CGAA IUGGCAG
1712	UGCCACC A GCUGUGC	GCACAGC CUGAUGAG X CGAA IGUGGCA
1715	CACCAGC U GUGCGCC	GGCGCAC CUGAUGAG X CGAA ICUGGUG
1722	UGUGCGC C CGAGGGC	GCCCUCG CUGAUGAG X CGAA ICGCACA
1723	GUGCGCC C GAGGGCA	UGCCCUC CUGAUGAG X CGAA IGCGCAC

Table 34

1730	CGAGGGC A CUGCUGG	CCAGCAG CUGAUGAG X CGAA ICCCUCG	
1732	AGGGCAC U GCUGGGG	CCCCAGC CUGAUGAG X CGAA IUGCCCU	_
1735	GCACUGC U GGGGUCC	GGACCCC CUGAUGAG X CGAA ICAGUGC	
1742	UGGGGUC C AGGGCCC	GGGCCCU CUGAUGAG X CGAA IACCCCA	
1743	GGGGUCC A GGGCCCA	UGGGCCC CUGAUGAG X CGAA IGACCCC	
1748	CCAGGGC C CACCCAG	CUGGGUG CUGAUGAG X CGAA ICCCUGG	
1749	CAGGGCC C ACCCAGU	ACUGGGU CUGAUGAG X CGAA IGCCCUG	
1750	AGGGCCC A CCCAGUG	CACUGGG CUGAUGAG X CGAA IGGCCCU	
1752	GGCCCAC C CAGUGUG	CACACUG CUGAUGAG X CGAA IUGGGCC	
1753	GCCCACC C AGUGUGU	ACACACU CUGAUGAG X CGAA IGUGGGC	
1754	CCCACCC A GUGUGUC	GACACAC CUGAUGAG X CGAA IGGUGGG	
1762	GUGUGUC A ACUGCAG	CUGCAGU CUGAUGAG X CGAA IACACAC	
1765	UGUCAAC U GCAGCCA	UGGCUGC CUGAUGAG X CGAA IUUGACA	
1768	CAACUGC A GCCAGUU	AACUGGC CUGAUGAG X CGAA ICAGUUG	
1771	CUGCAGC C AGUUCCU	AGGAACU CUGAUGAG X CGAA ICUGCAG	
1772	UGCAGCC A GUUCCUU	AAGGAAC CUGAUGAG X CGAA IGCUGCA	
1777	CCAGUUC C UUCGGGG	CCCCGAA CUGAUGAG X CGAA IAACUGG	
1778	CAGUUCC U UCGGGGC	GCCCCGA CUGAUGAG X CGAA IGAACUG	
1786	UCGGGGC C AGGAGUG	CACUCCU CUGAUGAG X CGAA ICCCCGA	
1787	CGGGGCC A GGAGUGC	GCACUCC CUGAUGAG X CGAA IGCCCCG	
1807	GGAAUGC C GAGUACU	AGUACUC CUGAUGAG X CGAA ICAUUCC	
1814	CGAGUAC U GCAGGGG	CCCCUGC CUGAUGAG X CGAA IUACUCG	
1817	GUACUGC A GGGGCUC	GAGCCCC CUGAUGAG X CGAA ICAGUAC	
1823	CAGGGGC U CCCCAGG	CCUGGGG CUGAUGAG X CGAA ICCCCUG	
1825	GGGGCUC C CCAGGGA	UCCCUGG CUGAUGAG X CGAA IAGCCCC	
1826	GGGCUCC C CAGGGAG	CUCCCUG CUGAUGAG X CGAA IGAGCCC	
1827	GGCUCCC C AGGGAGU	ACUCCCU CUGAUGAG X CGAA IGGAGCC	
1828	GCUCCCC A GGGAGUA	UACUCCC CUGAUGAG X CGAA IGGGAGC	
1845	UGAAUGC C AGGCACU	AGUGCCU CUGAUGAG X CGAA ICAUUCA	
1846	GAAUGCC A GGCACUG	CAGUGCC CUGAUGAG X CGAA IGCAUUC	
1850	GCCAGGC A CUGUUUG	CAAACAG CUGAUGAG X CGAA ICCUGGC	
1852	CAGGCAC U GUUUGCC	GGCAAAC CUGAUGAG X CGAA IUGCCUG	
1859	UGUUUGC C GUGCCAC	GUGGCAC CUGAUGAG X CGAA ICAAACA	
1864	GCCGUGC C ACCCUGA	UCAGGGU CUGAUGAG X CGAA ICACGGC	
1865	CCGUGCC A CCCUGAG	CUCAGGG CUGAUGAG X CGAA IGCACGG	
1867	GUGCCAC C CUGAGUG	CACUCAG CUGAUGAG X CGAA IUGGCAC	
1868	UGCCACC C UGAGUGU	ACACUCA CUGAUGAG X CGAA IGUGGCA	
1869	GCCACCC U GAGUGUC	GACACUC CUGAUGAG X CGAA IGGUGGC	
1877	GAGUGUC A GCCCCAG	CUGGGGC CUGAUGAG X CGAA IACACUC	
1880	UGUCAGC C CCAGAAU	AUUCUGG CUGAUGAG X CGAA ICUGACA	
1881	GUCAGCC C CAGAAUG	CAUUCUG CUGAUGAG X CGAA IGCUGAC	
1882	UCAGCCC C AGAAUGG	CCAUUCU CUGAUGAG X CGAA IGGCUGA	
1883	CAGCCCC A GAAUGGC	GCCAUUC CUGAUGAG X CGAA IGGGCUG	
1891	GAAUGGC U CAGUGAC	GUCACUG CUGAUGAG X CGAA ICCAUUC	
1893	AUGGCUC A GUGACCU	AGGUCAC CUGAUGAG X CGAA IAGCCAU	
1899	CAGUGAC C UGUUUUG	CAAAACA CUGAUGAG X CGAA IUCACUG	
1900	AGUGACC U GUUUUGG	CCAAAAC CUGAUGAG X CGAA IGUCACU	

Table 34

1910	UUUGGAC C GGAGGCU	AGCCUCC CUGAUGAG X CGAA IUCCAAA
1917	CGGAGGC U GACCAGU	ACUGGUC CUGAUGAG X CGAA ICCUCCG
1921	GGCUGAC C AGUGUGU	ACACACU CUGAUGAG X CGAA IUCAGCC
1922	GCUGACC A GUGUGUG	CACACAC CUGAUGAG X CGAA IGUCAGC
1932	GUGUGGC C UGUGCCC	GGGCACA CUGAUGAG X CGAA ICCACAC
1933	UGUGGCC U GUGCCCA	UGGGCAC CUGAUGAG X CGAA IGCCACA
1938	CCUGUGC C CACUAUA	UAUAGUG CUGAUGAG X CGAA ICACAGG
1939	CUGUGCC C ACUAUAA	UUAUAGU CUGAUGAG X CGAA IGCACAG
1940	UGUGCCC A CUAUAAG	CUUAUAG CUGAUGAG X CGAA IGGCACA
1942	UGCCCAC U AUAAGGA	UCCUUAU CUGAUGAG X CGAA IUGGGCA
1951	UAAGGAC C CUCCCUU	AAGGGAG CUGAUGAG X CGAA IUCCUUA
1952	AAGGACC C UCCCUUC	GAAGGGA CUGAUGAG X CGAA IGUCCUU
1953	AGGACCC U CCCUUCU	AGAAGGG CUGAUGAG X CGAA IGGUCCU
1955	GACCCUC C CUUCUGC	GCAGAAG CUGAUGAG X CGAA IAGGGUC
1956	ACCCUCC C UUCUGCG	. CGCAGAA CUGAUGAG X CGAA IGAGGGU
1957	CCCUCCC U UCUGCGU	ACGCAGA CUGAUGAG X CGAA IGGAGGG
1960	UCCCUUC U GCGUGGC	GCCACGC CUGAUGAG X CGAA IAAGGGA
1968	GCGUGGC C CGCUGCC	GGCAGCG CUGAUGAG X CGAA ICCACGC
1969	CGUGGCC C GCUGCCC	GGGCAGC CUGAUGAG X CGAA IGCCACG
1972	GGCCCGC U GCCCCAG	CUGGGGC CUGAUGAG X CGAA ICGGGCC
1975	CCGCUGC C CCAGCGG	CCGCUGG CUGAUGAG X CGAA ICAGCGG
1976	CGCUGCC C CAGCGGU	ACCGCUG CUGAUGAG X CGAA IGCAGCG
1977	GCUGCCC C AGCGGUG	CACCGCU CUGAUGAG X CGAA IGGCAGC ACACCGC CUGAUGAG X CGAA IGGGCAG
1978	CUGCCCC A GCGGUGU	GAGGUCA CUGAUGAG X CGAA IUUUCAC
1991	GUGAAAC C UGACCUC	- AGAGGUC CUGAUGAG X CGAA IGUUUCA
1992	UGAAACC U GACCUCU	UAGGAGA CUGAUGAG X CGAA IUCAGGU
1996	ACCUGAC C UCUCCUA CCUGACC U CUCCUAC	GUAGGAG CUGAUGAG X CGAA IGUCAGG
1997	IIGACCUC U CCUACAU	AUGUAGG CUGAUGAG X CGAA IAGGUCA
1999	ACCUCUC C UACAUGC	GCAUGUA CUGAUGAG X CGAA IAGAGGU
2001	CCUCUCC U ACAUGCC	GGCAUGU CUGAUGAG X CGAA IGAGAGG
2002	CUCCUAC A UGCCCAU	AUGGGCA CUGAUGAG X CGAA IUAGGAG
2009	UACAUGC C CAUCUGG	CCAGAUG CUGAUGAG X CGAA ICAUGUA
2010	ACAUGCC C AUCUGGA	UCCAGAU CUGAUGAG X CGAA IGCAUGU
2011	CAUGCCC A UCUGGAA	UUCCAGA CUGAUGAG X CGAA IGGCAUG
2014	GCCCAUC U GGAAGUU	AACUUCC CUGAUGAG X CGAA IAUGGGC
2024	AAGUUUC C AGAUGAG	CUCAUCU CUGAUGAG X CGAA IAAACUU
2025	AGUUUCC A GAUGAGG	CCUCAUC CUGAUGAG X CGAA IGAAACU
2040	AGGGCGC A UGCCAGC	GCUGGCA CUGAUGAG X CGAA ICGCCCU
2044	CGCAUGC C AGCCUUG	CAAGGCU CUGAUGAG X CGAA ICAUGCG
2045	GCAUGCC A GCCUUGC	GCAAGGC CUGAUGAG X CGAA IGCAUGC
2048	UGCCAGC C UUGCCCC	GGGGCAA CUGAUGAG X CGAA ICUGGCA
2049	GCCAGCC U UGCCCCA	UGGGGCA CUGAUGAG X CGAA IGCUGGC
2053	GCCUUGC C CCAUCAA	UUGAUGG CUGAUGAG X CGAA ICAAGGC
2054	CCUUGCC C CAUCAAC	GUUGAUG CUGAUGAG X CGAA IGCAAGG
2055	CUUGCCC C AUCAACU	AGUUGAU CUGAUGAG X CGAA IGGCAAG
2056	UUGCCCC A UCAACUG	CAGUUGA CUGAUGAG X CGAA IGGGCAA

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Table 34

		GUGCAGU CUGAUGAG X CGAA IAUGGGG
2059	CCCCAUC A ACUGCAC	
2062	CAUCAAC U GCACCCA	UGGGUGC CUGAUGAG X CGAA IUUGAUG
2065	CAACUGC A CCCACUC	GAGUGGG CUGAUGAG X CGAA ICAGUUG
2067	ACUGCAC C CACUCCU	AGGAGUG CUGAUGAG X CGAA IUGCAGU
2068	CUGCACC C ACUCCUG	CAGGAGU CUGAUGAG X CGAA IGUGCAG
2069	UGCACCC A CUCCUGU	ACAGGAG CUGAUGAG X CGAA IGGUGCA
2071	CACCCAC U CCUGUGU	ACACAGG CUGAUGAG X CGAA IUGGGUG
2073	CCCACUC C UGUGUGG	CCACACA CUGAUGAG X CGAA IAGUGGG
2074	CCACUCC U GUGUGGA	UCCACAC CUGAUGAG X CGAA IGAGUGG
2083	UGUGGAC C UGGAUGA	UCAUCCA CUGAUGAG X CGAA IUCCACA
2084	GUGGACC U GGAUGAC	GUCAUCC CUGAUGAG X CGAA IGUCCAC
2092	GGAUGAC A AGGGCUG	CAGCCCU CUGAUGAG X CGAA IUCAUCC
2098	CAAGGGC U GCCCCGC	GCGGGGC CUGAUGAG X CGAA ICCCUUG
2101	GGGCUGC C CCGCCGA	UCGGCGG CUGAUGAG X CGAA ICAGCCC
2102	GGCUGCC C CGCCGAG	CUCGGCG CUGAUGAG X CGAA IGCAGCC
2103	GCUGCCC C GCCGAGC	GCUCGGC CUGAUGAG X CGAA IGGCAGC
2106	GCCCCGC C GAGCAGA	UCUGCUC CUGAUGAG X CGAA ICGGGGC
2111	GCCGAGC A GAGAGCC	GGCUCUC CUGAUGAG X CGAA ICUCGGC
2118	AGAGAGC C AGCCCUC	GAGGGCU CUGAUGAG X CGAA ICUCUCU
2119	GAGAGCC A GCCCUCU	AGAGGGC CUGAUGAG X CGAA IGCUCUC
2122	AGCCAGC C CUCUGAC	GUCAGAG CUGAUGAG X CGAA ICUGGCU
2123	GCCAGCC C UCUGACG	CGUCAGA CUGAUGAG X CGAA IGCUGGC
2124	CCAGCCC U CUGACGU	ACGUCAG CUGAUGAG X CGAA IGGCUGG
2126	AGCCCUC U GACGUCC	GGACGUC CUGAUGAG X CGAA IAGGGCU
2133	UGACGUC C AUCAUCU	AGAUGAU CUGAUGAG X CGAA IACGUCA
2134	GACGUCC A UCAUCUC	GAGAUGA CUGAUGAG X CGAA IGACGUC
2137	GUCCAUC A UCUCUGC	GCAGAGA CUGAUGAG X CGAA IAUGGAC
2140	CAUCAUC U CUGCGGU	ACCGCAG CUGAUGAG X CGAA IAUGAUG
2142	UCAUCUC U GCGGUGG	CCACCGC CUGAUGAG X CGAA IAGAUGA
2155	GGUUGGC A UUCUGCU	AGCAGAA CUGAUGAG X CGAA ICCAACC
2159	GGCAUUC U GCUGGUC	GACCAGC CUGAUGAG X CGAA IAAUGCC
2162	AUUCUGC U GGUCGUG	CACGACC CUGAUGAG X CGAA ICAGAAU
2173	CGUGGUC U UGGGGGU	ACCCCCA CUGAUGAG X CGAA IACCACG
2185	GGUGGUC U UUGGGAU	AUCCCAA CUGAUGAG X CGAA IACCACC
2194	UGGGAUC C UCAUCAA	UUGAUGA CUGAUGAG X CGAA IAUCCCA
2195	GGGAUCC U CAUCAAG	CUUGAUG CUGAUGAG X CGAA IGAUCCC
2197	GAUCCUC A UCAAGCG	CGCUUGA CUGAUGAG X CGAA IAGGAUC
2200	CCUCAUC A AGCGACG	CGUCGCU CUGAUGAG X CGAA IAUGAGG
2210	CGACGGC A GCAGAAG	CUUCUGC CUGAUGAG X CGAA ICCGUCG
2213	CGGCAGC A GAAGAUC	GAUCUUC CUGAUGAG X CGAA ICUGCCG
2221	GAAGAUC C GGAAGUA	UACUUCC CUGAUGAG X CGAA IAUCUUC
2230	GAAGUAC A CGAUGCG	CGCAUCG CUGAUGAG X CGAA IUACUUC
2243	CGGAGAC U GCUGCAG	CUGCAGC CUGAUGAG X CGAA IUCUCCG
2246	AGACUGC U GCAGGAA	UUCCUGC CUGAUGAG X CGAA ICAGUCU
2249	CUGCUGC A GGAAACG	CGUTUCC CUGAUGAG X CGAA ICAGCAG
2261	ACGGAGC U GGUGGAG	CUCCACC CUGAUGAG X CGAA ICUCCGU
2270	GUGGAGC C GCUGACA	UGUCAGC CUGAUGAG X CGAA ICUCCAC

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Table 34

	Changes II Changes	AGGUGUC CUGAUGAG X CGAA ICGGCUC
2273	GAGCCGC U GACACCU	CGCUAGG CUGAUGAG X CGAA IUCAGCG
2277	CGCUGAC A CCUAGCG	UCCGCUA CUGAUGAG X CGAA IUGUCAG
2279	CUGACAC C UAGCGGA	
2280	UGACACC U AGCGGAG	CUCCGCU CUGAUGAG X CGAA IGUGUCA
2294	GCGAUGC C CAACCAG	CUGGUUG CUGAUGAG X CGAA ICAUCGC
2295	CGAUGCC C AACCAGG	CCUGGUU CUGAUGAG X CGAA IGCAUCG
2296	GAUGCCC A ACCAGGC	GCCUGGU CUGAUGAG X CGAA IGGCAUC
2299	GCCCAAC C AGGCGCA	UGCGCCU CUGAUGAG X CGAA IUUGGGC
2300	CCCAACC A GGCGCAG	CUGCGCC CUGAUGAG X CGAA IGUUGGG
2306	CAGGCGC A GAUGCGG	CCGCAUC CUGAUGAG X CGAA ICGCCUG
2317	GCGGAUC C UGAAAGA	UCUUUCA CUGAUGAG X CGAA IAUCCGC
2318	CGGAUCC U GAAAGAG	CUCUUUC CUGAUGAG X CGAA IGAUCCG
2333	ACGGAGC U GAGGAAG	CUUCCUC CUGAUGAG X CGAA ICUCCGU
2351	AAGGUGC U UGGAUCU	AGAUCCA CUGAUGAG X CGAA ICACCUU
2358	UUGGAUC U GGCGCUU	AAGCGCC CUGAUGAG X CGAA IAUCCAA
2364	CUGGCGC U UUUGGCA	UGCCAAA CUGAUGAG X CGAA ICGCCAG
2371	UUUUGGC A CAGUCUA	UAGACUG CUGAUGAG X CGAA ICCAAAA
2373	UUGGCAC A GUCUACA	UGUAGAC CUGAUGAG X CGAA IUGCCAA
2377	CACAGUC U ACAAGGG	CCCUUGU CUGAUGAG X CGAA IACUGUG
2380	AGUCUAC A AGGGCAU	AUGCCCU CUGAUGAG X CGAA IUAGACU
2386	CAAGGGC A UCUGGAU	AUCCAGA CUGAUGAG X CGAA ICCCUUG
2389	GGGCAUC U GGAUCCC	GGGAUCC CUGAUGAG X CGAA IAUGCCC
2395	CUGGAUC C CUGAUGG	CCAUCAG CUGAUGAG X CGAA IAUCCAG
2396	UGGAUCC C UGAUGGG	CCCAUCA CUGAUGAG X CGAA IGAUCCA
2397	GGAUCCC U GAUGGGG	CCCCAUC CUGAUGAG X CGAA IGGAUCC
2420	AAAAUUC C AGUGGCC	GGCCACU CUGAUGAG X CGAA IAAUUUU
2421	AAAUUCC A GUGGCCA	UGGCCAC CUGAUGAG X CGAA IGAAUUU
2427	CAGUGGC C AUCAAAG	CUUUGAU CUGAUGAG X CGAA ICCACUG
2428	AGUGGCC A UCAAAGU	ACUUUGA CUGAUGAG X CGAA IGCCACU
2431	GGCCAUC A AAGUGUU	AACACUU CUGAUGAG X CGAA IAUGGCC
2449	GGAAAAC A CAUCCCC	GGGGAUG CUGAUGAG X CGAA IUUUUCC
2451	AAAACAC A UCCCCCA	UGGGGGA CUGAUGAG X CGAA IUGUUUU
2454	ACACAUC C CCCAAAG	CUJUGGG CUGAUGAG X CGAA IAUGUGU
2455	CACAUCC C CCAAAGC	GCUUUGG CUGAUGAG X CGAA IGAUGUG
2456	ACAUCCC C CAAAGCC	GGCUUUG CUGAUGAG X CGAA IGGAUGU
2457	CAUCCCC C AAAGCCA	UGGCUUU CUGAUGAG X CGAA IGGGAUG
2458	AUCCCCC A AAGCCAA	UUGGCUU CUGAUGAG X CGAA IGGGGAU
2463	CCAAAGC C AACAAAG	CUUUGUU CUGAUGAG X CGAA ICUUUGG
2464	CAAAGCC A ACAAAGA	UCUUUGU CUGAUGAG X CGAA IGCUUUG
2467	AGCCAAC A AAGAAAU	AUUUCUU CUGAUGAG X CGAA IUUGGCU
2476	AGAAAUC U UAGACGA	UCGUCUA CUGAUGAG X CGAA IAUUUCU
2487	ACGAAGC A UACGUGA	UCACGUA CUGAUGAG X CGAA ICUUCGU
2499	UGAUGGC U GGUGUGG	CCACACC CUGAUGAG X CGAA ICCAUCA
2509	UGUGGGC U CCCCAUA	UAUGGGG CUGAUGAG X CGAA ICCCACA
2511	UGGGCUC C CCAUAUG	CAUAUGG CUGAUGAG X CGAA IAGCCCA
2512	GGGCUCC C CAUAUGU	ACAUAUG CUGAUGAG X CGAA IGAGCCC
2513	GGCUCCC C AUAUGUC	GACAUAU CUGAUGAG X CGAA IGGAGCC
		The state of the s

Table 34

2514	GCUCCCC A UAUGUCU	AGACAUA CUGAUGAG X CGAA IGGGAGC
2521	AUAUGUC U CCCGCCU	AGGCGGG CUGAUGAG X CGAA IACAUAU
2523	AUGUCUC C CGCCUUC	GAAGGCG CUGAUGAG X CGAA IAGACAU
2524	UGUCUCC C GCCUUCU	AGAAGGC CUGAUGAG X CGAA IGAGACA
2527	CUCCCGC C UUCUGGG	CCCAGAA CUGAUGAG X CGAA ICGGGAG
2528	UCCCGCC U UCUGGGC	GCCCAGA CUGAUGAG X CGAA IGCGGGA
2531	CGCCUUC U GGGCAUC	GAUGCCC CUGAUGAG X CGAA IAAGGCG
2536	UCUGGGC A UCUGCCU	AGGCAGA CUGAUGAG X CGAA ICCCAGA
2539	GGGCAUC U GCCUGAC	GUCAGGC CUGAUGAG X CGAA IAUGCCC
2542	CAUCUGC C UGACAUC	GAUGUCA CUGAUGAG X CGAA ICAGAUG
2543	AUCUGCC U GACAUCC	GGAUGUC CUGAUGAG X CGAA IGCAGAU
2547	GCCUGAC A UCCACGG	CCGUGGA CUGAUGAG X CGAA IUCAGGC
2550	UGACAUC C ACGGUGC	GCACCGU CUGAUGAG X CGAA IAUGUCA
2551	GACAUCC A CGGUGCA	UGCACCG CUGAUGAG X CGAA IGAUGUC
2558	ACGGUGC A GCUGGUG	CACCAGC CUGAUGAG X CGAA ICACCGU
2561	GUGCAGC U GGUGACA	UGUCACC CUGAUGAG X CGAA ICUGCAC
2568	UGGUGAC A CAGCUUA	UAAGCUG CUGAUGAG X CGAA IUCACCA
2570	GUGACAC A GCUUAUG	CAUAAGC CUGAUGAG X CGAA IUGUCAC
2573	ACACAGC U UAUGCCC	GGGCAUA CUGAUGAG X CGAA ICUGUGU
2579	CUUAUGC C CUAUGGC	GCCAUAG CUGAUGAG X CGAA ICAUAAG
2580	UUAUGCC C UAUGGCU	AGCCAUA CUGAUGAG X CGAA IGCAUAA
2581	UAUGCCC U AUGGCUG	CAGCCAU CUGAUGAG X CGAA IGGCAUA
2587	CUAUGGC U GCCUCUU	AAGAGGC CUGAUGAG X CGAA ICCAUAG
2590	UGGCUGC C UCUUAGA	UCUAAGA CUGAUGAG X CGAA ICAGCCA
2591	GGCUGCC U CUUAGAC	GUCUAAG CUGAUGAG X CGAA IGCAGCC
2593	CUGCCUC U UAGACCA	UGGUCUA CUGAUGAG X CGAA IAGGCAG
2599	CUUAGAC C AUGUCCG	CGGACAU CUGAUGAG X CGAA IUCUAAG
2600	UUAGACC A UGUCCGG	CCGGACA CUGAUGAG X CGAA IGUCUAA
2605	CCAUGUC C GGGAAAA	UUUUUCCC CUGAUGAG X CGAA IACAUGG
2614	GGAAAAC C GCGGACG	CGUCCGC CUGAUGAG X CGAA IUUUUCC
2623	CGGACGC C UGGGCUC	GAGCCCA CUGAUGAG X CGAA ICGUCCG
2624	GGACGCC U GGGCUCC	GGAGCCC CUGAUGAG X CGAA IGCGUCC
2629	CCUGGGC U CCCAGGA	UCCUGGG CUGAUGAG X CGAA ICCCAGG
2631	UGGGCUC C CAGGACC	GGUCCUG CUGAUGAG X CGAA IAGCCCA
2632	GGGCUCC C AGGACCU	AGGUCCU CUGAUGAG X CGAA IGAGCCC
2633	GGCUCCC A GGACCUG	CAGGUCC CUGAUGAG X CGAA IGGAGCC
2638	CCAGGAC C UGCUGAA	UUCAGCA CUGAUGAG X CGAA IUCCUGG
2639	CAGGACC U GCUGAAC	GUUCAGC CUGAUGAG X CGAA IGUCCUG
2642	GACCUGC U GAACUGG	CCAGUUC CUGAUGAG X CGAA ICAGGUC
2647	GCUGAAC U GGUGUAU	AUACACC CUGAUGAG X CGAA IUUCAGC
2657	UGUAUGC A GAUUGCC	GGCAAUC CUGAUGAG X CGAA ICAUACA
2664	AGAUUGC C AAGGGGA	UCCCCUU CUGAUGAG X CGAA ICAAUCU
2665	GAUUGCC A AGGGGAU	AUCCCCU CUGAUGAG X CGAA IGCAAUC
2677	GAUGAGC U ACCUGGA	UCCAGGU CUGAUGAG X CGAA ICUCAUC
2680	GAGCUAC C UGGAGGA	UCCUCCA CUGAUGAG X CGAA IUAGCUC
2681	AGCUACC U GGAGGAU	AUCCUCC CUGAUGAG X CGAA IGUAGCU
2696	GUGCGGC U CGUACAC	GUGUACG CUGAUGAG X CGAA ICCGCAC

Table 34

		THE COLUMN TWO COLUMN THE COLUMN	
2702	CUCGUAC A CAGGGAC	GUCCCUG CUGAUGAG X CGAA IUACGAG	
2704	CGUACAC A GGGACUU	AAGUCCC CUGAUGAG X CGAA IUGUACG	
2710	CAGGGAC U UGGCCGC	GCGGCCA CUGAUGAG X CGAA IUCCCUG	
2715	ACUUGGC C GCUCGGA	UCCGAGC CUGAUGAG X CGAA ICCAAGU	
2718	UGGCCGC U CGGAACG	CGUUCCG CUGAUGAG X CGAA ICGGCCA	
2729	AACGUGC U GGUCAAG	CUUGACC CUGAUGAG X CGAA ICACGUU	
2734	GCUGGUC A AGAGUCC	GGACUCU CUGAUGAG X CGAA IACCAGC	
2741	AAGAGUC C CAACCAU	AUGGUUG CUGAUGAG X CGAA IACUCUU	
2742	AGAGUCC C AACCAUG	CAUGGUU CUGAUGAG X CGAA IGACUCU	
2743	GAGUCCC A ACCAUGU	ACAUGGU CUGAUGAG X CGAA IGGACUC	
2746	UCCCAAC C AUGUCAA	UUGACAU CUGAUGAG X CGAA IUUGGGA	
2747	CCCAACC A UGUCAAA	UUUGACA CUGAUGAG X CGAA IGUUGGG	
2752	CCAUGUC A AAAUUAC	GUAAUUU CUGAUGAG X CGAA IACAUGG	
2760	AAAUUAC A GACUUCG	CGAAGUC CUGAUGAG X CGAA IUAAUUU	
2764	UACAGAC U UCGGGCU	AGCCCGA CUGAUGAG X CGAA IUCUGUA	
2771	UUCGGGC U GGCUCGG	CCGAGCC CUGAUGAG X CGAA ICCCGAA	
2775	GGCUGGC U CGGCUGC	GCAGCCG CUGAUGAG X CGAA ICCAGCC	
2780	GCUCGGC U GCUGGAC	GUCCAGC CUGAUGAG X CGAA ICCGAGC	
2783	CGGCUGC U GGACAUU	AAUGUCC CUGAUGAG X CGAA ICAGCCG	
2788	GCUGGAC A UUGACGA	UCGUCAA CUGAUGAG X CGAA IUCCAGC	
2799	ACGAGAC A GAGUACC	GGUACUC CUGAUGAG X CGAA IUCUCGU	-
2806	AGAGUAC C AUGCAGA	UCUGCAU CUGAUGAG X CGAA IUACUCU	
2807	GAGUACC A UGCAGAU	AUCUGCA CUGAUGAG X CGAA IGUACUC	
2811	ACCAUGC A GAUGGGG	CCCCAUC CUGAUGAG X CGAA ICAUGGU	
2821	UGGGGGC A AGGUGCC	GGCACCU CUGAUGAG X CGAA ICCCCCA	
2828	AAGGUGC C CAUCAAG	CUUGAUG CUGAUGAG X CGAA ICACCUU	-
2829	AGGUGCC C AUCAAGU	ACUUGAU CUGAUGAG X CGAA IGCACCU	-
2830	GGUGCCC A UCAAGUG	CACUUGA CUGAUGAG X CGAA IGGCACC	
2833	GCCCAUC A AGUGGAU	AUCCACU CUGAUGAG X CGAA IAUGGGC	
2846	AUGGCGC U GGAGUCC	GGACUCC CUGAUGAG X CGAA ICGCCAU GGAGAAU CUGAUGAG X CGAA IACUCCA	
2853	UGGAGUC C AUUCUCC	CGGAGAA CUGAUGAG X CGAA IACUCC	
2854	GGAGUCC A UUCUCCG	CCGGCGG CUGAUGAG X CGAA IAAUGGA	-
2858	UCCAUUC U CCGCCGG	CGCCGGC CUGAUGAG X CGAA TAAUGGA	+
2860	CAUUCUC C GCCGGCG	AACCGCC CUGAUGAG X CGAA ICGGAGA	
2863	UCUCCGC C GGCGGUU	UGGUGGG CUGAUGAG X CGAA IAGCCGC	
2872	GCGGUUC A CCCACCA	UCUGGUG CUGAUGAG X CGAA IMACCC	+
2874	GGUUCAC C CACCAGA	CUCUGGU CUGAUGAG X CGAA IGUGAAC	+
2875	GUUCACC C ACCAGAG	ACUCUGG CUGAUGAG X CGAA IGGUGAA	+
2876	UUCACCC A CCAGAGU	UCACUCU CUGAUGAG X CGAA IUGGGUG	+
2878	CACCCAC C AGAGUGA	AUCACUC CUGAUGAG X CGAA IGUGGGU	+
2879	ACCCACC A GAGUGAU	CCCACAC CUGAUGAG X CGAA IUCACAC	+
2907	GUGUGAC U GUGUGGG	AGUCAUC CUGAUGAG X CGAA ICUCCCA	+
2918	UGGGAGC U GAUGACU	CCCCAAA CUGAUGAG X CGAA IUCAUCA	+
2925	UGAUGAC U UUUGGGG	AAGGUUU CUGAUGAG X CGAA ICCCCAA	+
2934	UUGGGGC C AAACCUU	UAAGGUU CUGAUGAG X CGAA ICCCCAA	+
2935	UGGGGCC A AACCUUA	AUCGUAA CUGAUGAG X CGAA IUUUGGC	+
2939	GCCAAAC C UUACGAU	AUCGUAA CUGAUGAG A CGAA TUUUGGC	

Table 34

2940	CCAAACC U UACGAUG	CAUCGUA CUGAUGAG X CGAA IGUUUGG
2953	UGGGAUC C CAGCCCG	CGGGCUG CUGAUGAG X CGAA IAUCCCA
2954	GGGAUCC C AGCCCGG	CCGGGCU CUGAUGAG X CGAA IGAUCCC
2955	GGAUCCC A GCCCGGG	CCCGGGC CUGAUGAG X CGAA IGGAUCC
2958	UCCCAGC C CGGGAGA	UCUCCCG CUGAUGAG X CGAA ICUGGGA
2959	CCCAGCC C GGGAGAU	AUCUCCC CUGAUGAG X CGAA IGCUGGG
2968	GGAGAUC C CUGACCU	AGGUCAG CUGAUGAG X CGAA IAUCUCC
2969	GAGAUCC C UGACCUG	CAGGUCA CUGAUGAG X CGAA IGAUCUC
2970	AGAUCCC U GACCUGC	GCAGGUC CUGAUGAG X CGAA IGGAUCU
2974	CCCUGAC C UGCUGGA	UCCAGCA CUGAUGAG X CGAA IUCAGGG
2975	CCUGACC U GCUGGAA	UUCCAGC CUGAUGAG X CGAA IGUCAGG
2978	GACCUGC U GGAAAAG	CUUUUCC CUGAUGAG X CGAA ICAGGUC
2996	GAGCGGC U GCCCCAG	CUGGGGC CUGAUGAG X CGAA ICCGCUC
2999	CGGCUGC C CCAGCCC	GGGCUGG CUGAUGAG X CGAA ICAGCCG
3000	GGCUGCC C CAGCCCC	GGGGCUG CUGAUGAG X CGAA IGCAGCC
3001	GCUGCCC C AGCCCCC	GGGGGCU CUGAUGAG X CGAA IGGCAGC
3002	CUGCCCC A GCCCCCC	GGGGGC CUGAUGAG X CGAA IGGGCAG
3005	CCCCAGC C CCCCAUC	GAUGGGG CUGAUGAG X CGAA ICUGGGG
3006	CCCAGCC C CCCAUCU	AGAUGGG CUGAUGAG X CGAA IGCUGGG
3007	CCAGCCC C CCAUCUG	CAGAUGG CUGAUGAG X CGAA IGGCUGG
3008	CAGCCCC C CAUCUGC	GCAGAUG CUGAUGAG X CGAA IGGGCUG
3009	AGCCCCC C AUCUGCA	UGCAGAU CUGAUGAG X CGAA IGGGGCU
3010	GCCCCCC A UCUGCAC	GUGCAGA CUGAUGAG X CGAA IGGGGGC
3013	CCCCAUC U GCACCAU	AUGGUGC CUGAUGAG X CGAA IAUGGGG
3016	CAUCUGC A CCAUUGA	UCAAUGG CUGAUGAG X CGAA ICAGAUG
3018	UCUGCAC C AUUGAUG	CAUCAAU CUGAUGAG X CGAA IUGCAGA
3019	CUGCACC A UUGAUGU	ACAUCAA CUGAUGAG X CGAA IGUGCAG
3028	UGAUGUC U ACAUGAU	AUCAUGU CUGAUGAG X CGAA IACAUCA
3031	UGUCUAC A UGAUCAU	AUGAUCA CUGAUGAG X CGAA IUAGACA
3037	CAUGAUC A UGGUCAA	UUGACCA CUGAUGAG X CGAA IAUCAUG
3043	CAUGGUC A AAUGUUG	CAACAUU CUGAUGAG X CGAA IACCAUG
3061	GAUUGAC U CUGAAUG	CAUUCAG CUGAUGAG X CGAA IUCAAUC
3063	UUGACUC U GAAUGUC	GACAUUC CUGAUGAG X CGAA IAGUCAA
3074	UGUCGGC C AAGAUUC	GAAUCUU CUGAUGAG X CGAA ICCGACA
3075	GUCGGCC A AGAUUCC	GGAAUCU CUGAUGAG X CGAA IGCCGAC
3082	AAGAUUC C GGGAGUU	AACUCCC CUGAUGAG X CGAA IAAUCUU
3096	UGGUGUC U GAAUUCU	AGAAUUC CUGAUGAG X CGAA IACACCA
3103	UGAAUUC U CCCGCAU	AUGCGGG CUGAUGAG X CGAA IAAUUCA
3105	AAUUCUC C CGCAUGG	CCAUGCG CUGAUGAG X CGAA IAGAAUU
3106	AUUCUCC C GCAUGGC	GCCAUGC CUGAUGAG X CGAA IGAGAAU
3109	CUCCCGC A UGGCCAG	CUGGCCA CUGAUGAG X CGAA ICGGGAG
3114	GCAUGGC C AGGGACC	GGUCCCU CUGAUGAG X CGAA ICCAUGC
3115	CAUGGCC A GGGACCC	GGGUCCC CUGAUGAG X CGAA IGCCAUG
3121	CAGGGAC C CCCAGCG	CGCUGGG CUGAUGAG X CGAA IUCCCUG
3122	AGGGACC C CCAGCGC	GCGCUGG CUGAUGAG X CGAA IGUCCCU
3123	GGGACCC C CAGCGCU	AGCGCUG CUGAUGAG X CGAA IGGUCCC
3124	GGACCCC C AGCGCUU	AAGCGCU CUGAUGAG X CGAA IGGGUCC

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Table 34

3125	GACCCCC A GCGCUUU	AAAGCGC CUGAUGAG X CGAA IGGGGUC
3130	CCAGCGC U UUGUGGU	ACCACAA CUGAUGAG X CGAA ICGCUGG
3139	UGUGGUC A UCCAGAA	UUCUGGA CUGAUGAG X CGAA IACCACA
3142	GGUCAUC C AGAAUGA	UCAUUCU CUGAUGAG X CGAA IAUGACC
3143	GUCAUCC A GAAUGAG	CUCAUUC CUGAUGAG X CGAA IGAUGAC
3154	UGAGGAC U UGGGCCC	GGGCCCA CUGAUGAG X CGAA IUCCUCA
3160	CUUGGGC C CAGCCAG	CUGGCUG CUGAUGAG X CGAA ICCCAAG
3161	UUGGGCC C AGCCAGU	ACUGGCU CUGAUGAG X CGAA IGCCCAA
3162	UGGGCCC A GCCAGUC	GACUGGC CUGAUGAG X CGAA IGGCCCA
3165	GCCCAGC C AGUCCCU	AGGGACU CUGAUGAG X CGAA ICUGGGC
3166	CCCAGCC A GUCCCUU	AAGGGAC CUGAUGAG X CGAA IGCUGGG
3170	GCCAGUC C CUUGGAC	GUCCAAG CUGAUGAG X CGAA IACUGGC
3171	CCAGUCC C UUGGACA	UGUCCAA CUGAUGAG X CGAA IGACUGG
3172	CAGUCCC U UGGACAG	CUGUCCA CUGAUGAG X CGAA IGGACUG
3178	CUUGGAC A GCACCUU	AAGGUGC CUGAUGAG X CGAA IUCCAAG
3181	GGACAGC A CCUUCUA	UAGAAGG CUGAUGAG X CGAA ICUGUCC
3183	ACAGCAC C UUCUACC	GGUAGAA CUGAUGAG X CGAA IUGCUGU
3184	CAGCACC U UCUACCG	CGGUAGA CUGAUGAG X CGAA IGUGCUG
3187	CACCUUC U ACCGCUC	GAGCGGU CUGAUGAG X CGAA IAAGGUG
3190	CUUCUAC C GCUCACU	AGUGAGC CUGAUGAG X CGAA IUAGAAG
3193	CUACCGC U CACUGCU	AGCAGUG CUGAUGAG X CGAA ICGGUAG
3195	ACCGCUC A CUGCUGG	CCAGCAG CUGAUGAG X CGAA IAGCGGU
3197	CGCUCAC U GCUGGAG	CUCCAGC CUGAUGAG X CGAA IUGAGCG
3200	UCACUGC U GGAGGAC	GUCCUCC CUGAUGAG X CGAA ICAGUGA
3214	CGAUGAC A UGGGGGA	UCCCCCA CUGAUGAG X CGAA IUCAUCG
3223	GGGGGAC C UGGUGGA	UCCACCA CUGAUGAG X CGAA IUCCCCC
3224	GGGGACC U GGUGGAU	AUCCACC CUGAUGAG X CGAA IGUCCCC
3234	UGGAUGC U GAGGAGU	ACUCCUC CUGAUGAG X CGAA ICAUCCA
3245	GAGUAUC U GGUACCC	GGGUACC CUGAUGAG X CGAA IAUACUC
3251	CUGGUAC C CCAGCAG	CUGCUGG CUGAUGAG X CGAA IUACCAG
3252	UGGUACC C CAGCAGG	CCUGCUG CUGAUGAG X CGAA IGUACCA
3253	GGUACCC C AGCAGGG	CCCUGCU CUGAUGAG X CGAA IGGUACC
3254	GUACCCC A GCAGGGC	GCCCUGC CUGAUGAG X CGAA IGGGUAC
3257	CCCCAGC A GGGCUUC	GAAGCCC CUGAUGAG X CGAA ICUGGGG
3262	GCAGGGC U UCUUCUG	CAGAAGA CUGAUGAG X CGAA ICCCUGC
3265	GGGCUUC U UCUGUCC	GGACAGA CUGAUGAG X CGAA IAAGCCC
3268	CUUCUUC U GUCCAGA	UCUGGAC CUGAUGAG X CGAA IAAGAAG
3272	UUCUGUC C AGACCCU	AGGGUCU CUGAUGAG X CGAA IACAGAA
3273	UCUGUCC A GACCCUG	CAGGGUC CUGAUGAG X CGAA IGACAGA
3277	UCCAGAC C CUGCCCC	GGGGCAG CUGAUGAG X CGAA IUCUGGA
3278	CCAGACC C UGCCCCG	CGGGGCA CUGAUGAG X CGAA IGUCUGG
3279	CAGACCC U GCCCCGG	CCGGGGC CUGAUGAG X CGAA IGGUCUG
3282	ACCCUGC C CCGGGCG	CGCCCGG CUGAUGAG X CGAA ICAGGGU
3283	cccucce e cccccc	GCGCCCG CUGAUGAG X CGAA IGCAGGG
3284	CCUGCCC C GGGCGCU	AGCGCCC CUGAUGAG X CGAA IGGCAGG
3291	CGGGCGC U GGGGGCA	UGCCCCC CUGAUGAG X CGAA ICGCCCG
3298	UGGGGGC A UGGUCCA	UGGACCA CUGAUGAG X CGAA ICCCCCA

490

Table 34

		14010 54
3304	CAUGGUC C ACCACAG	CUGUGGU CUGAUGAG X CGAA IACCAUG
3305	AUGGUCC A CCACAGG	CCUGUGG CUGAUGAG X CGAA IGACCAU
3307	GGUCCAC C ACAGGCA	UGCCUGU CUGAUGAG X CGAA IUGGACC
3308	GUCCACC A CAGGCAC	GUGCCUG CUGAUGAG X CGAA IGUGGAC
3310	CCACCAC A GGCACCG	CGGUGCC CUGAUGAG X CGAA IUGGUGG
3314	CACAGGC A CCGCAGC	GCUGCGG CUGAUGAG X CGAA ICCUGUG
3316	CAGGCAC C GCAGCUC	GAGCUGC CUGAUGAG X CGAA IUGCCUG
3319	GCACCGC A GCUCAUC	GAUGAGC CUGAUGAG X CGAA ICGGUGC
3322	CCGCAGC U CAUCUAC	GUAGAUG CUGAUGAG X CGAA ICUGCGG
3324	GCAGCUC A UCUACCA	UGGUAGA CUGAUGAG X CGAA IAGCUGC
3327	GCUCAUC U ACCAGGA	UCCUGGU CUGAUGAG X CGAA IAUGAGC
3330	CAUCUAC C AGGAGUG	CACUCCU CUGAUGAG X CGAA IUAGAUG
3331	AUCUACC A GGAGUGG	CCACUCC CUGAUGAG X CGAA IGUAGAU
3349	UGGGGAC C UGACACU	AGUGUCA CUGAUGAG X CGAA IUCCCCA
3350	GGGGACC U GACACUA	UAGUGUC CUGAUGAG X CGAA IGUCCCC
3354	ACCUGAC A CUAGGGC	GCCCUAG CUGAUGAG X CGAA IUCAGGU
3356	CUGACAC U AGGGCUG	CAGCCCU CUGAUGAG X CGAA IUGUCAG
3362	CUAGGGC U GGAGCCC	GGGCUCC CUGAUGAG X CGAA ICCCUAG
3368	CUGGAGC C CUCUGAA	UUCAGAG CUGAUGAG X CGAA ICUCCAG
3369	UGGAGCC C UCUGAAG	CUUCAGA CUGAUGAG X CGAA IGCUCCA
3370	GGAGCCC U CUGAAGA	UCUUCAG CUGAUGAG X CGAA IGGCUCC
3372	AGCCCUC U GAAGAGG	CCUCUUC CUGAUGAG X CGAA IAGGGCU
3384	AGGAGGC C CCCAGGU	ACCUGGG CUGAUGAG X CGAA ICCUCCU
3385	GGAGGCC C CCAGGUC	GACCUGG CUGAUGAG X CGAA IGCCUCC
3386	GAGGCCC C CAGGUCU	AGACCUG CUGAUGAG X CGAA IGGCCUC
3387	AGGCCCC C AGGUCUC	GAGACCU CUGAUGAG X CGAA IGGGCCU GGAGACC CUGAUGAG X CGAA IGGGGCC
3388	GGCCCCC A GGUCUCC	CCAGUGG CUGAUGAG X CGAA IACCUGG
3393	CCAGGUC U CCACUGG	UGCCAGU CUGAUGAG X CGAA TACCOGG
3395	AGGUCUC C ACUGGCA	GUGCCAGU CUGAUGAG X CGAA TAGACCO
3396	GGUCUCC A CUGGCAC	GGGUGCC CUGAUGAG X CGAA IUGGAGA
3398	UCUCCAC U GGCACCC	CGGAGGG CUGAUGAG X CGAA ICCAGUG
3402	CACUGGC A CCCUCCG	UUCGGAG CUGAUGAG X CGAA IUGCCAG
3404	CUGGCAC C CUCCGAA	CUUCGGA CUGAUGAG X CGAA IGUGCCA
3405	UGGCACC C UCCGAAG	CCUUCGG CUGAUGAG X CGAA IGGUGCC
3406	GGCACCC U CCGAAGG CACCCUC C GAAGGGG	CCCCUUC CUGAUGAG X CGAA IAGGGUG
3408	AAGGGGC U GGCUCCG	CGGAGCC CUGAUGAG X CGAA ICCCCUU
3417		ACAUCGG CUGAUGAG X CGAA ICCAGCC
3421	GGCUGGC U CCGAUGU CUGGCUC C GAUGUAU	AUACAUC CUGAUGAG X CGAA IAGCCAG
3423	UGGUGAC C UGGGAAU	AUUCCCA CUGAUGAG X CGAA IUCACCA
3442	GGUGACC U GGGAAUG	CAUUCCC CUGAUGAG X CGAA IGUCACC
3443	UGGGGGC A GCCAAGG	CCUUGGC CUGAUGAG X CGAA ICCCCCA
3456	GGGCAGC C AAGGGGC	GCCCCUU CUGAUGAG X CGAA ICUGCCC
3459	GGCAGCC A AGGGGCU	AGCCCCU CUGAUGAG X CGAA IGCUGCC
3460	AAGGGC U GCAAAGC	GCUUUGC CUGAUGAG X CGAA ICCCCUU
	GGGCUGC A AAGCCUC	GAGGCUU CUGAUGAG X CGAA ICAGCCC
3470	GCAAAGC C UCCCCAC	GUGGGGA CUGAUGAG X CGAA ICUUUGC
3475	GCAAAGC C OCCCCAC	

Table 34

3476	CAAAGCC U CCCCACA	UGUGGGG CUGAUGAG X CGAA IGCUUUG
3478	AAGCCUC C CCACACA	UGUGUGG CUGAUGAG X CGAA IAGGCUU
3479	AGCCUCC C CACACAU	AUGUGUG CUGAUGAG X CGAA IGAGGCU
3479	GCCUCCC C ACACAUG	CAUGUGU CUGAUGAG X CGAA IGGAGGC
3481	CCUCCCC A CACAUGA	UCAUGUG CUGAUGAG X CGAA IGGGAGG
3483	UCCCCAC A CAUGACC	GGUCAUG CUGAUGAG X CGAA IUGGGGA
3485	CCCACAC A UGACCCC	GGGGUCA CUGAUGAG X CGAA IUGUGGG
3490	ACAUGAC C CCAGCCC	GGGCUGG CUGAUGAG X CGAA IUCAUGU
3491	CAUGACC C CAGCCCU	AGGGCUG CUGAUGAG X CGAA IGUCAUG
3492	AUGACCC C AGCCCUC	GAGGGCU CUGAUGAG X CGAA IGGUCAU
3493	UGACCCC A GCCCUCU	AGAGGGC CUGAUGAG X CGAA IGGGUCA
3496	CCCCAGC C CUCUACA	UGUAGAG CUGAUGAG X CGAA ICUGGGG
3497	CCCAGCC C UCUACAG	CUGUAGA CUGAUGAG X CGAA IGCUGGG
3498	CCAGCCC U CUACAGC	GCUGUAG CUGAUGAG X CGAA IGGCUGG
3500	AGCCCUC U ACAGCGG	CCGCUGU CUGAUGAG X CGAA IAGGGCU
3503	CCUCUAC A GCGGUAC	GUACCGC CUGAUGAG X CGAA IUAGAGG
3511	GCGGUAC A GUGAGGA	UCCUCAC CUGAUGAG X CGAA IUACCGC
3520	UGAGGAC C CCACAGU	ACUGUGG CUGAUGAG X CGAA IUCCUCA
3521	GAGGACC C CACAGUA	UACUGUG CUGAUGAG X CGAA IGUCCUC
3522	AGGACCC C ACAGUAC	GUACUGU CUGAUGAG X CGAA IGGUCCU
3523	GGACCCC A CAGUACC	GGUACUG CUGAUGAG X CGAA IGGGUCC
3525	ACCCCAC A GUACCCC	GGGGUAC CUGAUGAG X CGAA IUGGGGU
3530	ACAGUAC C CCUGCCC	GGGCAGG CUGAUGAG X CGAA IUACUGU
3531	CAGUACC C CUGCCCU	AGGGCAG CUGAUGAG X CGAA IGUACUG
3532	AGUACCC C UGCCCUC	GAGGGCA CUGAUGAG X CGAA IGGUACU
3533	GUACCCC U GCCCUCU	AGAGGGC CUGAUGAG X CGAA IGGGUAC
3536	CCCCUGC C CUCUGAG	CUCAGAG CUGAUGAG X CGAA ICAGGGG
3537	CCCUGCC C UCUGAGA	UCUCAGA CUGAUGAG X CGAA IGCAGGG
3538	CCUGCCC U CUGAGAC	GUCUCAG CUGAUGAG X CGAA IGGCAGG
3540	UGCCCUC U GAGACUG	CAGUCUC CUGAUGAG X CGAA IAGGGCA
3546	CUGAGAC U GAUGGCU	AGCCAUC CUGAUGAG X CGAA IUCUCAG
3553	UGAUGGC U ACGUUGC	GCAACGU CUGAUGAG X CGAA ICCAUCA
3561	ACGUUGC C CCCCUGA	UCAGGGG CUGAUGAG X CGAA 1CAACGU
3562	CGUUGCC C CCCUGAC	GUCAGGG CUGAUGAG X CGAA IGCAACG
3563	GUUGCCC C CCUGACC	GGUCAGG CUGAUGAG X CGAA IGGCAAC
3564	UUGCCCC C CUGACCU	AGGUCAG CUGAUGAG X CGAA IGGGCAA
3565	UGCCCCC C UGACCUG	CAGGUCA CUGAUGAG X CGAA IGGGGCA
3566	GCCCCCC U GACCUGC	GCAGGUC CUGAUGAG X CGAA 1GGGGGC
3570	CCCUGAC C UGCAGCC	GGCUGCA CUGAUGAG X CGAA IUCAGGG
3571	CCUGACC U GCAGCCC	GGGCUGC CUGAUGAG X CGAA IGUCAGG
3574	GACCUGC A GCCCCCA	UGGGGGC CUGAUGAG X CGAA ICAGGUC
3577	CUGCAGC C CCCAGCC	GGCUGGG CUGAUGAG X CGAA ICUGCAG
3578	UGCAGCC C CCAGCCU	AGGCUGG CUGAUGAG X CGAA IGCUGCA
3579	GCAGCCC C CAGCCUG	CAGGCUG CUGAUGAG X CGAA IGGCUGC
3580	CAGCCCC C AGCCUGA	UCAGGCU CUGAUGAG X CGAA IGGGCUG
3581	AGCCCCC A GCCUGAA	UUCAGGC CUGAUGAG X CGAA IGGGGCU AUAUUCA CUGAUGAG X CGAA ICUGGGG
3584	CCCCAGC C UGAAUAU	AUAUUCA CUGAUGAG A CGAA TCOGGGG

Table 34

		CAUAUUC CUGAUGAG X CGAA IGCUGGG
3585	CCCAGCC U GAAUAUG	UCUGGCU CUGAUGAG X CGAA IUUCACA
3598	UGUGAAC C AGCCAGA	AUCUGGC CUGAUGAG X CGAA IGUCAC
3599	GUGAACC A GCCAGAU	AACAUCU CUGAUGAG X CGAA ICUGGUU
3602	AACCAGC C AGAUGUU	GAACAUC CUGAUGAG X CGAA IGCUGGU
3603	ACCAGCC A GAUGUUC	GGCCUGG CUGAUGAG X CGAA IGCUGGO GGCCUGG CUGAUGAG X CGAA ICCGAAC
3614	GUUCGGC C CCAGCCC	GGGCUGG CUGAUGAG X CGAA ICCGAA GGGGCUG CUGAUGAG X CGAA IGCCGAA
3615	UUCGGCC C CAGCCCC	
3616	UCGGCCC C AGCCCCC	GGGGGCU CUGAUGAG X CGAA IGGCCGA AGGGGGC CUGAUGAG X CGAA IGGGCCG
3617	CGGCCCC A GCCCCCU	CGAAGGG CUGAUGAG X CGAA ICUGGGG
3620	CCCCAGC C CCCUUCG	GCGAAGG CUGAUGAG X CGAA ICCUGGG
3621	CCCAGCC C CCUUCGC	GCGAAGG CUGAUGAG X CGAA IGCCUGG
3622	CCAGCCC C CUUCGCC	GGCGAA CUGAUGAG X CGAA IGGGCUG
3623	CAGCCCC C UUCGCCC	GGGCGA CUGAUGAG X CGAA IGGGGCU
3624	AGCCCCC U UCGCCCC	CUCUCGG CUGAUGAG X CGAA ICGAAGG
3629	CCUUCGC C CCGAGAG	CUCUCG CUGAUGAG X CGAA IGCGAAG
3630	CUUCGCC C CGAGAGG	CCCUCUC CUGAUGAG X CGAA IGCGGAA
3631	UUCGCCC C GAGAGGG	GGCAGAG CUGAUGAG X CGAA ICCCUCU
3640	AGAGGGC C CUCUGCC	AGGCAGA CUGAUGAG X CGAA ICCCCUC
3641	GAGGGCC C UCUGCCU	CAGGCAG CUGAUGAG X CGAA IGGCCCU
3642	AGGGCCC U CUGCCUG	AGCAGGC CUGAUGAG X CGAA IAGGGCC
3644	GGCCCUC U GCCUGCU	GGCAGCA CUGAUGAG X CGAA ICAGAGG
. 3647	CCUCUGC C UGCUGCC	GGGCAGC CUGAUGAG X CGAA IGCAGAG
3648	CUCUGCC U GCUGCCC	GUCGGGC CUGAUGAG X CGAA ICAGGCA
3651	UGCCUGC U GCCCGAC	CAGGUCG CUGAUGAG X CGAA ICAGCAG
3654	CUGCUGC C CGACCUG	GCAGGUC CUGAUGAG X CGAA IGCAGCA
3655	UGCUGCC C GACCUGC GCCCGAC C UGCUGGU	ACCAGCA CUGAUGAG X CGAA IUCGGGC
3659	CCCGACC U GCUGGUG	CACCAGC CUGAUGAG X CGAA IGUCGGG
3660	GACCUGC U GGUGCCA	UGGCACC CUGAUGAG X CGAA ICAGGUC
3663	CUGGUGC C ACUCUGG	CCAGAGU CUGAUGAG X CGAA ICACCAG
3669	UGGUGCC A CUCUGGA	UCCAGAG CUGAUGAG X CGAA IGCACCA
3670	GUGCCAC U CUGGAAA	UUUCCAG CUGAUGAG X CGAA IUGGCAC
3672	GCCACUC U GGAAAGG	CCUUUCC CUGAUGAG X CGAA IAGUGGC
3674	GAAAGGC C CAAGACU	AGUCUUG CUGAUGAG X CGAA ICCUUUC
3684	AAAGGCC C AAGACUC	GAGUCUU CUGAUGAG X CGAA IGCCUUU
3685	AAGGCCC A AGACUCU	AGAGUCU CUGAUGAG X CGAA IGGCCUU
3690	CCAAGAC U CUCUCCC	GGGAGAG CUGAUGAG X CGAA IUCUUGG
3692	AAGACUC U CUCCCCA	UGGGGAG CUGAUGAG X CGAA IAGUCUU
3694	GACUCUC U CCCCAGG	CCUGGGG CUGAUGAG X CGAA IAGAGUC
3696	CUCUCUC C CCAGGGA	UCCCUGG CUGAUGAG X CGAA IAGAGAG
3697	UCUCUCC C CAGGGAA	UUCCCUG CUGAUGAG X CGAA IGAGAGA
3698	CUCUCCC C AGGGAAG	CUUCCCU CUGAUGAG X CGAA IGGAGAG
3699	UCUCCCC A GGGAAGA	UCUUCCC CUGAUGAG X CGAA IGGGAGA
3718	GGUCGUC A AAGACGU	ACGUCUU CUGAUGAG X CGAA IACGACC
3732	UUUUUGC C UUUGGGG	CCCCAAA CUGAUGAG X CGAA ICAAAAA
3733	UUUUGCC U UUGGGGG	CCCCCAA CUGAUGAG X CGAA IGCAAAA
3744	GGGGUGC C GUGGAGA	UCUCCAC CUGAUGAG X CGAA ICACCCC

Table 34

3754	GGAGAAC C CCGAGUA	UACUCGG CUGAUGAG X CGAA IUUCUCC
3755	GAGAACC C CGAGUAC	GUACUCG CUGAUGAG X CGAA IGUUCUC
3756	AGAACCC C GAGUACU	AGUACUC CUGAUGAG X CGAA IGGUUCU
3763	CGAGUAC U UGACACC	GGUGUCA CUGAUGAG X CGAA IUACUCG
3768	ACUUGAC A CCCCAGG	CCUGGGG CUGAUGAG X CGAA IUCAAGU
3770	UUGACAC C CCAGGGA	UCCCUGG CUGAUGAG X CGAA IUGUCAA
3771	UGACACC C CAGGGAG	CUCCCUG CUGAUGAG X CGAA IGUGUCA
3772	GACACCC C AGGGAGG	CCUCCCU CUGAUGAG X CGAA IGGUGUC
3773	ACACCCC A GGGAGGA	UCCUCCC CUGAUGAG X CGAA IGGGUGU
3783	GAGGAGC U GCCCCUC	GAGGGGC CUGAUGAG X CGAA ICUCCUC
3786	GAGCUGC C CCUCAGC	GCUGAGG CUGAUGAG X CGAA ICAGCUC
3787	AGCUGCC C CUCAGCC	GGCUGAG CUGAUGAG X CGAA IGCAGCU
3788	GCUGCCC C UCAGCCC	GGGCUGA CUGAUGAG X CGAA IGGCAGC
3789	CUGCCCC U CAGCCCC	GGGGCUG CUGAUGAG X CGAA IGGGCAG
3791	GCCCCUC A GCCCCAC	GUGGGGC CUGAUGAG X CGAA IAGGGGC
3794	CCUCAGC C CCACCCU	AGGGUGG CUGAUGAG X CGAA ICUGAGG
3795	CUCAGCC C CACCCUC	GAGGGUG CUGAUGAG X CGAA IGCUGAG
3796	UCAGCCC C ACCCUCC	GGAGGGU CUGAUGAG X CGAA IGGCUGA
3797	CAGCCCC A CCCUCCU	AGGAGGG CUGAUGAG X CGAA IGGGCUG
3799	GCCCCAC C CUCCUCC	GGAGGAG CUGAUGAG X CGAA IUGGGGC
3800	CCCCACC C UCCUCCU	AGGAGGA CUGAUGAG X CGAA IGUGGGG
3801	CCCACCC U CCUCCUG	CAGGAGG CUGAUGAG X CGAA IGGUGGG
3803	CACCCUC C UCCUGCC	GGCAGGA CUGAUGAG X CGAA IAGGGUG
3804	ACCCUCC U CCUGCCU	AGGCAGG CUGAUGAG X CGAA IGAGGGU
3806	cencene e nacenne	GAAGGCA CUGAUGAG X CGAA IAGGAGG
3807	CUCCUCC U GCCUUCA	UGAAGGC CUGAUGAG X CGAA IGAGGAG
3810	CUCCUGC C UUCAGCC	GGCUGAA CUGAUGAG X CGAA ICAGGAG
3811	UCCUGCC U UCAGCCC	GGGCUGA CUGAUGAG X CGAA IGCAGGA
3814	UGCCUUC A GCCCAGC	GCUGGGC CUGAUGAG X CGAA IAAGGCA
3817	CUUCAGO C CAGCOUU	AAGGCUG CUGAUGAG X CGAA ICUGAAG
3818	UUCAGCC C AGCCUUC	GAAGGCU CUGAUGAG X CGAA IGCUGAA
3819	UCAGCCC A GCCUUCG	CGAAGGC CUGAUGAG X CGAA IGGCUGA
3822	GCCCAGC C UUCGACA	UGUCGAA CUGAUGAG X CGAA ICUGGGC
3823	CCCAGCC U UCGACAA	UUGUCGA CUGAUGAG X CGAA IGCUGGG
3829	CUUCGAC A ACCUCUA	UAGAGGU CUGAUGAG X CGAA IUCGAAG
3832	CGACAAC C UCUAUUA	UAAUAGA CUGAUGAG X CGAA IUUGUCG
3833	GACAACC U CUAUUAC	GUAAUAG CUGAUGAG X CGAA IGUUGUC
3835	CAACCUC U AUUACUG	CAGUAAU CUGAUGAG X CGAA IAGGUUG
3841	CUAUUAC U GGGACCA	UGGUCCC CUGAUGAG X CGAA IUAAUAG
3847	CUGGGAC C AGGACCC	GGGUCCU CUGAUGAG X CGAA IUCCCAG
3848	UGGGACC A GGACCCA	UGGGUCC CUGAUGAG X CGAA IGUCCCA
3853	CCAGGAC C CACCAGA	UCUGGUG CUGAUGAG X CGAA IUCCUGG
3854	CAGGACC C ACCAGAG	CUCUGGU CUGAUGAG X CGAA IGUCCUG
3855	AGGACCC A CCAGAGC	GCUCUGG CUGAUGAG X CGAA IGGUCCU
3857	GACCCAC C AGAGCGG	CCGCUCU CUGAUGAG X CGAA IUGGGUC
3858	ACCCACC A GAGCGGG	CCCGCUC CUGAUGAG X CGAA IGUGGGU
3870	GGGGGGC U CCACCCA	UGGGUGG CUGAUGAG X CGAA ICCCCCC
20,0	1 2223000 0 00101011	

Table 34

3872	GGGGCUC C ACCCAGC	GCUGGGU CUGAUGAG X CGAA IAGCCCC
3873	GGGCUCC A CCCAGCA	UGCUGGG CUGAUGAG X CGAA IGAGCCC
3875	GCUCCAC C CAGCACC	GGUGCUG CUGAUGAG X CGAA IUGGAGC
3876	CUCCACC C AGCACCU	AGGUGCU CUGAUGAG X CGAA IGUGGAG
3877	UCCACCC A GCACCUU	AAGGUGC CUGAUGAG X CGAA IGGUGGA
3880	ACCCAGC A CCUUCAA	UUGAAGG CUGAUGAG X CGAA ICUGGGU
3882	CCAGCAC C UUCAAAG	CUUUGAA CUGAUGAG X CGAA IUGCUGG
3883	CAGCACC U UCAAAGG	CCUUUGA CUGAUGAG X CGAA IGUGCUG
3886	CACCUUC A AAGGGAC	GUCCCUU CUGAUGAG X CGAA IAAGGUG
3894	AAGGGAC A CCUACGG	CCGUAGG CUGAUGAG X CGAA IUCCCUU
3896	GGGACAC C UACGGCA	UGCCGUA CUGAUGAG X CGAA IUGUCCC
3897	GGACACC U ACGGCAG	CUGCCGU CUGAUGAG X CGAA IGUGUCC
3903	CUACGGC A GAGAACC	GGUUCUC CUGAUGAG X CGAA ICCGUAG
3910	AGAGAAC C CAGAGUA	UACUCUG CUGAUGAG X CGAA IUUCUCU
3911	GAGAACC C AGAGUAC	GUACUCU CUGAUGAG X CGAA IGUUCUC
3912	AGAACCC A GAGUACC	GGUACUC CUGAUGAG X CGAA IGGUUCU
3919	AGAGUAC C UGGGUCU	AGACCCA CUGAUGAG X CGAA IUACUCU
3920	GAGUACC U GGGUCUG	CAGACCC CUGAUGAG X CGAA IGUACUC
3926	CUGGGUC U GGACGUG	CACGUCC CUGAUGAG X CGAA IACCCAG
3935	GACGUGC C AGUGUGA	UCACACU CUGAUGAG X CGAA ICACGUC
3936	ACGUGCC A GUGUGAA	UUCACAC CUGAUGAG X CGAA IGCACGU
3945	UGUGAAC C AGAAGGC	GCCUUCU CUGAUGAG X CGAA IUUCACA
3946	GUGAACC A GAAGGCC	GGCCUUC CUGAUGAG X CGAA IGUUCAC
3953	AGAAGGC C AAGUCCG	CGGACUU CUGAUGAG X CGAA ICCUUCU
3954	GAAGGCC A AGUCCGC	GCGGACU CUGAUGAG X CGAA IGCCUUC
3959	CCAAGUC C GCAGAAG	CUUCUGC CUGAUGAG X CGAA IACUUGG
3962	AGUCCGC A GAAGCCC	GGGCUUC CUGAUGAG X CGAA ICGGACU
3968	CAGAAGC C CUGAUGU	ACAUCAG CUGAUGAG X CGAA ICUUCUG
3969	AGAAGCC C UGAUGUG	CACAUCA CUGAUGAG X CGAA IGCUUCU
3970	GAAGCCC U GAUGUGU	ACACAUC CUGAUGAG X CGAA IGGCUUC
3979	AUGUGUC C UCAGGGA	UCCCUGA CUGAUGAG X CGAA IACACAU
3980	UGUGUCC U CAGGGAG	CUCCCUG CUGAUGAG X CGAA IGACACA
3982	UGUCCUC A GGGAGCA	UGCUCCC CUGAUGAG X CGAA IAGGACA
3989	AGGGAGC A GGGAAGG	CCUUCCC CUGAUGAG X CGAA ICUCCCU GAAGUCA CUGAUGAG X CGAA ICCUUCC
3998	GGAAGGC C UGACUUC	AGAAGUC CUGAUGAG X CGAA ICCUUC
3999	GAAGGCC U GACUUCU	CAGCAGA CUGAUGAG X CGAA IUCAGGC
4003	GCCUGAC U UCUGCUG	UGCCAGC CUGAUGAG X CGAA IUCAGGC
4006	UGACUUC U GCUGGCA	UGAUGCC CUGAUGAG X CGAA IAAGUCA UGAUGCC CUGAUGAG X CGAA ICAGAAG
4009	CUUCUGC U GGCAUCA	CUCUUGA CUGAUGAG X CGAA ICAGAAG
4013	UGCUGGC A UCAAGAG	CACCUCU CUGAUGAG X CGAA IAUGCCA
4016	UGGCAUC A AGAGGUG	GUCGGAG CUGAUGAG X CGAA ICCCUCC
4031	GGAGGGC C CUCCGAC	GUCGGA CUGAUGAG X CGAA ICCCUC
4032	GAGGGCC C UCCGACC	UGGUCGG CUGAUGAG X CGAA IGCCCU
4033	AGGGCCC U CCGACCA	AGUGGUC CUGAUGAG X CGAA IAGGGCC
4035	GGCCCUC C GACCACU	UGGAAGU CUGAUGAG X CGAA IUCGGAG
4039	CUCCGAC C ACUUCCA	CUGGAAG CUGAUGAG X CGAA IGUCGGA
4040	UCCGACC A CUUCCAG	COGGARG CUGAUGAG X CGAA IGUCGGA

Table 34

4042	CGACCAC U UCCAGGG	CCCUGGA CUGAUGAG X CGAA IUGGUCG
4045	CCACUUC C AGGGGAA	UUCCCCU CUGAUGAG X CGAA IAAGUGG
4046	CACUUCC A GGGGAAC	GUUCCCC CUGAUGAG X CGAA IGAAGUG
4054	GGGGAAC C UGCCAUG	CAUGGCA CUGAUGAG X CGAA IUUCCCC
4055	GGGAACC U GCCAUGC	GCAUGGC CUGAUGAG X CGAA IGUUCCC
4058	AACCUGC C AUGCCAG	CUGGCAU CUGAUGAG X CGAA ICAGGUU
4059	ACCUGCC A UGCCAGG	CCUGGCA CUGAUGAG X CGAA IGCAGGU
4063	GCCAUGC C AGGAACC	GGUUCCU CUGAUGAG X CGAA ICAUGGC
4064	CCAUGCC A GGAACCU	AGGUUCC CUGAUGAG X CGAA IGCAUGG
4070	CAGGAAC C UGUCCUA	UAGGACA CUGAUGAG X CGAA IUUCCUG
4071	AGGAACC U GUCCUAA	UUAGGAC CUGAUGAG X CGAA IGUUCCU
4075	ACCUGUC C UAAGGAA	UUCCUUA CUGAUGAG X CGAA IACAGGU
4076	CCUGUCC U AAGGAAC	GUUCCUU CUGAUGAG X CGAA IGACAGG
4084	AAGGAAC C UUCCUUC	GAAGGAA CUGAUGAG X CGAA IUUCCUU
4085	AGGAACC U UCCUUCC	GGAAGGA CUGAUGAG X CGAA IGUUCCU
4088	AACCUUC C UUCCUGC	GCAGGAA CUGAUGAG X CGAA IAAGGUU
4089	ACCUUCC U UCCUGCU	AGCAGGA CUGAUGAG X CGAA IGAAGGU
4092	UUCCUUC C UGCUUGA	UCAAGCA CUGAUGAG X CGAA IAAGGAA
4093	UCCUUCC U GCUUGAG	CUCAAGC CUGAUGAG X CGAA IGAAGGA
4096	UUCCUGC U UGAGUUC	GAACUCA CUGAUGAG X CGAA ICAGGAA
4104	UGAGUUC C CAGAUGG	CCAUCUG CUGAUGAG X CGAA IAACUCA
4105	GAGUUCC C AGAUGGC	GCCAUCU CUGAUGAG X CGAA IGAACUC
4106	AGUUCCC A GAUGGCU	AGCCAUC CUGAUGAG X CGAA IGGAACU
4113	AGAUGGC U GGAAGGG	CCCUUCC CUGAUGAG X CGAA ICCAUCU
4124	AGGGGUC C AGCCUCG	CGAGGCU CUGAUGAG X CGAA IACCCCU
4125	GGGGUCC A GCCUCGU	ACGAGGC CUGAUGAG X CGAA IGACCCC
4128	GUCCAGC C UCGUUGG	CCAACGA CUGAUGAG X CGAA ICUGGAC
4129	UCCAGCC U CGUUGGA	UCCAACG CUGAUGAG X CGAA IGCUGGA
4145	GAGGAAC A GCACUGG	CCAGUGC CUGAUGAG X CGAA IUUCCUC
4148	GAACAGC A CUGGGGA	UCCCCAG CUGAUGAG X CGAA ICUGUUC
4150	ACAGCAC U GGGGAGU	ACUCCCC CUGAUGAG X CGAA IUGCUGU
4159	GGGAGUC U UUGUGGA	UCCACAA CUGAUGAG X CGAA IACUCCC
4170	UGGAUUC U GAGGCCC	GGGCCUC CUGAUGAG X CGAA IAAUCCA
4176	CUGAGGC C CUGCCCA	UGGGCAG CUGAUGAG X CGAA ICCUCAG
4177	UGAGGCC C UGCCCAA	UUGGGCA CUGAUGAG X CGAA IGCCUCA
4178	GAGGCCC U GCCCAAU	AUUGGGC CUGAUGAG X CGAA IGGCCUC
4181	GCCCUGC C CAAUGAG	CUCAUUG CUGAUGAG X CGAA ICAGGGC
4182	CCCUGCC C AAUGAGA	UCUCAUU CUGAUGAG X CGAA IGCAGGG
4183	CCUGCCC A AUGAGAC	GUCUCAU CUGAUGAG X CGAA IGGCAGG
4191	AUGAGAC U CUAGGGU	ACCCUAG CUGAUGAG X CGAA IUCUCAU
4193	GAGACUC U AGGGUCC	GGACCCU CUGAUGAG X CGAA IAGUCUC
4200	UAGGGUC C AGUGGAU	AUCCACU CUGAUGAG X CGAA IACCCUA
4201	AGGGUCC A GUGGAUG	CAUCCAC CUGAUGAG X CGAA IGACCCU
4210	UGGAUGC C ACAGCCC	GGGCUGU CUGAUGAG X CGAA ICAUCCA
4211	GGAUGCC A CAGCCCA	UGGGCUG CUGAUGAG X CGAA IGCAUCC
4213	AUGCCAC A GCCCAGC	GCUGGGC CUGAUGAG X CGAA IUGGCAU
4216	CCACAGC C CAGCUUG	CAAGCUG CUGAUGAG X CGAA ICUGUGG

Table 34

4217	CACAGCC C AGCUUGG	CCAAGCU CUGAUGAG X CGAA IGCUGUG
4218	ACAGCCC A GCUUGGC	GCCAAGC CUGAUGAG X CGAA IGGCUGU
4221	GCCCAGC U UGGCCCU	AGGGCCA CUGAUGAG X CGAA ICUGGGC
4226	GCUUGGC C CUUUCCU	AGGAAAG CUGAUGAG X CGAA ICCAAGC
4227	CUUGGCC C UUUCCUU	AAGGAAA CUGAUGAG X CGAA IGCCAAG
4228	UUGGCCC U UUCCUUC	GAAGGAA CUGAUGAG X CGAA IGGCCAA
4232	CCCUUUC C UUCCAGA	UCUGGAA CUGAUGAG X CGAA IAAAGGG
4233	CCUUUCC U UCCAGAU	AUCUGGA CUGAUGAG X CGAA IGAAAGG
4236	UUCCUUC C AGAUCCU	AGGAUCU CUGAUGAG X CGAA IAAGGAA
4237	UCCUUCC A GAUCCUG	CAGGAUC CUGAUGAG X CGAA IGAAGGA
4242	CCAGAUC C UGGGUAC	GUACCCA CUGAUGAG X CGAA IAUCUGG
4243	CAGAUCC U GGGUACU	AGUACCC CUGAUGAG X CGAA IGAUCUG
4250	UGGGUAC U GAAAGCC	GGCUUUC CUGAUGAG X CGAA IUACCCA
4257	UGAAAGC C UUAGGGA	UCCCUAA CUGAUGAG X CGAA ICUUUCA
4258	GAAAGCC U UAGGGAA	UUCCCUA CUGAUGAG X CGAA IGCUUUC
4268	GGGAAGC U GGCCUGA	UCAGGCC CUGAUGAG X CGAA ICUUCCC
4272	AGCUGGC C UGAGAGG	CCUCUCA CUGAUGAG X CGAA ICCAGCU
4273	GCUGGCC U GAGAGGG	CCCUCUC CUGAUGAG X CGAA IGCCAGC
4289	AAGCGGC C CUAAGGG	CCCUUAG CUGAUGAG X CGAA ICCGCUU
4290	AGCGGCC C UAAGGGA	UCCCUUA CUGAUGAG X CGAA IGCCGCU
4291	GCGGCCC U AAGGGAG	CUCCCUU CUGAUGAG X CGAA IGGCCGC
4303	GAGUGUC U AAGAACA	UGUUCUU CUGAUGAG X CGAA IACACUC
4310	UAAGAAC A AAAGCGA	UCGCUUU CUGAUGAG X CGAA IUUCUUA
4319	AAGCGAC C CAUUCAG	CUGAAUG CUGAUGAG X CGAA IUCGCUU
4320	AGCGACC C AUUCAGA	UCUGAAU CUGAUGAG X CGAA IGUCGCU
4321	GCGACCC A UUCAGAG	CUCUGAA CUGAUGAG X CGAA IGGUCGC
4325	CCCAUUC A GAGACUG	CAGUCUC CUGAUGAG X CGAA IAAUGGG
4331	CAGAGAC U GUCCCUG	CAGGGAC CUGAUGAG X CGAA IUCUCUG
4335	GACUGUC C CUGAAAC	GUUUCAG CUGAUGAG X CGAA IACAGUC
4336	ACUGUCC C UGAAACC	GGUUUCA CUGAUGAG X CGAA IGACAGU
4337	CUGUCCC U GAAACCU	AGGUUUC CUGAUGAG X CGAA IGGACAG
4343	CUGAAAC C UAGUACU	AGUACUA CUGAUGAG X CGAA IUUUCAG
4344	UGAAACC U AGUACUG	CAGUACU CUGAUGAG X CGAA IGUUUCA
4350	CUAGUAC U GCCCCCC	GGGGGGC CUGAUGAG X CGAA IUACUAG
4353	GUACUGC C CCCCAUG	CAUGGGG CUGAUGAG X CGAA ICAGUAC
4354	UACUGCC C CCCAUGA	UCAUGGG CUGAUGAG X CGAA IGCAGUA
4355	ACUGCCC C CCAUGAG	CUCAUGG CUGAUGAG X CGAA IGGCAGU
4356	CUGCCCC C CAUGAGG	CCUCAUG CUGAUGAG X CGAA IGGGCAG
4357	UGCCCCC C AUGAGGA	UCCUCAU CUGAUGAG X CGAA IGGGGCA
4358	GCCCCCC A UGAGGAA	UUCCUCA CUGAUGAG X CGAA IGGGGGC
4371	AAGGAAC A GCAAUGG	CCAUUGC CUGAUGAG X CGAA IUUCCUU
4374	GAACAGC A AUGGUGU	ACACCAU CUGAUGAG X CGAA ICUGUUC
4383	UGGUGUC A GUAUCCA	UGGAUAC CUGAUGAG X CGAA IACACCA
4389	CAGUAUC C AGGCUUU	AAAGCCU CUGAUGAG X CGAA IAUACUG
4390	AGUAUCC A GGCUUUG	CAAAGCC CUGAUGAG X CGAA IGAUACU
4394	UCCAGGC U UUGUACA	UGUACAA CUGAUGAG X CGAA ICCUGGA
4401	UUUGUAC A GAGUGCU	AGCACUC CUGAUGAG X CGAA IUACAAA

Table 34

4408	AGAGUGC U UUUCUGU	ACAGAAA CUGAUGAG X CGAA ICACUCU
4413	GCUUUUC U GUUUAGU	ACUAAAC CUGAUGAG X CGAA IAAAAGC
4427	UUUUUAC U UUUUUUG	CAAAAA CUGAUGAG X CGAA IUAAAAA
4464	UAAAGAC C CAGGGGG	CCCCCUG CUGAUGAG X CGAA IUCUUUA
4465	AAAGACC C AGGGGGA	UCCCCCU CUGAUGAG X CGAA IGUCUUU
4466	AAGACCC A GGGGGAG	CUCCCCC CUGAUGAG X CGAA IGGUCUU

Seq Accession No. = HSERB2R (Human c-erb-B-2 mRNA; 4473 bp)
Core Sequence = CUGAUGAG X CGAA (X = GCCGAAAGGC or other stem II)

Table 35

Table 35: HBV Strains and Accession numbers

Accession	Name
Number	
AF100308.1	AF100308 Hepatitis B virus strain 2-18, complete
AB026815.1	AB026815 Hepatitis B virus DNA, complete genome,
AB033559.1	AB033559 Hepatitis B virus DNA, complete genome,
AB033558.1	AB033558 Hepatitis B virus DNA, complete genome,
AB033557.1	AB033557 Hepatitis B virus DNA, complete genome,
AB033556.1	AB033556 Hepatitis B virus DNA, complete genome,
AB033555.1	AB033555 Hepatitis B virus DNA, complete genome,
AB033554.1	AB033554 Hepatitis B virus DNA, complete genome,
AB033553.1	AB033553 Hepatitis B virus DNA, complete genome,
AB033552.1	AB033552 Hepatitis B virus DNA, complete genome,
AB033551.1	AB033551 Hepatitis B virus DNA, complete genome,
AB033550.1	AB033550 Hepatitis B virus DNA, complete genome
AF143308.1	AF143308 Hepatitis B virus clone WB1254, complete
AF143307.1	AF143307 Hepatitis B virus clone RM518, complete
AF143306.1	AF143306 Hepatitis B virus clone RM517, complete
AF143305.1	AF143305 Hepatitis B virus clone RM501, complete
AF143304.1	AF143304 Hepatitis B virus clone HD319, complete
AF143303.1	AF143303 Hepatitis B virus clone HD1406, complete
AF143302.1	AF143302 Hepatitis B virus clone HD1402, complete
AF143301.1	AF143301 Hepatitis B virus clone BW1903, complete
AF143300.1	AF143300 Hepatitis B virus clone 7832-G4, complete
AF143299.1	AF143299 Hepatitis B virus clone 7744-G9, complete
AF143298.1	AF143298 Hepatitis B virus clone 7720-G8, complete
AB026814.1	AB026814 Hepatitis B virus DNA, complete genome,
AB026813.1	AB026813 Hepatitis B virus DNA, complete genome,
AB026812.1	AB026812 Hepatitis B virus DNA, complete genome,
AB026811.1	AB026811 Hepatitis B virus DNA, complete genome,
AJ131956.1	HBV131956 Hepatitis B virus complete genome,
AF151735.1	AF151735 Hepatitis B virus, complete genome
AF090842.1	AF090842 Hepatitis B virus strain G5.27295, complete
AF090841.1	AF090841 Hepatitis B virus strain G4.27241, complete
AF090840.1	AF090840 Hepatitis B virus strain G3.27270, complete
AF090839.1	AF090839 Hepatitis B virus strain G2.27246, complete
AF090838.1	AF090838 Hepatitis B virus strain P1.27239, complete
Y18858.1	HBV18858 Hepatitis B virus complete genome, isolate
Y18857.1	HBV18857 Hepatitis B virus complete genome, isolate
D12980.1	HPBCG Hepatitis B virus subtype adr(SRADR) DNA,
Y18856.1	HBV18856 Hepatitis B virus complete genome, isolate
Y18855.1	HBV18855 Hepatitis B virus complete genome, isolate
AJ131133.1	HBV131133 Hepatitis B virus, complete genome, strain
X80925.1	HBVP6PCXX Hepatitis B virus (patient 6) complete
X80926.1	HBVP5PCXX Hepatitis B virus (patient 5) complete
X80924.1	HBVP4PCXX Hepatitis B virus (patient 4) complete
AF100309.1	Hepatitis B virus strain 56, complete genome

Table 35

AF068756.1 AF068756 Hepatitis B virus, complete geno AF043593.1 AF043593 Hepatitis B virus isolate 6/89, com Y07587.1 HEVAYWGEN Hepatitis B virus, complete gen D28880.1 D28880 Hepatitis B virus DNA, complete genome, X98076.1 HEVDEFVP3 Hepatitis B virus complete genome,	mplete ome strain
Y07587.1 HBVAYWGEN Hepatitis B virus, complete general D28880.1 D28880 Hepatitis B virus DNA, complete genome.	ome strain
D28880.1 D28880 Hepatitis B virus DNA, complete genome,	strain
	strain
VACABLE 1 PRODEFUES Henatitis B virus complete genome	
X98075.1 HBVDEFVP2 Hepatitis B virus complete genome	
X98074.1 HBVDEFVP1 Hepatitis B virus complete genome	
X98077.1 HBVCGWITY Hepatitis B virus complete genome, w	ild type
X98072.1 HBVCGINSC Hepatitis B virus complete genome	
X98073.1 HBVCGINCX Hepatitis B virus complete genome	
U95551.1 U95551 Hepatitis B virus subtype ayw, complete	e genome
D23684.1 HPBC6T588 Hepatitis B virus (C6-TKB588) complet	te genome
D23683.1 HPBC5HKO2 Hepatitis B virus (C5-HBVKO2) complet	te genome
D23682.1 HPBB5HKO1 Hepatitis B virus (B5-HBVKO1) complet	te genome
D23681.1 HPBC4HST2 Hepatitis B virus (C4-HBVST2) complete	te genome
D23680.1 HPBB4HST1 Hepatitis B virus (B4-HBVST1) comple	
D00331.1 HPBADW3 Hepatitis B virus genome, complete	
D00330.1 HPBADW2 Hepatitis B virus genome, complete	
DS0489.1 HPBAllA Hepatitis B virus DNA, complete ge	
D23679.1 HPBA3HMS2 Hepatitis B virus (A3-HBVMS2) comple	te genome
D23678.1 HPBA2HYS2 Hepatitis B virus (A2-HBVYS2) comple	te genome
D23677.1 HPBA1HKK2 Hepatitis B virus (A1-HBVKK2) comple	
D16665.1 HPBADRM Hepatitis B virus DNA, complete ge	
D00329.1 HPBADW1 Hepatitis B virus (HBV) genome, comple	
X97851.1 HBVP6CSX Hepatitis B virus (patient 6) complet	
X97850.1 HBVP4CSX Hepatitis B virus (patient 4) complete	te genome
X97849.1 HBVP3CSX Hepatitis B virus (patient 3) complet	
X97848.1 HBVP2CSX Hepatitis B virus (patient 2) complete	te genome
X51970.1 HVHEPB Hepatitis B virus (HBV 991) complete	genome
M38636.1 HPBCGADR Hepatitis B virus, subtype adr, comple	
X59795.1 HBVAYWMCG Hepatitis B virus (ayw subtype m	
M38454.1 HPBADR1CG Hepatitis B virus , complete ge	enome ot a
M32138.1 HPBHBVAA Hepatitis B virus variant HBV-alphal,	, complete
J02203.1 HPBAYW Human hepatitis B virus (subtype ayw),	comprete
M12906.1 HPBADRA Hepatitis B virus subtype adr, comple	te genome
M54923.1 HPBADWZ Hepatitis B virus (subtype adw), compl	ere genome
L27106.1 HPBMUT Hepatitis B virus mutant complete o	genome

Table 36

Table 36: HBV Substrate Sequence

NT Position*	Substrate	Seq ID
82	CUAUCGUCCCCUUCUUCAUC	1
101	CUACCGUUCCGGCC	2
159	CUUCUCAUCU	3
184	CUUCCCUUCACCAC	4
269	GACUCUCAGAAUGUCAACGAC	5
381	CUGUAGGCAUAAAUGGUCUG	6
401	GUUCACCAGCACCAUGCAACUUUUU	7
424	UUUCACGUCUGCCUAAUCAUC	8
524	AUUUGGAGCUUC	9
562	CUGACUUCUUUCCUUCUAUUC	10
649	CUCACCAUACCGCACUCA	11
667	GGCAAGCUAUUCUGUG	12
717	GGAAGUAAUUUGGAAGAC	13
758	CAGCUAUGUCAAUGUUAA	14
783	CUAAAAUCGGCCUAAAAUCAGAC	15
812	CAUUUCCUGUCUCACUUUUGGAAGAG	16
887	UCCUGCUUACAGAC	17
922	CAACACUUCCGGAAACUACUGUUGUUAG	18
989	CUCGCCUCGCAGACGAAGGUCUC	19
1009	CAAUCGCCGCGUCGCAGAAG	20
1031	AUCUCAAUCUCGGGAAUCUCAA	21
1052	AUGUUAGUAUCCCUUGGACUC	22
1072	CAUAAGGUGGGAAACUUUACUG	23
1109	CUGUACCUAUUCUUUAAAUCC	24
1127	CUGAGUGGCAAACUCCC	25
1271	CCAAAUAUCUGCCCUUGGACAA	26
1297	AUUAAACCAUAUUAUCCUGAACA	27
1319	AUGCAGUUAAUCAUUACUUCAAAACUA	28
1340	AAACUAGGCAUUA	29
1370	AGGCGGGCAUUCUAUAUAAGAGAG	30
1393	GAAACUACGCGCAGCGCCUCAUUUUGU	31
1412	CAUUUUGUGGGUCACCAUA	32
1441	CAAGAGCUACAGCAUGGG	33

LOCUS HPBADR1CG 3221 bp DNA circular VRL

06-MAR-1995

DEFINITION Hepatitis B virus , complete genome.

ACCESSION M38454

^{*}The nucleotide number referred to in that table is the position of the 5' end of the oligo in this sequence.

Table 37

Table 37: Human HBV Hammerhead Ribozyme and Target Sequence

Pos	Substrate	Seq ID	Ribozyme	Rz Seq II
	CCACCACT T TCCACCAA	34	UUGGUGGA CUGAUGAG X CGAA AGUGGUGG	2543
	CACCACTT T CCACCAAA	35	UUUGGUGG CUGAUGAG X CGAA AAGUGGUG	2544
	ACCACTTT C CACCAAAC	36	GUUUGGUG CUGAUGAG X CGAA AAAGUGGU	2545
	ACCAAACT C TTCAAGAT	37	AUCUUGAA CUGAUGAG X CGAA AGUUUGGU	2546
	CAAACTCT T CAAGATCC	38	GGAUCUUG CUGAUGAG X CGAA AGAGUUUG	2547
	AAACTCT C AAGATCC	39	GGGAUCUU CUGAUGAG X CGAA AAGAGUUU	2548
		40	GACUCUGG CUGAUGAG X CGAA AUCUUGAA	2549
	TTCAAGAT C CCAGAGTC CCCAGAGT C AGGGCCCT	41	AGGGCCCU CUGAUGAG X CGAA ACUCUGGG	2550
		42	CAGGAAAG CUGAUGAG X CGAA ACAGGGCC	2551
	GGCCCTGT A CTTTCCTG	43	CAGCAGGA CUGAUGAG X CGAA AGUACAGG	2552
	CCTGTACT T TCCTGCTG	44	CCAGCAGG CUGAUGAG X CGAA AAGUACAG	2553
57	CTGTACTT T CCTGCTGG	45	ACCAGCAG CUGAUGAG X CGAA AAAGUACA	2554
58	TGTACTTT C CTGCTGGT	46	CUGAACUG CUGAUGAG X CGAA AGCCACCA	2555
71	TGGTGGCT C CAGTTCAG	47	UGUUCCUG CUGAUGAG X CGAA ACUGGAGC	2556
76	GCTCCAGT T CAGGAACA	4.7	CUGUUCCU CUGAUGAG X CGAA AACUGGAG	2557
77	CTCCAGTT C AGGAACAG	49	AGUAUUCU CUGAUGAG X CGAA AGCAGGGC	2558
97	GCCCTGCT C AGAATACT	50	AGAGACAG CUGAUGAG X CGAA AUUCUGAG	2559
103	CTCAGAAT A CTGTCTCT	51	AUGGCAGA CUGAUGAG X CGAA ACAGUAUU	2560
108	AATACTGT C TCTGCCAT	52	AUAUGGCA CUGAUGAG X CGAA AGACAGUA	2561
110	TACTGTCT C TGCCATAT	52	AUUGACGA CUGAUGAG X CGAA AUGGCAGA	2562
117	TCTGCCAT A TCGTCAAT	54	AGAUUGAC CUGAUGAG X CGAA AUAUGGCA	2563
119	TGCCATAT C GTCAATCT	55	AUAAGAUU CUGAUGAG X CGAA ACGAUAUG	2564
122	CATATOGT C AATOTTAT	56	UUCGAUAA CUGAUGAG X CGAA AUUGACGA	2565
126	TCGTCAAT C TTATCGAA	57	UCUUCGAU CUGAUGAG X CGAA AGAUUGAC	2566
128	GTCAATCT T ATCGAAGA	58	GUCUUCGA CUGAUGAG X CGAA AAGAUUGA	2567
129	TCAATCTT A TCGAAGAC	59	CAGUCUUC CUGAUGAG X CGAA AUAAGAUU	2568
131	AATCITAT C GAAGACTG	60	AUGUUCGG CUGAUGAG X CGAA ACAGGGUC	2569
150	GACCCTGT A CCGAACAT	61	CCUGAUGC CUGAUGAG X CGAA AUGUUCUC	2570
168	GAGAACAT C GCATCAGG	62	GGAGUCCU CUGAUGAG X CGAA AUGCGAUG	2571
173	CATCGCAT C AGGACTCC	63	GGUCCUAG CUGAUGAG X CGAA AGUCCUGA	2572
180	TCAGGACT C CTAGGACC		AGGGGUCC CUGAUGAG X CGAA AGGAGUCC	2573
183	GGACTCCT A GGACCCCT	64	UGUAACAC CUGAUGAG X CGAA AGCAGGGG	2574
195	CCCCTGCT C GTGTTACA	66	CCGCCUGU CUGAUGAG X CGAA ACACGAGC	2575
200	GCTCGTGT T ACAGGCGG	67	CCCGCCUG CUGAUGAG X CGAA AACACGAG	2576
201	CTCGTGTT A CAGGCGGG		ACAAGAAA CUGAUGAG X CGAA ACCCCGCC	2577
212	GGCGGGGT T TTTCTTGT	68	AACAAGAA CUGAUGAG X CGAA AACCCCGC	2578
213	GCGGGGTT T TTCTTGTT	69 70	CAACAAGA CUGAUGAG X CGAA AAACCCCG	2579
214	CGGGGTTT T TCTTGTTG	70	UCAACAAG CUGAUGAG X CGAA AAAACCCC	2580
215	GGGGTTTT T CTTGTTGA		GUCAACAA CUGAUGAG X CGAA AAAAACCC	2581
216	GGGTTTTT C TTGTTGAC	72	UUGUCAAC CUGAUGAG X CGAA AGAAAAAC	2582
218	GTTTTTCT T GTTGACAA		UUUUUGUC CUGAUGAG X CGAA ACAAGAAA	2583
221	TTTCTTGT T GACAAAAA	74	AUUGUGAG CUGAUGAG X CGAA AUUUUUGU	2584
231	ACAAAAAT C CTCACAAT	75	GGUAUUGU CUGAUGAG X CGAA AGGAUUUU	2589
234	AAAATCCT C ACAATACC	76	CUCUGUGG CUGAUGAG X CGAA AUGUGUGAG	2586
240	CTCACAAT A CCACAGAG	77	CUCUGUGG CUGAUGAG X CGAA AUUGUGAG CGAGUCUA CUGAUGAG X CGAA ACUCUGUG	2587
250	CACAGAGT C TAGACTCG	78	CACGAGUC CUGAUGAG X CGAA ACCUCUG CACGAGUC CUGAUGAG X CGAA AGACUCUG	2588
252	CAGAGTCT A GACTCGTG	79	UCCACCAC CUGAUGAG X CGAA AGACUCUG UCCACCAC CUGAUGAG X CGAA AGUCUAGA	2589
257	TCTAGACT C GTGGTGGA	80	AUUGAGAG CUGAUGAG X CGAA AGUCCACC	2590
268	GGTGGACT T CTCTCAAT	81	AUUGAGAG CUGAUGAG A CGAM AGUCCACC	

Table 37

260	GTGGACTT C TCTCAATT	82	AAUUGAGA CUGAUGAG X CGAA AAGUCCAC	2591
269	GGACTTCT C TCAATTTT	83	AAAAUUGA CUGAUGAG X CGAA AGAAGUCC	2592
273	ACTICICI C AATTITCT	84	AGAAAAUU CUGAUGAG X CGAA AGAGAAGU	2593
273	CTCTCAAT T TTCTAGGG	85	CCCUAGAA CUGAUGAG X CGAA AUUGAGAG	2594
	TCTCAATT T TCTAGGGG	86	CCCCUAGA CUGAUGAG X CGAA AAUUGAGA	2595
278	CTCAATT T CTAGGGG	87	CCCCCUAG CUGAUGAG X CGAA AAAUUGAG	2596
279	TCAATTT C TAGGGGGA	88	UCCCCCUA CUGAUGAG X CGAA AAAAUUGA	2597
280	AATTTTCT A GGGGGAAC	89	GUUCCCCC CUGAUGAG X CGAA AGAAAAUU	2598
	CCGTGTGT C TTGGCCAA	90	UUGGCCAA CUGAUGAG X CGAA ACACACGG	2599
301	GTGTGTCT T GGCCAAAA	91	UUUUGGCC CUGAUGAG X CGAA AGACACAC	2600
303	GCCAAAAT T CGCAGTCC	92	GGACUGCG CUGAUGAG X CGAA AUUUUGGC	2601
313	CCAAAATT C GCAGTCCC	93	GGGACUGC CUGAUGAG X CGAA AAUUUUGG	2602
314	TTCGCAGT C CCAAATCT	94	AGAUUUGG CUGAUGAG X CGAA ACUGCGAA	2603
320	TCCCAAAT C TCCAGTCA	95	UGACUGGA CUGAUGAG X CGAA AUUUGGGA	2604
327	CCAAATCT C CAGTCACT	96	AGUGACUG CUGAUGAG X CGAA AGAUUUGG	2605
329	TCTCCAGT C ACTCACCA	97	UGGUGAGU CUGAUGAG X CGAA ACUGGAGA	2606
334		98	AGGUUGGU CUGAUGAG X CGAA AGUGACUG	2607
338	CAGTCACT C ACCAACCT CAACCTGT T GTCCTCCA	99	UGGAGGAC CUGAUGAG X CGAA ACAGGUUG	2608
349		100	AAUUGGAG CUGAUGAG X CGAA ACAACAGG	2609
352	CCTGTTGT C CTCCAATT	101	ACAAAUUG CUGAUGAG X CGAA AGGACAAC	2610
355	GTTGTCCT C CAATTTGT	102	CCAGGACA CUGAUGAG X CGAA AUUGGAGG	2611
360	CCTCCAAT T TGTCCTGG	103	ACCAGGAC CUGAUGAG X CGAA AAUUGGAG	2612
361	CTCCAATT T GTCCTGGT	103	AUAACCAG CUGAUGAG X CGAA ACAAAUUG	2613
364	CAATTIGT C CTGGTTAT GTCCTGGT T ATCGCTGG	105	CCAGCGAU CUGAUGAG X CGAA ACCAGGAC	2614
370	TCCTGGT A TCGCTGGA	106	UCCAGCGA CUGAUGAG X CGAA AACCAGGA	2615
371	CTGGTTAT C GCTGGATG	107	CAUCCAGC CUGAUGAG X CGAA AUAACCAG	2616
373	GGATGTGT C TGCGGCGT	108	ACGCCGCA CUGAUGAG X CGAA ACACAUCC	2617
385	TGCGGCGT T TTATCATC	109	GAUGAUAA CUGAUGAG X CGAA ACGCCGCA	2618
394	GCGGCGTT T TATCATCT	110	AGAUGAUA CUGAUGAG X CGAA AACGCCGC	2619
	CGGCGTT T TATCATCT	111	AAGAUGAU CUGAUGAG X CGAA AAACGCCG	2620
396	GGCGTTT A TCATCTTC	112	GAAGAUGA CUGAUGAG X CGAA AAAACGCC	2621
397	CGTTTTAT C ATCTTCCT	113	AGGAAGAU CUGAUGAG X CGAA AUAAAACG	2622
402	TTTATCAT C TTCCTCTG	114	CAGAGGAA CUGAUGAG X CGAA AUGAUAAA	2623
404	TATCATCT T CCTCTGCA	115	UGCAGAGG CUGAUGAG X CGAA AGAUGAUA	2624
405	ATCATCTT C CTCTGCAT	116	AUGCAGAG CUGAUGAG X CGAA AAGAUGAU	2625
408	ATCTTCCT C TGCATCCT	117	AGGAUGCA CUGAUGAG X CGAA AGGAAGAU	2626
414	CTCTGCAT C CTGCTGCT	118	AGCAGCAG CUGAUGAG X CGAA AUGCAGAG	2627
423	CTGCTGCT A TGCCTCAT	119	AUGAGGCA CUGAUGAG X CGAA AGCAGCAG	2628
429	CTATGCCT C ATCTTCTT	120	AAGAAGAU CUGAUGAG X CGAA AGGCAUAG	2629
432	TGCCTCAT C TTCTTGTT	121	AACAAGAA CUGAUGAG X CGAA AUGAGGCA	2630
434	CCTCATCT T CTTGTTGG	122	CCAACAAG CUGAUGAG X CGAA AGAUGAGG	2631
435	CTCATCTT C TTGTTGGT	123	ACCAACAA CUGAUGAG X CGAA AAGAUGAG	2632
437	CATCTTCT T GTTGGTTC	124	GAACCAAC CUGAUGAG X CGAA AGAAGAUG	2633
440	CTTCTTGT T GGTTCTTC	125	GAAGAACC CUGAUGAG X CGAA ACAAGAAG	2634
444	TTGTTGGT T CTTCTGGA	126	UCCAGAAG CUGAUGAG X CGAA ACCAACAA	2635
445	TGTTGGTT C TTCTGGAC	127	GUCCAGAA CUGAUGAG X CGAA AACCAACA	2636
447	TTGGTTCT T CTGGACTA	128	UAGUCCAG CUGAUGAG X CGAA AGAACCAA	2637
448	TGGTTCTT C TGGACTAT	129	AUAGUCCA CUGAUGAG X CGAA AAGAACCA	2638
455	TCTGGACT A TCAAGGTA	130	UACCUUGA CUGAUGAG X CGAA AGUCCAGA	2639
457	TGGACTAT C AAGGTATG	131	CAUACCUU CUGAUGAG X CGAA AUAGUCCA	2640
463	ATCAAGGT A TGTTGCCC	132	GGGCAACA CUGAUGAG X CGAA ACCUUGAU	2641
	1 2121002 11 12210000	<u> </u>		

Table 3/

467	AGGTATGT T GCCCGTTT	133	AAACGGGC CUGAUGAG X CGAA ACAUACCU	2642
474	TTGCCCGT T TGTCCTCT	134	AGAGGACA CUGAUGAG X CGAA ACGGGCAA	2643
475	TGCCCGTT T GTCCTCTA	135	UAGAGGAC CUGAUGAG X CGAA AACGGGCA	2644
478	CCGTTTGT C CTCTAATT	136	AAUUAGAG CUGAUGAG X CGAA ACAAACGG	2645
481	TTTGTCCT C TAATTCCA	137	UGGAAUUA CUGAUGAG X CGAA AGGACAAA	2646
483	TGTCCTCT A ATTCCAGG	138	CCUGGAAU CUGAUGAG X CGAA AGAGGACA	2647
486	CCTCTAAT T CCAGGATC	139	GAUCCUGG CUGAUGAG X CGAA AUUAGAGG	2648
487	CTCTAATT C CAGGATCA	140	UGAUCCUG CUGAUGAG X CGAA AAUUAGAG	2649
494	TCCAGGAT C ATCAACAA	141	UUGUUGAU CUGAUGAG X CGAA AUCCUGGA	2650
497	AGGATCAT C AACAACCA	142	UGGUUGUU CUGAUGAG X CGAA AUGAUCCU	2651
535	GCACAACT C CTGCTCAA	143	UUGAGCAG CUGAUGAG X CGAA AGUUGUGC	2652
541	CTCCTGCT C AAGGAACC	144	GGUUCCUU CUGAUGAG X CGAA AGCAGGAG	2653
551	AGGAACCT C TATGTTTC	145	GAAACAUA CUGAUGAG X CGAA AGGUUCCU	2654
553	GAACCTCT A TGTTTCCC	146	GGGAAACA CUGAUGAG X CGAA AGAGGUUC	2655
557	CTCTATGT T TCCCTCAT	147	AUGAGGGA CUGAUGAG X CGAA ACAUAGAG	2656
558	TCTATGTT T CCCTCATG	148	CAUGAGGG CUGAUGAG X CGAA AACAUAGA	2657
559	CTATGTTT C CCTCATGT	149	ACAUGAGG CUGAUGAG X CGAA AAACAUAG	2658
563	GTTTCCCT C ATGTTGCT	150	AGCAACAU CUGAUGAG X CGAA AGGGAAAC	2659
568	CCTCATGT T GCTGTACA	151	UGUACAGC CUGAUGAG X CGAA ACAUGAGG	2660
574	GTTGCTGT A CAAAACCT	152	AGGUUUUG CUGAUGAG X CGAA ACAGCAAC	2661
583	CAAAACCT A CGGACGGA	153	UCCGUCCG CUGAUGAG X CGAA AGGUUUUG	2662
604	GCACCTGT A TTCCCATC	154	GAUGGGAA CUGAUGAG X CGAA ACAGGUGC	2663
606	ACCTGTAT T CCCATCCC	155	GGGAUGGG CUGAUGAG X CGAA AUACAGGU	2664
607	CCTGTATT C CCATCCCA	156	UGGGAUGG CUGAUGAG X CGAA AAUACAGG	2665
612	ATTCCCAT C CCATCATC	157	GAUGAUGG CUGAUGAG X CGAA AUGGGAAU	2666
617	CATCCCAT C ATCTTGGG	158	CCCAAGAU CUGAUGAG X CGAA AUGGGAUG	2667
620	CCCATCAT C TTGGGCTT	159	AAGCCCAA CUGAUGAG X CGAA AUGAUGGG	2668
622	CATCATCT T GGGCTTTC	160	GAAAGCCC CUGAUGAG X CGAA AGAUGAUG	2669
628	CTTGGGCT T TCGCAAAA	161	UUUUGCGA CUGAUGAG X CGAA AGCCCAAG	2670
629	TTGGGCTT T CGCAAAAT	162	AUJUUGOG CUGAUGAG X OGAA AAGCCCAA	2671
630	TGGGCTTT C GCAAAATA	163	UAUUUUGC CUGAUGAG X CGAA AAAGCCCA	2672
638	CGCAAAAT A CCTATGGG	164	CCCAUAGG CUGAUGAG X CGAA AUUUUGCG	2673
642	AAATACCT A TGGGAGTG	165	CACUCCCA CUGAUGAG X'CGAA AGGUAUUU	2674
656	GTGGGCCT C AGTCCGTT	166	AACGGACU CUGAUGAG X CGAA AGGCCCAC	2675
660	GCCTCAGT C CGTTTCTC	167	GAGAAACG CUGAUGAG X CGAA ACUGAGGC	2676
664	CAGTCCGT T TCTCTTGG	168	CCAAGAGA CUGAUGAG X CGAA ACGGACUG	2677
665	AGTCCGTT T CTCTTGGC	169	GCCAAGAG CUGAUGAG X CGAA AACGGACU	2678
666	GTCCGTTT C TCTTGGCT	170	AGCCAAGA CUGAUGAG X CGAA AAACGGAC	2679
668	CCGTTTCT C TTGGCTCA	171	UGAGCCAA CUGAUGAG X CGAA AGAAACGG	2680
670	GTTTCTCT T GGCTCAGT	172	ACUGAGCC CUGAUGAG X CGAA AGAGAAAC	2681
675	TCTTGGCT C AGTTTACT	173	AGUAAACU CUGAUGAG X CGAA AGCCAAGA	2682
679	GGCTCAGT T TACTAGTG	174	CACUAGUA CUGAUGAG X CGAA ACUGAGCC	2683
680	GCTCAGTT T ACTAGTGC	175	GCACUAGU CUGAUGAG X CGAA AACUGAGC	2684
681	CTCAGTTT A CTAGTGCC	176	GGCACUAG CUGAUGAG X CGAA AAACUGAG	2685
684	AGTTTACT A GTGCCATT	177	AAUGGCAC CUGAUGAG X CGAA AGUAAACU	2686
692	AGTGCCAT T TGTTCAGT	178	ACUGAACA CUGAUGAG X CGAA AUGGCACU	2687
693	GTGCCATT T GTTCAGTG	179	CACUGAAC CUGAUGAG X CGAA AAUGGCAC	2688
696	CCATTTGT T CAGTGGTT	180	AACCACUG CUGAUGAG X CGAA ACAAAUGG	2689
697	CATTTGTT C AGTGGTTC	181	GAACCACU CUGAUGAG X CGAA AACAAAUG	2690
704	TCAGTGGT T CGTAGGGC	182	GCCCUACG CUGAUGAG X CGAA ACCACUGA	2691
			AGCCCUAC CUGAUGAG X CGAA AACCACUG	2692

Table 37

			GAAAGCCC CUGAUGAG X CGAA ACGAACCA	2693
708	TGGTTCGT A GGGCTTTC	184	GUGGGGGA CUGAUGAG X CGAA ACCAACCA GUGGGGGA CUGAUGAG X CGAA AGCCCUAC	2694
714	GTAGGGCT T TCCCCCAC	185	AGUGGGGG CUGAUGAG X CGAA AGCCCUAC	2695
715	TAGGGCTT T CCCCCACT	186		2696
716	AGGGCTTT C CCCCACTG	187	CAGUGGGG CUGAUGAG X CGAA AAAGCCCU	2697
726	CCCACTGT C TGGCTTTC	188	GAAAGCCA CUGAUGAG X CGAA ACAGUGGG	2698
732	GTCTGGCT T TCAGTTAT	189	AUAACUGA CUGAUGAG X CGAA AGCCAGAC	2699
733	TCTGGCTT T CAGTTATA	190	UAUAACUG CUGAUGAG X CGAA AAGCCAGA	
734	CTGGCTTT C AGTTATAT	191	AUAUAACU CUGAUGAG X CGAA AAAGCCAG	2700
738	CTTTCAGT T ATATGGAT	192	AUCCAUAU CUGAUGAG X CGAA ACUGAAAG	
739	TTTCAGTT A TATGGATG	193	CAUCCAUA CUGAUGAG X CGAA AACUGAAA	2702
741	TCAGTTAT A TGGATGAT	194	AUCAUCCA CUGAUGAG X CGAA AUAACUGA	2703
755	GATGTGGT T TTGGGGGC	195	GCCCCCAA CUGAUGAG X CGAA ACCACAUC	
756	ATGTGGTT T TGGGGGCC	196	GGCCCCCA CUGAUGAG X CGAA AACCACAU	2705
757	TGTGGTTT T GGGGGCCA	197	UGGCCCCC CUGAUGAG X CGAA AAACCACA	2706
769	GGCCAAGT C TGTACAAC	198	GUUGUACA CUGAUGAG X CGAA ACUUGGCC	2707
773	AAGTCTGT A CAACATCT	199	AGAUGUUG CUGAUGAG X CGAA ACAGACUU	2708
780	TACAACAT C TTGAGTCC	200	GGACUCAA CUGAUGAG X CGAA AUGUUGUA	2709
782	CAACATCT T GAGTCCCT	201	AGGGACUC CUGAUGAG X CGAA AGAUGUUG	2710
787	TCTTGAGT C CCTTTATG	202	CAUAAAGG CUGAUGAG X CGAA ACUCAAGA	2711
791	GAGTCCCT T TATGCCGC	203	GCGGCAUA CUGAUGAG X CGAA AGGGACUC	2712
792	AGTCCCTT T ATGCCGCT	204	AGCGGCAU CUGAUGAG X CGAA AAGGGACU	2713
793	GTCCCTTT A TGCCGCTG	205	CAGCGGCA CUGAUGAG X CGAA AAAGGGAC	2714
803 -	GCCGCTGT T ACCAATTT	206	AAAUUGGU CUGAUGAG X CGAA ACAGCGGC	2715
804	CCGCTGTT A CCAATTTT	207	AAAAUUGG CUGAUGAG X CGAA AACAGCGG	2716
810	TTACCAAT T TTCTTTTG	208	CAAAAGAA CUGAUGAG X CGAA AUUGGUAA	2717
811	TACCAATT T TCTTTTGT	209	ACAAAAGA CUGAUGAG X CGAA AAUUGGUA	2718
812	ACCAATTT T CTTTTGTC	210	GACAAAAG CUGAUGAG X CGAA AAAUUGGU	2719
813	CCAATTTT C TTTTGTCT	211	AGACAAAA CUGAUGAG X CGAA AAAAUUGG	2720
815	AATTITCT T TIGICTIT	212	AAAGACAA CUGAUGAG X CGAA AGAAAAUU	2721
816	ATTTTCTT T TGTCTTTG	213	CAAAGACA CUGAUGAG X CGAA AAGAAAAU	2722
817	TTTTCTTT T GTCTTTGG	214	CCAAAGAC CUGAUGAG X CGAA AAAGAAAA	2723
820	TCTTTTGT C TTTGGGTA	215	UACCCAAA CUGAUGAG X CGAA ACAAAAGA	2724
822	TTTTGTCT T TGGGTATA	216	UAUACCCA CUGAUGAG X CGAA AGACAAAA	2725
823	TTTGTCTT T GGGTATAC	217	GUAUACCC CUGAUGAG X CGAA AAGACAAA	2726
828	CTTTGGGT A TACATTTA	218	UAAAUGUA CUGAUGAG X CGAA ACCCAAAG	2727
830	TTGGGTAT A CATTTAAA	219	UUUAAAUG CUGAUGAG X CGAA AUACCCAA	2728
834	GTATACAT T TAAACCCT	220	AGGGUUUA CUGAUGAG X CGAA AUGUAUAC	2729
835	TATACATT T AAACCCTC	221	GAGGGUUU CUGAUGAG X CGAA AAUGUAUA	2730
836	ATACATTT A AACCCTCA	222	UGAGGGUU CUGAUGAG X CGAA AAAUGUAU	2731
843	TAAACCCT C ACAAAACA	223	UGUUUUGU CUGAUGAG X CGAA AGGGUUUA	2732
865	ATGGGGAT A TTCCCTTA	224	UAAGGGAA CUGAUGAG X CGAA AUCCCCAU	2733
867	GGGGATAT T CCCTTAAC	225	GUUAAGGG CUGAUGAG X CGAA AUAUCCCC	2734
868	GGGATATT C CCTTAACT	226	AGUUAAGG CUGAUGAG X CGAA AAUAUCCC	2735
872	TATTCCCT T AACTTCAT	227	AUGAAGUU CUGAUGAG X CGAA AGGGAAUA	2736
873	ATTCCCTT A ACTTCATG	228	CAUGAAGU CUGAUGAG X CGAA AAGGGAAU	2737
877	CCTTAACT T CATGGGAT	229	AUCCCAUG CUGAUGAG X CGAA AGUUAAGG	2738
878	CTTAACTT C ATGGGATA	230	UAUCCCAU CUGAUGAG X CGAA AAGUUAAG	2739
886	CATGGGAT A TGTAATTG	231	CAAUUACA CUGAUGAG X CGAA AUCCCAUG	2740
890	GGATATGT A ATTGGGAG	232	CUCCCAAU CUGAUGAG X CGAA ACAUAUCC	2741
893	TATGTAAT T GGGAGTTG	233	CAACUCCC CUGAUGAG X CGAA AUUACAUA	2742
900	TTGGGAGT T GGGGCACA	234	UGUGCCCC CUGAUGAG X CGAA ACUCCCAA	2743
200				

Table 3/

		235	CCUGUGGC CUGAUGAG X CGAA AUGUGCCC	2011
910	GGGCACAT T GCCACAGG	235	UUGUACAA CUGAUGAG X CGAA AUGUUCCU	2744
924	AGGAACAT A TTGTACAA GAACATAT T GTACAAAA	236	UUUUGUAC CUGAUGAG X CGAA AUAUGUUC	2745
926		237	AUJUUUUG CUGAUGAG X CGAA ACAAUAUG	2746
929	CATATTGT A CAAAAAAT		CACAUUUU CUGAUGAG X CGAA AUUUUUUUG	2747
938	CAAAAAAT C AAAATGTG	239	UUUCCUAA CUGAUGAG X CGAA ACUUUUUUG	2748
948	AAATGTGT T TTAGGAAA			
949	AATGTGTT T TAGGAAAC	241	GUUUCCUA CUGAUGAG X CGAA AACACAUU AGUUUCCU CUGAUGAG X CGAA AAACACAU	2750
950	ATGTGTTT T AGGAAACT	242		2751
951	TGTGTTTT A GGAAACTT	243	AAGUUUCC CUGAUGAG X CGAA AAAACACA UUUACAGG CUGAUGAG X CGAA AGUUUCCU	2752
959	AGGAAACT T CCTGTAAA		GUUUACAG CUGAUGAG X CGAA AGUUUCCU	
960	GGAAACTT C CTGTAAAC	245		2754
965	CTTCCTGT A AACAGGCC	246	GGCCUGUU CUGAUGAG X CGAA ACAGGAAG	2755
975	ACAGGCCT A TTGATTGG	247	CCAAUCAA CUGAUGAG X CGAA AGGCCUGU	2756
977	AGGCCTAT T GATTGGAA	248	UUCCAAUC CUGAUGAG X CGAA AUAGGCCU	2757
981	CTATTGAT T GGAAAGTA	249	UACUUUCC CUGAUGAG X CGAA AUCAAUAG	2758
989	TGGAAAGT A TGTCAACG	250	CGUUGACA CUGAUGAG X CGAA ACUUUCCA	2759
993	AAGTATGT C AACGAATT	251	AAUUCGUU CUGAUGAG X CGAA ACAUACUU	2760
1001	CAACGAAT T GTGGGTCT	252	AGACCCAC CUGAUGAG X CGAA AUUCGUUG	2761
1008	TTGTGGGT C TTTTGGGG	253	CCCCAAAA CUGAUGAG X CGAA ACCCACAA	2762
1010	GTGGGTCT T TTGGGGTT	254	AACCCCAA CUGAUGAG X CGAA AGACCCAC	2763
1011	TGGGTCTT T TGGGGTTT	255	AAACCCCA CUGAUGAG X CGAA AAGACCCA	2764
1012	GGGTCTTT T GGGGTTTG	256	CAAACCCC CUGAUGAG X CGAA AAAGACCC	2765
1018	TTTGGGGT T TGCCGCCC	257	GGGCGGCA CUGAUGAG X CGAA ACCCCAAA	2766
1019	TTGGGGTT T GCCGCCCC	258	GGGGCGC CUGAUGAG X CGAA AACCCCAA	2767
1029	CCGCCCCT T TCACGCAA	259	UUGCGUGA CUGAUGAG X CGAA AGGGGCGG	2768
1030	CGCCCCTT T CACGCAAT	260	AUUGCGUG CUGAUGAG X CGAA AAGGGGCG	2769
1031	GCCCCTTT C ACGCAATG	261	CAUUGCGU CUGAUGAG X CGAA AAAGGGGC AAGCAGAA CUGAUGAG X CGAA AUCCACAU	2770
1045	ATGTGGAT A TTCTGCTT	262		2771
1047	GTGGATAT T CTGCTTTA	263	UAAAGCAG CUGAUGAG X CGAA AUAUCCAC	2773
1048	TGGATATT C TGCTTTAA	264	UUAAAGCA CUGAUGAG X CGAA AAUAUCCA AGGCAUUA CUGAUGAG X CGAA AGCAGAAU	2773
1053	ATTCTGCT T TAATGCCT	265		2775
1054	TTCTGCTT T AATGCCTT TCTGCTTT A ATGCCTTT	266	AAGGCAUU CUGAUGAG X CGAA AAGCAGAA AAAGGCAU CUGAUGAG X CGAA AAAGCAGA	2776
1055		268	UGCAUAUA CUGAUGAG X CGAA AGGCAUUA	2777
1062	TAATGCCT T TATATGCA AATGCCTT T ATATGCAT	269	AUGCAUAU CUGAUGAG X CGAA AAGGCAUU	2778
1063			CAUGCAUA CUGAUGAG X CGAA AAGGCAU	2779
1064	ATGCCTTT A TATGCATG GCCTTTAT A TGCATGCA	270	UGCAUGCA CUGAUGAG X CGAA AUAAAGGC	2780
1066	GCCTTTAT A TGCATGCA GCATGCAT A CAAGCAAA	271	UUUGCUUG CUGAUGAG X CGAA AUGCAUGC	2781
1076	AACAGGCT T TTACTTTC	272	GAAAGUAA CUGAUGAG X CGAA AGCCUGUU	2782
1092	ACAGGCT T TTACTTTCT	274	AGAAAGUA CUGAUGAG X CGAA AAGCCUGU	2783
1093	CAGGCTT T ACTTTCT	274	GAGAAAGU CUGAUGAG X CGAA AAAGCCUG	2784
1094	AGGCTTT A CTTTCTCG	275	CGAGAAAG CUGAUGAG X CGAA AAAAGCCU	2785
1095	CTTTTACT T TCTCGCCA	277	UGGCGAGA CUGAUGAG X CGAA AGUAAAAG	2786
1098	TTTTACT T TCTCGCCAA	278	UUGGCGAGA CUGAUGAG X CGAA AAGUAAAA	2787
	TTTACTT C TOGCCAAC	279	GUUGGCGAG CUGAUGAG X CGAA AAAGUAAA	2788
1100		280	AAGUUGGC CUGAUGAG X CGAA AAAGUAAA	2789
1102	TACTITCT C GCCAACTT CGCCAACT T ACAAGGCC	281	GCCUUGU CUGAUGAG X CGAA AGUUGGCG	2790
1110	GCCAACT T ACAAGGCC	281	AGGCCUUG CUGAUGAG X CGAA AAGUUGGC	2790
1111	CAAGGCCT T TCTAAGTA	282	UACUUAGA CUGAUGAG X CGAA AGGCCUUG	2792
		283	UIIACUUAGA CUGAUGAG X CGAA AAGGCCUU	2792
1121	AGGCCTT T CTAAGTAA AGGCCTTT C TAAGTAAA	284	UUUACUUA CUGAUGAG X CGAA AAAGGCCU	2793
1122	AGGCCITI C TAAGTAAA	285	OUDACOUN COGNOGAG X CONA MANGGCCO	1 2/34

Table 37

1124	GCCTTTCT A AGTAAACA	286	UGUUUACU CUGAUGAG X CGAA AGAAAGGC	2795
1128	TICTAAGT A AACAGTAT	287	AUACUGUU CUGAUGAG X CGAA ACUUAGAA	2796
1135	TAAACAGT A TGTGAACC	288	GGUUCACA CUGAUGAG X CGAA ACUGUUUA	2797
1145	GTGAACCT T TACCCCGT	289	ACGGGGUA CUGAUGAG X CGAA AGGUUCAC	2798
1146	TGAACCTT T ACCCCGTT	290	AACGGGGU CUGAUGAG X CGAA AAGGUUCA	2799
1147	GAACCTTT A CCCCGTTG	291	CAACGGGG CUGAUGAG X CGAA AAAGGUUC	2800
1154	TACCCCGT T GCTCGGCA	292	UGCCGAGC CUGAUGAG X CGAA ACGGGGUA	2801
1158	CCGTTGCT C GGCAACGG	293	CCGUUGCC CUGAUGAG X CGAA AGCAACGG	2802
1173	GGCCTGGT C TATGCCAA	294	UUGGCAUA CUGAUGAG X CGAA ACCAGGCC	2803
1175	CCTGGTCT A TGCCAAGT	295	ACUUGGCA CUGAUGAG X CGAA AGACCAGG	2804
1186	CCAAGTGT T TGCTGACG	296	CGUCAGCA CUGAUGAG X CGAA ACACUUGG	2805
1187	CAAGTGTT T GCTGACGC	297	GCGUCAGC CUGAUGAG X CGAA AACACUUG	2806
1209	CCACTGGT T GGGGCTTG	298	CAAGCCCC CUGAUGAG X CGAA ACCAGUGG	2807
1216	TTGGGGCT T GGCCATAG	299	CUAUGGCC CUGAUGAG X CGAA AGCCCCAA	2808
1223	TTGGCCAT A GGCCATCA	300	UGAUGGCC CUGAUGAG X CGAA AUGGCCAA	2809
1230	TAGGCCAT C AGCGCATG	301	CAUGCGCU CUGAUGAG X CGAA AUGGCCUA	2810
1249	TGGAACCT T TGTGTCTC	302	GAGACACA CUGAUGAG X CGAA AGGUUCCA	2811
1250	GGAACCTT T GTGTCTCC	303	GGAGACAC CUGAUGAG X CGAA AAGGUUCC	2812
1255	CTTTGTGT C TCCTCTGC	304	GCAGAGGA CUGAUGAG X CGAA ACACAAAG	2813
1257	TTGTGTCT C CTCTGCCG	305	CGGCAGAG CUGAUGAG X CGAA AGACACAA	2814
1260	TGTCTCCT C TGCCGATC	306	GAUCGGCA CUGAUGAG X CGAA AGGAGACA	2815
1268	CTGCCGAT C CATACCGC	307	GCGGUAUG CUGAUGAG X CGAA AUCGGCAG	2816
1272	CGATCCAT A CCGCGGAA	308	UUCCGCGG CUGAUGAG X CGAA AUGGAUCG	2817
1283	GCGGAACT C CTAGCCGC	309	GCGGCUAG CUGAUGAG X CGAA AGUUCCGC	2818
1285	GAACTCCT A GCCGCTTG	310	CAAGCGGC CUGAUGAG X CGAA AGGAGUUC	2819
1293	TAGCCGCT T GTTTTGCT	311	AGCAAAAC CUGAUGAG X CGAA AGCGGCUA	2820
1296	CCGCTTGT T TTGCTCGC	312	GCGAGCAA CUGAUGAG X CGAA ACAAGCGG	2821
1297	CGCTTGTT T TGCTCGCA	313	UGCGAGCA CUGAUGAG X CGAA AACAAGCG	2822
1298	GCTTGTTT T GCTCGCAG	314	CUGCGAGC CUGAUGAG X CGAA AAACAAGC	2823
1302	GTTTTGCT C GCAGCAGG	315	CCUGCUGC CUGAUGAG X CGAA AGCAAAAC	2824
1312	CAGCAGGT C TGGGGCAA	316	UUGCCCCA CUGAUGAG X CGAA ACCUGCUG	2825
1325	GCAAAACT C ATCGGGAC	317	GUCCCGAU CUGAUGAG X CGAA AGUUUUGC	2826
1328	AAACTCAT C GGGACTGA	318	UCAGUCCC CUGAUGAG X CGAA AUGAGUUU	2827
1341	CTGACAAT T CTGTCGTG	319	CACGACAG CUGAUGAG X CGAA AUUGUCAG	2828
1342	TGACAATT C TGTCGTGC	320	GCACGACA CUGAUGAG X CGAA AAUUGUCA	2829
1346	AATTCTGT C GTGCTCTC	321	GAGAGCAC CUGAUGAG X CGAA ACAGAAUU	2830
1352	GTCGTGCT C TCCCGCAA	322	UUGCGGGA CUGAUGAG X CGAA AGCACGAC	2831
1354	CGTGCTCT C CCGCAAAT	323	AUUUGCGG CUGAUGAG X CGAA AGAGCACG	2832
1363	CCGCAAAT A TACATCAT	324	AUGAUGUA CUGAUGAG X CGAA AUUUGCGG	2833
1365	GCAAATAT A CATCATTT	325	AAAUGAUG CUGAUGAG X CGAA AUAUUUGC	2834
1369	ATATACAT C ATTTCCAT	326	AUGGAAAU CUGAUGAG X CGAA AUGUAUAU	2835
1372	TACATCAT T TCCATGGC	327	GCCAUGGA CUGAUGAG X CGAA AUGAUGUA	2836
1373	ACATCATT T CCATGGCT	328	AGCCAUGG CUGAUGAG X CGAA AAUGAUGU	2837
1374	CATCATTT C CATGGCTG	329	CAGCCAUG CUGAUGAG X CGAA AAAUGAUG	2838
1385	TGGCTGCT A GGCTGTGC	330	GCACAGCC CUGAUGAG X CGAA AGCAGCCA	2839
1406	AACTGGAT C CTACGCGG	331	CCGCGUAG CUGAUGAG X CGAA AUCCAGUU	2840
1409	TGGATCCT A CGCGGGAC	332	GUCCCGCG CUGAUGAG X CGAA AGGAUCCA	2841
1420	CGGGACGT C CTTTGTTT	333	AAACAAAG CUGAUGAG X CGAA ACGUCCCG	2842
1423	GACGTCCT T TGTTTACG	334	CGUAAACA CUGAUGAG X CGAA AGGACGUC	2843
1424	ACGTCCTT T GTTTACGT	335	ACGUAAAC CUGAUGAG X CGAA AAGGACGU	2844
1427	TCCTTTGT T TACGTCCC	336	GGGACGUA CUGAUGAG X CGAA ACAAAGGA	2845

Table 37

1428					
1439	1428	CCTTTGTT T ACGTCCCG	337	CGGGACGU CUGAUGAG X CGAA AACAAAGG	2846
1438 GETTAGGT C COGTOGGC 339 CCCGACGG CUGAUGAG X COAA AGGUAAC 2849 1449 CQUTGAAT C CCGCGGAC 341 GUCCGCGG CUGAUGAG X COAA AGGUAGAC 2849 1449 CQUTGAAT C CCGCGGAC 341 GUCCGCGG CUGAUGAG X COAA AGGUAGGC 2851 1477 GOGCCCCT C CCGGGACC 342 GGCCCCGG CUGAUGAG X COAA AGGUAGGC 2851 1477 GOGCCCCT C CCGGGACC 344 AGACCCCC CUGAUGAG X COAA AGGUAGGC 2851 1484 TTGGGGCT C TACCGCCC 344 AGACCCCC CUGAUGAG X COAA AGCCGCCCA 2851 1486 GGCGCCT C TACCGCCC 345 CGGGGGGG CUGAUGAG X COAA AGCCGCCCA 2851 1496 CGCCCCCT T CTCCGCCT 346 AGGCGGGG CUGAUGAG X CGAA AGCCCCC 2854 1497 GCCCCCCT T CTCCGCCT 346 AGGCGGGG CUGAUGAG X CGAA AGCCGCCC 2854 1497 CGCCCCT T CTCCGCTA 347 UAGGCGGG CUGAUGAG X CGAA AGCCGCCC 2854 1499 CCGCTTCT C CGCCTA 348 AGAGCGGG CUGAUGAG X CGAA AGCCGCCC 2856 1499 CCGCTTCT C CGCCTA 348 AGAGCGGG CUGAUGAG X CGAA AGCCGCCC 2856 1590 CCCCCCTT T C TACCGCCT 349 CCGUAGAG CUGAUGAG X CGAA AGCAGCGC 2857 1590 CCGCTTCT C CGCCTA 351 CCGUCGG CUGAUGAG X CGAA AGCAGCGC 2857 1591 CCGCCCCCT T CTTCCCCC 352 CCCCCCGGG CUGAUGAG X CGAA ACAGAGGG 2857 1593 CCGCACCT C TTTTACCG 352 CCCCCCGGG CUGAUGAG X CGAA ACAGAGG 2859 1594 CCGCACCT C TTTTACCG 353 CCCCCGGG CUGAUGAG X CGAA ACAGAGG 2861 1594 CCGCACCT C TTTTACCG 354 CCCCUGAG CUGAUGAG X CGAA ACAGAGG 2861 1595 CCTCTCTT A CGCGCGAC 355 CCCCCGGG CUGAUGAG X CGAA ACAGAGG 2861 1596 CTCTCTT T ACCGCGAC 356 GUCCGCGU CUGAUGAG X CGAA ACAGAGG 2861 1596 CTCTCTT T ACCGCGAC 356 GUCCGCGU CUGAUGAG X CGAA ACAGAGG 2861 1596 CTCTCTT T ACCGCGAC 356 GUCCGCGU CUGAUGAG X CGAA ACAGAGG 2865 1596 CTCTCCT T CACTCTC 357 AGUCCCCC CUGAUGAG X CGAA ACAGAGG 2865 1596 CTCCCCT T CTCATCTC 356 GUCCAGGG CUGAUGAG X CGAA ACAGAGG 2866 1596 CTCCCCT T CTCATCTC 356 GUCCAGGG CUGAUGAG X CGAA ACAGAGG 2867 1597 CTCCCCT T CTCATCTC 356 GUCCAGGG CUGAUGAG X CGAA ACAGAG		CTTTGTTT A CGTCCCGT	338	ACGGGACG CUGAUGAG X CGAA AAACAAAG	2847
1495 COGTIGAT C COCCOGGC 341 GICCOCCC CUGAINGA K CGAA ANUCAGCS 2851 1465 CORACCCCT C COCGGGCC 342 GICCOCCCC CUGAINGA K CGAA ANUCAGCS 2851 1477 GOGCCCCT C GOGGCTCT 343 AGAGCCCC CUGAINGA K CGAA AGCGCCCA 2852 1484 TTOGGGCT C TACCOCCCC 344 GGCGGGIL CUGAINGA K CGAA AGCGCCCA 2852 1486 GGGCCCCT A CCCCCCCC 345 CGGGGGGIL CUGAINGA K CGAA AGCCCCCA 2854 1486 CGGCCCCCT C TCCCCCCC 345 CGGGGGGIL CUGAINGA K CGAA AGCCCCCA 2854 1496 CGCCCCCT T CTCCCCCT 346 AGGCGGGG CUGAINGA K CGAA AGCCCCCA 2854 1497 CGCCCCCT T CTCCCCCT 347 LUGAINGAG KUGAINGA K CGAA AGCCCCCA 2854 1497 CGCCCCCT T CTCCCCCT 347 LUGAINGAG KUGAINGA K CGAA AGCCCCCA 2854 1499 CGCCCCCT T CTCCCCCT 348 AGGCGGGG CUGAINGA K CGAA AGCCCCCA 2856 1499 CGCCCCCT T CTCCCCCT 347 LUGAINGAG KUGAINGA K CGAA AGCCCCCA 2856 1505 CTCCCCCT T CTCCCCCT 348 AGCGCGGG CUGAINGA K CGAA AGANGCGG 2857 1507 CCCCCCTRT T GTACCGAC 350 GUCCGUIAC CUGAINGA K CGAA AGANGCGG 2858 1507 CCCCCCTRT T GTACCGAC 351 ACCCUCGG CUGAINGA K CGAA AGANGCGG 2858 1510 CCTATITOT A CCCGACCOT 351 ACCCUCGG CUGAINGA K CGAA ACANDAG CUGAINGA K CGAC 2850 1534 GCGCACCT C TCTTTACCG 352 GCCCCCGUI CUGAINGA K CGAA ACANDAG CUGAINGA K CGAC 2850 1534 GCGCACCT C TCTTTACCG 354 CCCCULAA CUGAINGA K CGAA ACANDAG CUGAINGA K CGAC 2861 1539 ACCTCTCT T ACCCGCAC 356 GUCCCCCUI CUGAINGA K CGAA AGANGAG CUGAINGA K CGAC 2861 1540 CCCCCCTT T CTCCCCC 356 GUCCCCCUI CUGAINGA K CGAA AGANGAG CUGAINGA K CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1433	GTTTACGT C CCGTCGGC	339		2848
1465	1438	CGTCCCGT C GGCGCTGA	340		2849
1455	1449	CGCTGAAT C CCGCGGAC	341	GUCCGCGG CUGAUGAG X CGAA AUUCAGCG	2850
1477 GGGCCCCT T GGGGCTCT 343 AGAGCCCC CURADAG X CGAA AGCCCCA 2853 1486 GGGGCCCT A CCCCCCCC 344 GGGGGGGG CURADAG X CGAA AGCCCCA 2854 1486 CGCCCCCCT T CTCCGCCT 345 GGGGGGG CURADAG X CGAA AGCCCCA 2854 1497 CGCCCCCCT T CTCCGCCT 346 AGGCGGGG CURADAG X CGAA AGCGGGGG X CGAA AGCGGGG X CGAA AGCGGGGG X CGAA AGCGGGG X CGAA AGCGGGGG X CGAA AGCGGGG X		CGACCCCT C CCGGGGCC	342	GGCCCCGG CUGAUGAG X CGAA AGGGGUCG	
1486		GGGCCGCT T GGGGCTCT	343	AGAGCCCC CUGAUGAG X CGAA AGCGGCCC	2852
1486 GGGGCTCT A CCGCCCCCCCCCCCCCCCCCCCCCCCCC		TTGGGGCT C TACCGCCC	344	GGGCGGUA CUGAUGAG X CGAA AGCCCCAA	2853
1497 COCCOCTT C TOCCCCTA 347 LIAGROCGA CUGARIGAS X CGAA AMACCOCC 2856 1499 COCCTTCT C COCCTATT 348 ANLIAGOCC CUGARIGAS X CGAA AMACCOCC 2858 1595 CTCCCCCTAT T CTACCCG 349 COCUACAA CUGARIGAS X CGAA AMACCCCAC 2858 1507 CCCCCTAT T GTACCGAA 350 GUCAGAAC CUGARIGAS X CGAA AMACCCCAC 2858 1510 CCCATTOTA A COCCACCT 351 ACQCUIGGG CUGARIGAS X CGAA AMACCCCCC 2851 1510 CCCATTOTA A COCCACCT 351 ACQCUIGGG CUGARIGAS X CGAA ACACHINGG 2861 1534 CCCCACCT C CACCGGGC 352 CCCCCCGU CUGARIGAS X CGAA ACACHINGG 2861 1535 CCCACCT C TITACCCGA 354 CCCCUAAA CUGARIGAS X CGAA ACACHINGG 2861 1536 GCACCTCT C TITACCCGA 355 CCCCCCGU CUGARIGAS X CGAA ACACHINGG 2861 1538 ACCTICTCT T TACCCCGA 355 UCCCCCGU CUGARIGAS X CGAA ACACHINGG 2863 1539 CCTCTCTT T ACCCCGAC 356 UCCCCCGU CUGARIGAS X CGAA ACACHINGG 2865 1540 CCTCTCTT A CCCCCGAC 356 GUCCCCCC CUGARIGAS X CGAA ACACHINGG 2865 1540 CCTCTCTT A CCCCCGAC 356 GUCCCCCC CUGARIGAS X CGAA ACACHINGG 2865 1540 CCTCCCCCT C TOTCCCTT 359 ANGUCACC CUGARIGAS X CGAA ACACHINGG 2865 1553 CTCCCCCT C TOTCCCTT 359 ANGUCACC CUGARIGAS X CGAA ACACHINGG 2865 1554 TOTCCCCT C TOTCCCT 350 ANGUCACA CUGARIGAS X CGAA ACCGGCAC 2869 1555 CTCCCCCT C TOTCCCT 350 ANGUCACA CUGARIGAS X CGAA ACCGGCAC 2869 1566 TOTCCCTT C ATCTCCCC 361 CCAGARIGA CUGARIGAS X CGAA ACCGCACAC 2869 1566 TOTCCTTCAT C TACTCCCC 362 CCGCAGRIG CUGARIGAS X CGAA ACCGCAC 2870 1589 CTCCCCCT T CACCTCCC 362 CCGCAGRIG CUGARIGAS X CGAA ACCGCAC 2871 1589 CTCCCCCT T CACCTCCC 365 CCGCAGRIG CUGARIGAS X CGAA ACCGCAC 2871 1589 CTCCCCCT T CACCTCCC 366 CCGCAGRIG CUGARIGAS X CGAA ACCGCAC 2871 1599 CTCCCCCT T CACCTCCC 367 CCACAGRIG CUGARIGAS X CGAA ACCGCAC 2871 1591 CTCCCCCT T CACCTCCC 367 CCACAGRIG CUGARIGAS X CGAA ACCGCAC 2871 1593 ACTCCCTT T CACCTCTC 366 CCCCCCC CUGARIGAS X CGAA ACCGCCAC 2871		GGGGCTCT A CCGCCCGC	345		2854
1497 GCCGCTT C TCCGCCTA 347 MAGRICGGA CUGAUGAG X CGAA AAAGCGGC 2856 1499 CCGCTTCT C CGCCTAT 348 AAALAGGC CUGAUGAG X CGAA AAAGCGG 2857 1595 CTCGCCCTAT TGTACCGG 349 CCGGUACAA CUGAUGAG X CGAA AAAGCGGC 2858 1597 CCGCCTAT TGTACCGG 349 CCGGUACAA CUGAUGAG X CGAA AAAGCGGC 2858 1597 CCGCCTAT TGTACCGGA 350 GUCGGUAC CUGAUGAG X CGAA AAAGAGGG 2858 1510 CCTATTOT A CCGACGGG 351 ACGGUCGG CUGAUGAG X CGAA ACAAUAGG 2850 1539 CCGCACCGT C TGTACCGG 354 CCCCGUG CUGAUGAG X CGAA ACAAUAGG 2861 1534 GCGCCCCG C CACGGGGC 352 CCCCCGUG CUGAUGAG X CGAA ACAAUAGG 2861 1536 GCACCTCT C TTTACGCG 354 CCCCGUGAA CUGAUGAG X CGAA ACAAUAGG 2861 1538 ACCTCTCT T TACGCGGA 355 UCCCCGUG CUGAUGAG X CGAA ACAAGGGC 2861 1539 CCTCTCTT T ACGCGGAC 355 UCCCCGUG CUGAUGAG X CGAA ACAAGAGG 2861 1540 CCTCTCTT T ACGCGGAC 356 GUCCGCGU CUGAUGAG X CGAA AAAGAAGG 2865 1540 CCTCTCTT A CGCGGAC 356 GUCCGCGU CUGAUGAG X CGAA AAAGAAGG 2865 1540 CCTCTCTT A CGCCGAC 356 ACGCCCGC UGAUGAG X CGAA AAAGAAGG 2865 1540 CCTCCCCCT C TACCCCT 357 AAGUCCCGC CUGAUGAG X CGAA AAAGAAGG 2865 1541 CCCCGCGAC C CCCCCTCTG 358 AAGCCGC CUGAUGAG X CGAA AAAGAAGG 2865 1543 CCCCCCCCT C TCTCCCC 361 AAGUCCCC CUGAUGAG X CGAA AAAGAAGG 2866 1544 CTCCCCCT C TCTCCCC 361 AAGUCCAC CUGAUGAG X CGAA AAAGACG 2867 1555 CTCCCCCT C TCTCTCT 359 AAGUCCAC CUGAUGAG X CGAA AAAGACG 2867 1556 TCTCCCCT C TCTCTCT 359 AAGUCCAC CUGAUGAG X CGAA AAAGACG 2867 1557 CTCCCCCT C TCTCTCC 361 ACAAUGAC CUGAUGAG X CGAA AAAGACG 2869 1568 TCTCCCCT C TCTCTCC 361 ACAAUGAC CUGAUGAG X CGAA AAAGACG 2870 1569 CTTCTCAT C TCCCTCT 365 ACGCACAG CUGAUGAG X CGAA AAAGACG 2871 1589 CTCCCCCT C TCCCCC 365 ACGCACAG CUGAUGAG X CCAA AAAGACCA 2871 1589 CTCCCCCT C TCCCCC 365 ACGCACAG CUGAUGAG X CCAA AAAGACCA 2871 1589 CTCCCCCT C TCCCCC 365 ACGCACAG CUGAUGAG X CCAA AAAGACCA 2871 1589 CTCCCCCT C TCCCCC 366 ACGCACAC CUGAUGAG X CCAA AAAGACCA 2871 1589 CTCCCCCT C TCCCCC 366 ACGCACAC CUGAUGAG X CCAA AAAGACAC 2871	1496	CGCCCGCT T CTCCGCCT	346	AGGCGGAG CUGAUGAG X CGAA AGCGGGCG	2855
1499			347	UAGGCGGA CUGAUGAG X CGAA AAGCGGGC	2856
1507 CONCETNI T GITACCIAC 350 GICCOGIAC CIGARIGAG X CHAA AUAGGCGC 2859 1510 COTATIOT A COGACCOT 351 ACCOURGE CHANINGS CACAA ACAGGGCGC 2861 1534 COCACCOT C CACGGGGC 352 GCCCCCGIG CUGARIGAG X CGAA ACAGGGCGC 2861 1534 GCGCACCT C TCTITACGC 353 GCCCCCGIG CUGARIGAG X CGAA ACAGGGCGC 2861 1536 GCACCCTC C TCTITACGC 354 CCCCUAAA CUGARIGAG X CGAA ACAGGGCC 2862 1538 ACCTICTCT T TACGCGGA 355 CCCCCCGIG CUGARIGAG X CGAA ACAGGGCC 2863 1539 CCTCTCTT T TACGCGA 356 CUCCCGCC UGARIGAG X CGAA ACAGGGCC 2863 1540 CTCTCTTT A CGCGGAC 356 CUCCCGCC UGARIGAG X CGAA ACAGGGCG 2865 1540 CCTCTCTT A CGCGGAC 356 CUCCCGCC UGARIGAG X CGAA ACAGGGC 2865 1540 CCTCCCTT A CGCGGAC 357 ADUCCCCC UGARIGAG X CGAA ACAGGGC 2865 1540 CCTCCCCT C TOTGCCTT 359 AAGGCACA CUCARIGAG X CGAA ACAGGGAG 2865 1541 CCGCGACT C TOTGCCTT 359 AAGGCACA CUCARIGAG X CGAA ACAGGGAG 2867 1552 CTCCCCCT C TOTGCCTT 359 AAGGCACA CUCARIGAG X CGAA ACAGGGAG 2867 1553 CTCCCCCT C TOTGCCTT 359 AAGGCACA CUCARIGAG X CGAA ACAGGGAG 2869 1564 TOTCCCTT C TACTCTCC 361 CACARIGAG CUGARIGAG X CCAA ACAGGACA 2871 1556 TOCCTTCT C ATCTCCC 362 COGCARAI CUCARIGAG X CCAA ACAGGCACA 2871 1569 TOTCCCTT C TACTCTCC 363 CUCCAGGAC CUGARIGAG X CCAA ACAGGCACA 2871 1569 TOTCCATC T COCCCGAC 363 CUCCAGGC CUGARIGAG X CCAA ACAGGCACA 2871 1589 TOTGCACT T C GCTTCAC 364 CUGARIGAC CUCARIGAG X CCAA ACAGGCACA 2871 1599 ACTTCCCTT C ACCCTCTC 366 CUGARIGAC CUCARIGAG X CCAA ACAGGCACA 2873 1591 ACTTCCCTT C TACCTCTC 366 CUGARIGAC CUCARIGAG X CCAA ACAGGCACA 2873 1593 ACTTCCCTT C TACCTCTC 366 CUGARIGAC CUCARIGAG X CCAA ACAGGCACA 2873 1594 CTTCCCTT C TACCTCTC 366 CUGARIGAC CUCARIGAG X CCAA ACAGCCACA 2873 1595 CTTCCCTT C TACCTCTC 366 CUGARIGAC CUCARIGAG X CCAA ACAGCCACA 2873 1667 CCCCACGT T CCCCACC 367 CACARGGC CUGARIGAG X CCAA ACAGCCACA 2873 1667 CTCCACCT C COCCACAC 367 CACARGGC CUGARI		CCGCTTCT C CGCCTATT	348		2857
1510 CCCANTOT A COGACCOT 351 ACCOURGE CIGAURIA X CGAA ACAMIAGE 2860 1519 CCCANCOT C CACGGGGC 352 ACCOURGE CIGAURIA X CGAA ACAMIAGE 2861 1519 CCGACCOT C CACGGGGC 352 ACCOURGE CIGAURIA X CGAA ACAMIAGE 2861 1534 CCGACCOT C TITTACG 354 CCCCCURA CIGAURIA X CGAA ACAMIAGE 2861 1536 GCACCTC C TITTACG 354 CCCCURA CIGAURIA X CGAA ACAMIAGE 2861 1538 ACCTCTCT T TAGCGGA 355 UCCCCCURA CIGAURIA X CGAA ACAMAGGC 2861 1538 ACCTCTCT T TAGCGGA 356 GUCCGCGU CUGAURIA X CGAA ACAMAGG 2864 1539 CCTCTCTT A CCCCCCACT 357 ACCCCCCCC CUGAURIA X CGAA ACAMAGG 2865 1540 CCTCTCTT A CCCCCCACT 357 ACCCCCCC CUGAURIA X CCAA ACAMAGG 2865 1540 CCTCTCTT A CCCCCCACT 357 ACCCCCCC CUGAURIA X CCAA ACAMAGG 2865 1540 CCTCTCTT A CCCCCCCC 357 ACCCCCCC CUGAURIA X CCAA ACAMAGG 2865 1540 CCTCTCTT A CCCCCCCC 358 ACAGCCGG CUGAURIA X CCAA ACAGCAC 2867 1555 CTCCCCCC C TAGTCCC 359 ACAGCCCCC CUGAURIA X CCAA ACCCCACC 2867 1555 CTCCCCCC C TAGTCCC 361 CCCAAURIA X CCAA ACCCCACC 2869 1554 CTCCCCCC C TAGTCCC 361 CCCAAURIA X CCAA ACCCCACC 2869 1556 TOTCCCCT C TAGTCCC 361 CCCAAURIA CUGAURIA X CCAA ACCCCACC 2870 1556 CTCCCCCT C TCCCCCC 362 CCCCCARRIA CUGAURIA X CCAA ACCCCAC 2870 1559 CTCCCCCT C TCCCCCCC 362 CCCCCARRIA CUGAURIA X CCAA ARGACACA 2870 1559 CTCCCCCT C TCCCCCCC 364 CGGARRIA CUGAURIA X CCAA ARGACACA 2871 1559 CTCCCCCT C TCCCCCCC 364 CGGARRIA CUGAURIA X CCAA ARGACACA 2871 1559 CTCCCCCT C TCCCCCCC 366 CGGARRIA CUGAURIA X CCAA ARGACACA 2871 1559 CTCCCCCCT C TCCCCCCC 366 CGGARRIA CUGAURIA X CCAA ARGACACA 2871 1559 CTCCCCCCT C TCCCCCCC 366 CGGARRIA CUGAURIA X CCAA ARGACACA 2871 1559 CTCCCCCCT C TCCCCCTC 367 CCCAAGCC UCAURIA X CCAA ARGACACA 2871 1559 CTCCCCCCC C TCCCCCC 367 CCCAAGCC UCAURIA X CCAA ARGACCAA 2871 1559 CTCCCCCCC C TCCCCCCC CUGAURIA X CCAA ARGACCAA 2871 1651 CCCCACCCC C CCCCCCC CUGAURIA X CCAA ARGACCACA	1505	CTCCGCCT A TTGTACCG	349	CGGUACAA CUGAUGAG X CGAA AGGCGGAG	2858
1519 CCCARCOTT C CACGOGGC 352 CCCCCCGIG CUGAUGAG X CGAA ACCGUCGG 2861 1534 CCCACCCT C TCTTTACG 353 CCUCACGG CUGAUGAG X CGAA ACCGUCGG 2862 1536 CCCCCCC TCTTTACGG 354 CCCCCCGC CUGAUGAG X CGAA ACCGUCGG 2863 1538 ACCTCCTT T TACGCG 354 CCCCCCGC UCAUGAGA X CGAA ACAGUCGC 2863 1538 ACCTCCTT T TACGCG 355 UCCCCCGU CUGAUGAG X CGAA ACAGUCGC 2863 1539 CCCTCCTT T ACGCGGAC 356 UCCCCCGC UCAUGAGA X CGAA ACAGAGG 2865 1549 CCCCCCTT T ACGCGGAC 356 UCCCCCGC UCAUGAGA X CGAA ACAGAGG 2865 1549 CCCCCCCT T TACGCGAC 357 AGUCCCCC UCAUGAGA X CGAA ACAGAGG 2865 1549 CCCCCCCT T T TACGCGAC 358 ACCCCCCT UCAUGAGA X CGAA ACAGAGG 2866 1549 CCCCCCCT T T T T T T T T T T T T T T	1507	CCGCCTAT T GTACCGAC	350		
1519 COCACCOT C CACCOCCC 352 COCCCCCC CUGAUGAG X COAA ACQUICCCC 2861 1534 GORECTCT C TITACCCCC 354 COCCUAAA CUGAUGAG X COAA ACQUICCCC 2862 1538 ACCTICTCT T TACCCCCC 354 COCCUAAA CUGAUGAG X COAA ACQUICCCC 2863 1539 CCTCTCTT T ACCCCCCCC 355 CUCCCCCCC CUGAUGAG X COAA ACQUICCCC 2865 1540 CCTCTCTT T ACCCCCCCC 356 CUCCCCCCC CUGAUGAG X COAA AAAAGAGAC 2865 1540 CCTCCCTT A CCCCCCCCC 357 AGUICCCCC CUGAUGAG X COAA AAAAGAGAC 2865 1540 CCCCCCCC C TACCCCTT 359 AAGCACA CUGAUGAG X COAA AAACAGAC 2865 1553 CTCCCCCCT C TACCCCT 359 AAGCACA CUGAUGAG X COAA AAACAGAC 2865 1553 CTCCCCCT C TACCCCT 359 AAGCACA CUGAUGAG X COAA AACAGACA 2869 1564 TOTOCCTT C TACCCCC 362 CCCCAGAC CUGAUGAG X COAA AACAGACA 2869 1565 TOTOCCCT C TACCCCC 362 CCCCAGAC CUGAUGAG X COAA AACAGACA 2870 1566 TOTOCCTT C TACCCCC 362 CCCCAGAC CUGAUGAG X COAA AACAGCCA 2870 1569 CTCTCCAT C TACCCCC 362 CCCCAGAC CUGAUGAG X COAA AACAGCCA 2871 1589 CTCCCCCT C TACCCCC 362 CCCCAGAC CUGAUGAG X COAA AACAGCCA 2871 1589 CTCCCCCT C TACCCCC 362 CCCCAGAC CUGAUGAG X COAA AACAGCCA 2871 1589 CTCCCCCT C TACCCCC 364 CUCCAGAC CUGAUGAG X COAA AACAGCCA 2871 1589 CTCCCCCT C TACCCCCC 365 CUCCAGCAC CUGAUGAG X COAA AACAGCCA 2871 1589 ACTCCCCT T CACCCTCC 365 CUCCAGCAC CUGAUGAG X COAA AACAGCAC 2874 1593 ACTCCCCT T CACCCTC 366 CUCCAGCAC CUGAUGAG X COAA AACAGCAA 2873 1594 CTTCCCTT C ACCCTCC 367 CCACAGCC CUGAUGAG X COAA AACAGCAAC 2875 1594 CTTCCCTT C ACCCTCC 367 CCACAGCC CUGAUGAG X COAA AACAGCCAA 2876 1595 CTTCCCTT C ACCCTCC 367 CCACAGCC CUGAUGAG X COAA AACAGCCAAC 2876 1667 ACCACCT C TOCACCTC 368 GACGUCA CUGAUGAG X COAA AACAGCCAAC 2876 1667 ACCACCT C TOCACCTC 367 CCACAGCC CUGAUGAG X COAA AACAGCCAAC 2876 1668 TACCTCCT C TACCCTCC 367 CCACAGCC CUGAUGAG X COAA AACAGCCAAC 2880 1669 ACCACCT C TOCACCTC 378 ACUCCCCC CUGAUGAG X COAA AACAGCAAC 2881 1667	1510	CCTATTGT A CCGACCGT	351	ACGGUCGG CUGAUGAG X CGAA ACAAUAGG	2860
1534 GOGRACT C TCTTTACG 353 COUANAGA CUGAUGAG X CGAA AGGUGGC 2862 1536 GCACCTCT C TTTACGCG 354 CCGCUGAA CUGAUGAG X CGAA AAGGUGC 2863 1539 CCTCTCTT T ACGCGGAA 355 UCCGCGUA CUGAUGAG X CGAA AAAGGAG 2864 1539 CCTCTCTT T ACGCGGAC 356 UCCGCGUA CUGAUGAG X CGAA AAAAGAGAG 2865 1539 CCTCTCTT T ACGCGGAC 357 AGUCCGCC CUGAUGAG X CGAA AAAAGAGAG 2865 1549 CCTCCTCTT A CGCGGAC 357 AGUCCGCC CUGAUGAG X CGAA AAAAGAGAG 2865 1549 CCTCCCGT C TGTGCCTT 358 AAGGACAC CUGAUGAG X CGAA AAAAGAGAG 2866 1549 CCTCCCGT C TGTGCCTT 359 AAGGACAC CUGAUGAG X CGAA AAAAGAGAG 2866 1553 CTCTCCCGT C TGTGCCTT 359 AAGGACAC CUGAUGAG X CGAA AAAGAGAG 2869 1563 CTCTCCCT C TCACTCT 350 AAGGACAC CUGAUGAG X CGAA AAGGCACA 2869 1564 TGTGCCTT C TCACTCT 361 GCAGAUGA CUGAUGAG X CGAA AAGGCACA 2869 1564 TGTGCCTT C TCACTCT 362 CGGGAGAU CUGAUGAG X CGAA AAGGCACA 2871 1566 TGTCCTTC T CTCCCGGA 363 GUCCGGCA CUGAUGAG X CGAA AAGGACAC 2871 1569 CTCTCAT C TGCCGGAC 363 GUCCGGCA CUGAUGAG X CGAA AAGAGCAC 2871 1593 AGTCCCTT C ACCTTCAC 364 GUGAAGCC CUGAUGAG X CGAA AAGAGCAC 2873 1599 GTCCACTT C GCCTCAC 365 GUUGAGC CUGAUGAG X CGAA AAGAGCAC 2873 1593 ACTTCCCT T C ACCTTCAC 366 GUGAGGC CUGAUGAG X CGAA AAGAGCAC 2874 1593 ACTTCCCT T C ACCTCTC 366 CAGAGGGU CUGAUGAG X CGAA AAGAGCAC 2876 1599 CTCCACTC T C ACCTCTC 367 GCAGAGGU CUGAUGAG X CGAA AAGACAAG 2875 1599 CTCCACTC T C ACCTCTC 367 GCAGAGGU CUGAUGAG X CGAA AAGAGCAAG 2876 1599 CTCCACTC T C ACCTCTC 368 GAGGAGG CUGAUGAG X CGAA AAGAGCAAG 2876 1599 CTCCACTC T CACACTC 368 GAGGACC CUGAUGAG X CGAA AAGCCAAG 2876 1599 CTCCACTC T C ACCTCTC 368 GAGGACC CUGAUGAG X CGAA AAGCCAAG 2876 1591 CCCACAGT C TGCACATC 369 CCCCAUGC CUGAUGAG X CGAA AAGCCAAG 2876 1591 CCCACAGT C TGCACATC 369 CCCCAUGC CUGAUGAG X CGAA AACCCAAG 2876 1591 CCCACAGT C TGCACATC 3770 AGUCCAC CUGAUGAG X CGAA AACCCAAG 2879 1651 CCAAGGT T		CCGACCGT C CACGGGGC	352		
1516 GCACCTCT C TITACOCCO 354 COCCUDADA CUGAUGAG X CODA ACAGOGUC 2861 1538 ACCTCTCT T TACCCCCC 355 UCCCCCCUDA CUGAUGAG X CODA ACAGOGUC 2861 1539 CCTCTCTT T ACCCCCCCC 356 GUCCCCCC UCGAUGAG X CODA ACAGOGAC 2865 1540 CCCCCCCCT ACCCCCCCC 357 AGUICCCCC CUGAUGAG X CODA ACAGOGAC 2865 1540 CCCCCCCCC T CACCCCCT 358 CAGACCGC CUGAUGAG X CODA ACAGOGAC 2865 1551 CTCCCCCCC T CACCCCCT 359 AAGUCCCCC CUGAUGAG X CODA ACAGOGAC 2867 1553 CTCCCCCCC T CACCCCCC 359 AAGUCCAC CUGAUGAG X CODA ACGCCCAC 2869 1564 TOTOCCCT C TACTCTC 360 CAGAUGAC CUGAUGAG X CODA ACGCCCAC 2869 1565 CTCCCCCC T CATCCCC 361 CACAGUGA CUGAUGAG X CODA ACGCCCAC 2870 1566 CTCCCCCC T CACCCCC 362 COCCACAG UCGAUGAG X CODA ACGCCAC 2870 1569 CTCCCCCT C CACCCCC 363 GUCCGCCAC UCGAUGAG X CODA ACGCCAC 2871 1589 GTCCCCCT C TCCCCCC 365 GUUGAGCC CUGAUGAG X CODA ACGCCAC 2871 1593 ACTCCCCT T CACCTCCC 365 GUUGAGCC CUGAUGAG X CODA ACGCCAC 2871 1594 CTTCCCCT C TCCCCC 366 GUUGAGCC CUGAUGAG X CODA ACGCCAC 2871 1594 CTTCCCCT C TCCCCC 367 CCCCACGC CUGAUGAG X CODA ACGCCAC 2876 1595 CTCCCCCT T CACCTCCC 367 CCCCACGC UCGAUGAG X CODA ACGCCACA 2876 1596 CTCCCCCT C TCCCCC 368 GUUGAGCC CUGAUGAG X CODA ACGCCACA 2876 1597 CTCCCCT C TCCCCCC 368 GUUGAGCC CUGAUGAG X CODA ACGCCACA 2876 1598 CTCCCCCT C TCCCCC 369 CUCCAUGAG X CODA ACGCCACA 2876 1697 CCCCACGT C TCCCCCT 369 CUCCAUGAG X CODA ACGCCACA 2877 1697 CTCCCCT C TCCCCTCC 369 CUCCAUGAG X CODA ACGCCACA 2877 1697 CTCCCCT C TCCCCTCC 369 CUCCAUGAG X CODA ACGCCACA 2879 1651 CCCCACGT C TCCCCTCC 369 CUCCAUGAG X CODA ACGCCACA 2879 1653 CACCTCTC C TCCCCTCC 369 CUCCAUGAG X CODA ACGCCACA 2879 1651 CCCCACGT C TCCCCTCC 369 CUCCAUGAG X CODA ACGCCACA 2879 1653 CACCTCTC C TCCCCCT 370 ACUCCCC CUCCAUGAG X CODA ACCCUCCA 2880 1667 AGGCCTT T GCATTAA 370 UUAUGCCA CUCAUGAG X CODA ACCUCCA 2880 1667 TC		GCGCACCT C TCTTTACG	353		
1539 CCTCTCTT T ACGCGGAC 356 GUICGCGGU CUGAUGAG X CGAA AAGAGAG 2865 1540 CCTCTCTT A CGCGGACT 357 AGUICCGCG CUGAUGAG X CGAA AAGAGAG 2865 1549 CGGGGACT CCCGTCTG 358 CAGACGGG CUGAUGAG X CGAA AAGAGCGG 2867 1555 CTCCCGGT C TGTGCCTT 359 AAGGCACA CUGAUGAG X CGAA AAGGCACG 2867 1553 CTGTGCCTT CTCATCTG 360 CAGAUGAG CUGAUGAG X CGAA AAGGCACA 2869 1554 TGTGCCTT C TCATCTG 361 CAGAUGA CUGAUGAG X CGAA AAGGCACA 2870 1556 TGTCCCTT C TCATCTG 362 CGCGACAG CUGAUGAG X CGAA AAGGCACA 2870 1569 CTTCTCAT C TGCCGGAC 363 GUICGGCA CUGAUGAG X CGAA AAGGCACA 2871 1569 CTTCTCAT C TGCCGGAC 364 GUICAGGCA CUGAUGAG X CGAA AAGGCACA 2871 1589 TGTCCATT C CCTTCAC 365 GUICAGGCA CUGAUGAG X CGAA AAGGCACA 2871 1589 GTCCACTT C ACCTCTG 366 GUICAGGCA CUGAUGAG X CGAA AAGGCACA 2871 1593 ACTTCGCT T CACCTCTG 366 GUICAGGCA CUGAUGAG X CGAA AAGGCACA 2874 1593 ACTTCGCT T CACCTCTG 366 GUICAGGCA CUGAUGAG X CGAA AAGGCACA 2874 1594 CTTCCCTT C TGCCTCTC 367 CAGAGGG CUGAUGAG X CGAA AAGCCAAG 2875 1595 CTTCCCTC T CACCTCTG 367 CAGAGGG CUGAUGAG X CGAA AAGCCAAG 2876 1596 CTCCCCCT C TGCACGTC 368 ACGUGAC CUGAUGAG X CGAA AAGCCAAG 2876 1597 CTTCCCTT C TGCATGAG 369 CUCCAUGAG X CGAA AAGCCAAG 2876 1697 CTCACCT C TGCACGTC 368 ACGUGAC CUGAUGAG X CGAA AAGCCAAG 2876 1697 AGGCATT C TGCATGAG 369 CUCCAUGAG X CGAA AAGCCAAG 2877 1651 CCCAAGGT C TTCACTAA 370 UUAUGCAA CUGAUGAG X CGAA AAGCCAAG 2877 1653 CAAGGTCT T GACATGAG 371 UUUAUGCAA CUGAUGAG X CGAA AAGCCAAG 2877 1656 CTTCTGCAT T GACATGAG 372 AGUCCUCU CUGAUGAG X CGAA AAGCCAAG 2880 1667 AGAGGACT T TGCACTTC 373 AGUCCUC CUGAUGAG X CGAA AAGCCAAG 2881 1667 AGAGGACT T TGCACTTC 374 AGUCCUC CUGAUGAG X CGAA AAGCCAAG 2881 1667 AGAGGACT T TGCACTTC 374 AGUCCUC CUGAUGAG X CGAA AAGCCCAG 2881 1667 TGCACTT T CACCATGGAG 378 AGUCCUC CUGAUGAG X CGAA AAGCCCAG 2881 1667 TGCACTT T CACCATGGAG 378 CA			354		
1539 CCTCCTT T ACCCCCAC 356 GUCCCCCC UCAUGING X CORA ARAGRACIA 2865	1538	ACCTCTCT T TACGCGGA	355	UCCGCGUA CUGAUGAG X CGAA AGAGAGGU	
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1549 CONTROLOT T CONTROLOT 359 ARRIGADA CUGAUGAG X CGAA ACCOGGAG 2869 1553 CONTROLOT T CTCATCTG 360 CAGAUGAG CUGAUGAG X CGAA ACCOGGAG 2869 1564 TOTROCOT T CTCATCTG 361 CAGAUGAG CUGAUGAG X CGAA ACCOGGAG 2870 1566 TOTCOCTT C ACTOTCGC 362 CAGAUGAG CUGAUGAG X CGAA ARGEGACA 2870 1566 TOTCCTTC C ATCTCCC 363 CAGCGAGC CUGAUGAG X CGAA ARGEGACA 2871 1569 CTTCCATC T CACCCGAC 363 CUCCGGCA UGAUGAG X CGAA ARGEGACA 2871 1569 CTTCCATC T CACCCGAC 364 CUGCAGCA CUGAUGAG X CGAA ARGEGACA 2871 1589 TOTCCACT T CACCTCTC 364 CUGAAGCC CUGAUGAG X CGAA ARGUGCAC 2873 1589 GTCCACT T CACCTCTC 366 CAGAGGU CUGAUGAG X CGAA ARGUCCAC 2873 1589 CTTCACT C ACCCTCTC 366 CAGAGGU CUGAUGAG X CGAA ARGUCCAC 2873 1599 CTTCACC T CACCTCTC 367 CACAGAGGU CUGAUGAG X CGAA ARGUCCACA 2875 1599 CTTCACCT C ACCTCTC 368 GACGUCCA CUGAUGAG X CGAA ARGUCCACA 2875 1607 CTCCACCT C ACCTCTC 367 CACAGAGGU CUGAUGAG X CGAA ARGUCCACA 2875 1607 CTCCACCT C CACATGAG 369 CUCCAUGC CUGAUGAG X CGAA ARGUCCACA 2879 1607 CTCCACCT C TCCACCTT C ACCTCTC 367 CACAGAGCU CUGAUGAG X CGAA ARGUCCACA 2879 1607 CTCCACCT C TCCACCTT C ACCTCTC 367 CACAGAGCU CUGAUGAG X CGAA ARGCUCACA 2879 1607 CTCCACCT C TCCACCTT C ACCTCTC 367 CACAGAGCU CUGAUGAG X CCAA ARGCUCACA 2879 1607 CTCCACCT C TCCACACTT A TO UUAUGACC CUGAUGAG X CCAA ARGCUCACA 2879 1653 CACCCAAGCT C TCCACACTT 373 ARGUCCAC CUGAUGAG X CCAA ARGCUCAC 2880 1667 AGAGGACT C TCGACACTT 374 GAAAGGCC CUGAUGAG X CCAA ARGCUCAC 2881 1667 AGAGGACT C TCGACACTT 375 AUUCCUCU CUGAUGAG X CCAA ARGUCCAC 2881 1667 AGAGGACT T TCACCAACT 375 AUUCCUCU CUGAUGAG X CCAA ARGUCCAC 2881 1667 AGAGGACT T CACCAACTC 378 CACAGCCC CUGAUGAG X CCAA ARGUCCAC 2881 1676 TCGACTT C ARGCACCT 378 AGUCCUCU CUGAUGAG X CCAA ARGUCCAC 2881 1676 TCGACTT C ARGCACCT 378 AGUCCUCU CUGAUGAG X CCAA ARGUCCAC 2881 1676 TCGACTT C ARGCACCT 378 CAUCACACCAC C CACAGA	1540	CTCTCTTT A CGCGGACT	357		
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1564 TOTOCCTT C TOTACTOC 361 OCAGARGA CUGADAGA X CGAA AAGGCACA 2870 1566 TOTOCCTT C TATCTCCC 362 OCAGARGA CUGADAGA X CGAA AAGGCACA 2871 1569 TOTCCTTC C ATCTCCCC 363 OCCCGGCC CUGADAGA X CGAA AAGGCACA 2871 1588 TOTOCACT T CGCTTCAC 364 OUCAGACC CUGADAGA X CGAA AAGGCACA 2873 1589 TOTOCACT T CGCTTCAC 365 OUCAGAC CUGADAGA X CGAA AAGGCACA 2873 1593 ACTTCGCT T CACCTCTC 366 CAGAGGGC CUGADAGA X CGAA AAGGCACA 2873 1594 CTTCCCT T CACCTCTC 366 CAGAGGGC CUGADAGA X CGAA AAGGCACA 2873 1595 CTTCCCT T CACCTCTC 366 CAGAGGGC CUGADAGA X CGAA AAGCCACA 2873 1597 CTTCCCT C TOCACCTC 368 QACGUGCA CUGADAGA X CGAA AAGCCACA 2873 1697 CTTCCCCT C TOCACCTC 368 QACGUGCA CUGADAGA X CGAA AAGCCACA 2873 1697 CTTCCCCT C TOCACCTC 368 QACGUGCA CUGADAGA X CGAA AAGCCACA 2873 1697 CCCAAGGT C TOCACCTC 368 QACGUGCA CUGADAGA X CGAA AAGCCUCA 2875 1698 CACCAAGAC X CACCAA ACCCUCAGA 2876 1691 CACCAAGT X CACCAA 370 UUAUAGCA CUGADAGA X CGAA AAGCCUCA 2880 1696 AGAGGACT C TOGACAT 372 AGUCCUC CUGADAGA X CGAA AAGCCUCU 2881 1697 AGAGGACT C TOGACTT 373 AAGUCCCA CUGADAGA X CGAA AAGCCUCU 2881 1697 AGAGGACT C TOGACTT 374 GAAAGCC CUGADAGA X CGAA AAGUCCUCU 2882 1697 TOGACTT T CACCAAT 375 AUUACUGA CUGADAGA X CGAA AAGUCCUCU 2883 1677 TOGACTT T CACCAAT 375 AUUACUGA CUGADAGA X CGAA AAGUCCUCU 2881 1677 TOGACTT C AAGCAATC 377 ACAUCUCU CUGADAGA X CCAA AAGUCCUC 2881 1677 TOGACTT C AAGCAATC 377 ACAUCUCU CUGADAGA X CCAA AAGUCCUC 2881 1677 TOGACTT C AAGCAATC 378 AUUACUGA CUGADAGA X CCAA AAGUCCUC 2881 1677 TOGACTT C AAGCACCT 378 ACAUCUCU CUGADAGA X CCAA AAGUCCCA 2881 1677 TOGACTT C AAGCACCT 378 ACAUCUCU CUGADAGA X CCAA AAGUCCCA 2881 1677 TOGACTT C AAGCACCT 379 UAUACUCC CUGADAGA X CCAA AAGUCCCA 2881 1689 ACCAACTCT C AAGCACCT 378 AUUACUUC CUGADAGA X CCAA AAGUCCCA 2881 1710 GCCACAT	1555	CTCCCCGT C TGTGCCTT	359		
1566 TOCCTICT C ATCROCCO 362 COGCARAI CUGARGAG X COAA AGAGGCA 2871 1569 CTITICAT C TGCCCGAC 363 GUCCAGCA CUGARGAG X COAA AGAGGCA 2872 1588 TOTGCACT T CGCTTCAC 364 GUCAAGCC CUGARGAG X COAA AGUCCAC 2873 1589 GTCCACTT C CCTTCACC 365 GUCCAGCA CUGARGAG X COAA AGUCCAC 2873 1589 GTCCACTT C CCTTCACC 365 COUGAACC CUGARGAG X COAA AGUCCAC 2874 1593 ACTICGCT T CACCTCTO 366 CAGAGGU CUGARGAG X COAA AGUCCAC 2875 1594 CTTCCCTT C ACCTCTO 366 CAGAGGU CUGARGAG X COAA AGCCAAG 2875 1599 CTTCACCT C TOCACCTC 368 GACGUGCA CUGARGAG X COAA AGCCAAG 2876 1599 CTTCACCT C TOCACATA 368 GACGUACA CUGARGAG X COAA AGCCAAG 2877 1697 CTCCACGT C TGCATAA 376 CUCCAUGC CUGARGAG X COAA AGCCAAG 2878 1651 CCCAAGGT C TTCACTAT 371 UULUNGCA CUGARGAG X COAA AGCCUUG 2889 1653 CAAGGCAT C TTCACTAT 372 AGUCCUC UGARGAG X COAA AGCCUUG 2880 1657 AGGGCAT T TGCACTA 373 AGUCCACA CUGARGAG X COAA AGCCUUG 2881 1659 AGGACTCT T GACCATA 373 AGUCCACA CUGARGAG X COAA AGCCUUC 2882 1659 AGGACTCT TGCACTA 373 AGUCCACA CUGARGAG X COAA AGCCUUC 2882 1657 CTTCGACTT 374 GAAAGGCC UGARGAG X COAA AGCCUUC 2882 1657 CTTGGACTT T CAGCAAT 375 AGUCCUC UGARGAG X COAA AGCCUUC 2882 1676 TGCACTT C GACCATAG 376 CAUGCUC UGARGAG X COAA AGUCCAAC 2884 1676 TGCACTT C GACCATC 377 ACCUUCU UGARGAG X COAA AGUCCAAC 2884 1677 TGCACTTT C AGCCAAT 378 CAGUCCUU UGARGAG X COAA AGUCCAAC 2885 1689 ACCAACCT T GACCACT 378 CAGUCCUU UGARGAG X COAA AAGUCCAA 2885 1699 ACCACCT T GACCATC 378 CAGUCUU UGARGAG X COAA AAGUCCAA 2885 1699 ACCAACCT T GACCACT 378 CAGUCUU UGARGAG X COAA AAGUCCAAC 2885 1699 ACCAACCT T GACCACT 381 AGUCUUU UGARGAG X COAA AAGUCCAA 2885 1700 TAGGCATT C AAAGACCT 382 CAGUCUUU UGARGAG X COAA AAGUCCAAC 2889 1701 TGCATTT C AAAGACTC 382 CAGUCUUU UGARGAG X COAA AAGUCCAAC 2889 1702 TCTCTTCTT C AAAGACTC 382 CAGUCUUU UGARGAG X COAA AAGACCACA 2891	1563	CTGTGCCT T CTCATCTG	360		
1566	1564	TGTGCCTT C TCATCTGC	361		
1588	1566	TGCCTTCT C ATCTGCCG	362		
1588	1569	CTTCTCAT C TGCCGGAC	363		
1593 ACTTGGCT T CACCTETC 366 CAGAGGUG CUGAUGAG X CGAA AGGGAAGU 2875 1594 CTTGGCT C ACCTETCC 367 CACAGGGU CUGAUGAG X CGAA AGGGAAGU 2877 1599 CTTGACCT C TGCACGTC 368 GACGUGGA CUGAUGAG X CGAA AGGGAAGU 2877 1607 CTGCACGT C GCATGGAG 369 CUCCAUGC CUGAUGAG X CGAA AGGUGAG 2877 1651 CCCAAGGT C TGCATAA 370 UUAUGAGA CUGAUGAG X CGAA AGGCUGG 2879 1653 CACAGGTC T TGCATAA 371 UUAUGAGA CUGAUGAG X CGAA AGGCUGG 2880 1658 TCTTGCATA AGGGACTT 372 AGUCCUCU CUGAUGAG X CGAA AGACCUUG 2880 1658 TCTTGCAT A TGCATTA 373 AAGUCCA CUGAUGAG X CCAA AGGCUGG 2881 1657 AGGGACTT C TGGACTT 373 AAGUCCA CUGAUGAG X CCAA AGGCUCU 2882 1659 AGGCACTT C TGCACTT 374 GAAAGGCC CUGAUGAG X CCAA AGUCCUC 2883 1675 CTTGGACTT T CACCAAT 375 AUUGCUGA CUGAUGAG X CCAA AGUCCUC 2883 1676 TGGACTTT C TACCAAT 376 CAUUGCG CUGAUGAG X CCAA AGUCCUC 2883 1677 TGGACTTT C AGCCAATC 377 ACAUGCG CUGAUGAG X CCAA AGUCCCAA 2885 1678 AGCAATCT C AGCGACTG 378 CAUUGCG CUGAUGAG X CCAA AAGUCCAA 2885 1679 ACCACCT T GAGCCAT 377 ACAUGCC CUGAUGAG X CCAA AAGUCCAA 2885 1689 ACCAACTCT C AGCGACTG 378 CAUUGAGG CUGAUGAG X CCAA AAGUCCAA 2885 1699 ACCACCT T GAGCCAT 379 UAUGCCC CUGAUGAG X CCAA AAGUCCAA 2885 1700 TGAGCCAT A CTTCAAAG 380 CUUUGAGA CUGAUGAG X CCAA AAGUCCC 2887 1701 TGAGCCAT A CTTCAAAG 380 CUUUGAGA CUGAUGAG X CCAA AAGUCCC 2887 1710 CACCACTT C AAGAGCT 381 AGUCUUUC CUGAUGAG X CCAA AAGUCCC 2889 1711 GCATACTT C AAGAGCT 381 AGUCUUUC CUGAUGAG X CCAA AAGUCCC 2881 1725 CTCTCTTT T AATCAGT 382 CAGUCCUU CUGAUGAG X CCAA AAGUCCC 2881 1726 CTCTCTTT T AATCAGT 384 CACUCCUU CUGAUGAG X CCAA AAGUCCC 2891 1727 GTCTCTTT T AATCAGT 384 CACUCCUU CUGAUGAG X CCAA AAGUCCC 2891 1727 GTCTCTTT T AATCAGT 384 CACUCCUU CUGAUGAG X CCAA AAGUCCC 2891 1727 GTCTCTTT T AATCAGT 384 CACUCCUU CUGAUGAG X CCAA AAGUCCC 2892 1728 CTCTCTTTT T AATCAGT 384 CACUCCUU CUGAUGAG X C	1588	TGTGCACT T CGCTTCAC	364		
1594 CTTCOCTT C ACCTECTC 368 GCAGAGGG CUGAUGAG X CGAA AMGCGAAG 2876 1599 CTTCOCTT C TOCACGTC 368 GCAGAGGG CUGAUGAG X CGAA AMGCGAAG 2877 1599 CTTCACCT C TOCACGTC 368 GACGUGCA CUGAUGAG X CGAA AGGUGCAG 2877 1697 CTCCACCT C GCATGGAG 369 CUCCAGGG C CUGAUGAG X CGAA AGGUGCAG 2877 1698 CCCCAGGT C TOCACTAA 370 ULUAUGCA CUGAUGAG X CGAA AGCUUGG 2879 1653 CAMAGGTC T TOCATAA 371 ULUAUGCA CUGAUGAG X CGAA AGCUUGG 2880 1658 TCTTGCAT A AGAGGACT 372 AGUCCUC CUGAUGAG X CCAA AGCUUG 2880 1659 AGGACTCT T GGACTTT 373 AAGUCCAA CUGAUGAG X CGAA AGUCCUC 2880 1669 AGGACTCT T CAGCAAT 374 GAAAGUCC CUGAUGAG X CGAA AGUCCUC 2880 1676 TTGGACTT T CAGCAAT 375 AUUGCUG CUGAUGAG X CGAA AGUCCAA 2881 1676 TTGGACTT T CAGCAAT 375 AUUGCUG CUGAUGAG X CGAA AGUCCAA 2881 1677 TGGACTTT C AGCCAAT 376 CAUUGCUC CUGAUGAG X CGAA AAGUCCA 2885 1686 AGCAATOT C AAGCACGG 377 ACAUUGCU CUGAUGAG X CGAA AAGUCCA 2885 1687 ACCACCT T GAGCACTA 379 CAGUCCUC CUGAUGAG X CGAA AAGUCCA 2885 1686 AGCAATOT C AAGCACGG 379 CAGUCCUU CUGAUGAG X CGAA AAGUCCA 2886 1707 TGAGGCTT C GAGGCATA 379 UNIGCCUC CUGAUGAG X CGAA AAGUCCA 2886 1708 ACCACCT T GAGGCATA 379 UNIGCCUC CUGAUGAG X CGAA AAGUCCA 2886 1707 TGAGGCAT A CTTCAAAG 380 CUUCAAG CUGAUGAG X CGAA AAGUCCCU 2889 1708 ACCACCT T GAGGCATA 379 UNIGCCUC CUGAUGAG X CGAA AAGUCCCU 2889 1707 TGAGGCTT C TAAGACCT 381 AGUCUUU CUGAUGAG X CGAA AAGUCCCC 2889 1711 GCATACTT C AAGACCT 381 AGUCUUU CUGAUGAG X CGAA AAGUCCCC 2889 1726 TOTCTTT T AATGAGT 381 AGUCUUU CUGAUGAG X CGAA AAGUCCCC 2891 1727 TCTCTTTT T AATGAGT 384 CACUCAUU CUGAUGAG X CGAA AAGCACACA 2891 1728 TCTCTTTT T AATGAGT 385 CACUCCCC CUGAUGAG X CGAA AACACACAC 2891 1727 TCTCTTTT T AATGAGT 386 CACUCCCC CUGAUGAG X CGAA AACACACAC 2891 1728 TCTCTTTT T AATGAGT 386 CACUCCCCC CUGAUGAG X CGAA AACACACAC 289	1589		365		
1599 CTTCACCT C TOCACGTC 358 GACGUGGA CUGAUGGA X CGAA AGGUGAAG 2877 1607 CTCCACGT C GCATGGAG 369 GUCCAUGG CUGAUGGA X CGAA AGGUGAAG 2878 1651 CCCAAGGT C TICCACTAA 370 UUAUGAGA CUGAUGAG X CGAA AGCUUGGG 2879 1653 CACCAGGT C TICCATAA 371 UUAUGAGA CUGAUGAG X CGAA AGCUUGGG 2879 1658 TCTCGCAT A AGAGGACT 372 AGUCCQUC UGAUGAGA X CGAA AGACCUUG 2880 1658 TCTCGCAT A AGAGGACT 373 AGUCCQA CUGAUGAG X CGAA AGACCUUG 2881 1657 AGAGGACT C TICGACTT 373 AGUCCAA CUGAUGAG X CGAA AGUCCUU 2882 1659 AGAGGACT T TOCACAT 375 AGUCCAA CUGAUGAG X CCAA AGUCCUU 2882 1675 CTTGGACT T TOACCAT 375 AUUGCUGA CUGAUGAG X CCAA AGUCCUU 2881 1676 TTGGACTT C AGCAATG 376 CAUUGCGA CUGAUGAG X CCAA AGUCCAA 2881 1677 TGGACTT C AGCAATG 377 ACAUGCG UGAUGAGA X CCAA AGUCCAA 2885 1677 TGGACTT C AGCAATG 377 ACAUGCC UGAUGAGA X CCAA AAGUCCAA 2885 1678 AGCAATGT C AGCGACGG 378 CAUUGAGAG X CCAA AAGUCCAA 2885 1689 ACCAACT C AGCGACTG 379 UAUGCCUC UGAUGAGA X CCAA AAGUCCA 2885 1699 ACCACCT T GAGGCCTA 379 UAUGCCUC UGAUGAGA X CCAA AAGUCCCU 2887 1700 TGAGGCAT A CTTCAAAG 380 CUUUGAAG CUGAUGAG X CCAA AAGUCCCU 2887 1710 GCATACT C AAGAGCT 381 AGUCUUU CUGAUGAG X CCAA AAGUCCCU 2887 1711 GCATACTT C AAGAGCT 381 AGUCUUU CUGAUGAG X CCAA AAGUCCCU 2881 1712 TCTCTCTT T AATGGGT 382 CAGUCUUU CUGAUGAG X CCAA AAGUCCCU 2881 1713 GTCTCTTT T AATGGGT 384 CACUCAUU CUGAUGAG X CCAA AAGUCCCU 2891 1726 TOTCTCTT T AATGGGT 384 CACUCAUU CUGAUGAG X CCAA AAGUCCCU 2891 1727 GTCTCTTT T AATGGGT 384 CACUCAUU CUGAUGAG X CCAA AAGUCCCU 2891 1728 TCTCTCTTT T AATGGGT 384 CACUCAUU CUGAUGAG X CCAA AAGUCCCU 2891 1729 TCTCTCTTT T AATGGGT 385 CACUCCCC CUGAUGAG X CCAA AACACACAC 2891 1727 GTCTCTTT T AATGGGT 386 CCCCCCC CUGAUGAG X CCAA AACACACAC 2891 1728 TCTCTCTTT T AATGGGT 386 CCCCCCCC CUGAUGAG X CCAA AACACACCC 2891 1729 TCTCTCTTT T AATGGGT 386 CCCCCCC CUGAUGAG X CCCAA ACCACCAC 2892 1726 TCTCTCTTT T AATGGGT 386 CCCCCCC CUGAUGAG X CCCAA ACCACCAC 2895 1727	1593	ACTTCGCT T CACCTCTG	366		
1699 CTTOCACT C TUCACUTC 388 CUCCAUGG CUGAUGAG X CORA ACQUIGCAG 2879 1651 CCCAAGGT C TOCATGAA 370 ULUAUGCA CUCAUGAG X CORA ACQUIGCAG 2879 1653 CAAGGTCT T COCATAGAA 371 ULUAUGCA CUCAUGAG X CORA ACQUIGCAG 2879 1658 TCTTOCAT A AGAGGACT 372 AGUCCUCU CUGAUGAG X CORA AGACCUUG 2880 1658 TCTTOCAT A AGAGGACT 372 AGUCCUCU CUGAUGAG X CORA AGACCUUG 2881 1657 AGAGGACT C TTGACCAT 374 AGACCUCU CUGAUGAG X CORA AGACCUUG 2882 1659 AGGACTCT T GACCTTT 374 AGACCUCU CUGAUGAG X CORA AGACCUCUC 2882 1676 TOTGCATT T CACCCAT 375 AUJUCCUG CUGAUGAG X CORA AGACCUCA 2885 1676 TOGACTT T CACCCAT 376 CAUJUCCU CUGAUGAG X CORA AGUCCAA 2885 1677 TGGACTTT C AGCCATG 377 ACAUJUCCU CUGAUGAG X CORA AGACUCCA 2885 1686 AGCATACT C AGACACCG 378 CAGUCUCU UCAUGAGG X CORA AGAGUCCA 2885 1699 ACCGACT T GAGCACTG 379 CAGUCUCU UCAUGAGG X CORA AGAGUCCA 2886 1707 TCAAGCATT T GAGCACTG 379 CAGUCUU UCAUGAGG X CORA AGAGUCCA 2886 1707 TCAAGCACT A CTTCAAAG 380 CUUUGAAG CUGAUGAG X CORA AGUCCUCC 2889 1708 TCAAGCACTG 379 CAGUCUU UCAUGAGG X CORA AGUCCAC 2889 1700 TCAAGCACTG 370 CAGUCUUU UCAUGAGG X CORA AGUCCAC 2889 1710 GCATACTT C AAGACCTG 381 AGUCUUUU CUGAUGAG X CORA AGUCCUCC 2889 1711 GCATACTT C AAGACCTG 382 CAGUCUUU CUGAUGAG X CORA AGUCCUCC 2891 1726 TOTCTTTT T AATCAGTG 383 ACUCAUAU CUGAUGAG X CORA AGCCCACA 2891 1726 TOTCTTTT T AATCAGTG 384 CACCUCCCC CUGAUGAG X CORA AACACACAC 2891 1727 GTOTCTTT T AATCAGTG 384 CACCUCCCC CUGAUGAG X CORA AACACACAC 2892 1728 CTCTOTTTT T AATCAGTG 384 CACCUCCCC CUGAUGAG X CORA AACACACAC 2893 1727 GTOTCTTT T AATCAGTG 384 CACCUCCCC CUGAUGAG X CORA AACACACAC 2893 1728 CACCUCCCC CUGAUGAG X CORA AACACACAC 2893 1729 CTCTOTTTT T AATCAGTG 384 CACCUCCCC CUGAUGAG X CORA AACACACAC 2893 1729 CTCTOTTTT AATCAGGTG 384 CACCUCCCC CUGAUGAG X CORA AACACACAC 2893	1594	CTTCGCTT C ACCTCTGC	367		
1651 CCCARGOT C DEATOURS 389 UURUNIGEDA CUERURGA X CORA ACCUUGGE 2879 1653 CARGOTET T GORTANGA 371 UURUNIGE CUIGAURGA X CORA ACCUUGGE 2880 1658 TETTOROT A RADROGAET 372 AGUCCUCC UCRAUGAG X CORA AURCANGA 2881 1667 AGRICATET C TOGACTT 373 ARGUECA CUGAUGAG X CORA AURCANGA 2881 1669 AGRICTET C TOGACTT 374 GARAGUCC UCRAUGAG X CORA AURCANGA 2881 1675 CTTOGACTT T CACCART 375 AUUGCUGA CUGAUGAG X CORA AURCANGA 2881 1676 TTOGACTT T CACCART 375 AUUGCUGA CUGAUGAG X CORA AUGUCCU 2882 1677 TTOGACTT T CACCART 375 AUUGCUGA CUGAUGAG X CORA AUGUCCA 2885 1677 TTOGACTT C AGCARTOT 377 ACAUUGCU CUGAUGAG X CORA AUGUCCA 2885 1677 TGGACTT C AGCARTOT 377 ACAUUGCU CUGAUGAG X CORA AUGUCCA 2885 1686 AGCARTOT C AGCARTOT 377 ACAUUGCU CUGAUGAG X CORA AUGUCCA 2887 1686 AGCARTOT C AGCARCOT 378 CUGUCGU CUGAUGAG X CORA AUGUCCA 2887 1699 ACCARCOT C AGGACCTA 379 UURUCCUC CUGAUGAG X CORA AUGUCCO 2888 1700 TCAGGCAT A CTTCAAAG 380 CUUUGAG CUCAUGAG X CORA AUGUCCO 2888 1710 GCATACTT C AAGAGCT 381 AUUCUUU CUGAUGAG X CORA AUGUCCO 2889 1711 GCATACTT C AAGAGCT 381 AUUCUUU CUGAUGAG X CORA AUGUCCO 2889 1726 TOTOTOTT T AATCAGOT 382 AUUCUUU CUGAUGAG X CORA AUGUCCO 2891 1727 GTOTOTTT T AATCAGOT 384 CACUCAUU CUGAUGAG X CORA ACACACAC 2891 1728 TOTOTOTT T AATCAGOT 384 CACUCAUU CUGAUGAG X CORA ACACACAC 2891 1727 GTOTOTTT T AATCAGOT 385 CACUCCOC CUGAUGAG X CORA ACACACAC 2891 1728 TOTOTOTT T AATCAGOT 386 CCCUCCCC CUGAUGAG X CORA ACACACAC 2891 1729 TOTOTOTT T AATCAGOT 386 CCCUCCCC CUGAUGAG X CORA ACACACAC 2891 1721 TOTOTOTT T AATCAGOT 386 CCCUCCCC CUGAUGAG X CORA ACACACAC 2891 1727 GTOTOTTT T AATCAGOT 386 CCCUCCCC CUGAUGAG X CORA ACCACACC 2891 1728 TOTOTOTT T AATCAGOT 386 CCCUCCCC CUGAUGAG X CORA ACCACACAC 2891 1729 TOTOTOTT T AATCAGOT 386 CCCUCCCC CUGAUGAG X CORA AC	1599				
1651 CCCAAGGT C TUCATAA 370 UUUNDAGC CUGARDAGA X CGAA AGACCUUC 2880 1658 TCTTOCAT A AGAGGACT 372 AGUICCUC CUGAUGAG X CGAA AGACCCUUC 2881 1658 AGAGGACT C TOGACTT 373 AAGUICCACA CUGAUGAG X CGAA AUGCAAGA 2881 1659 AGGGACT T TOGACTT 374 GAAAGUIC CUGAUGAG X CGAA AGACCCUUC 2882 1659 AGGACTCT T GACCTTT 374 GAAAGUIC CUGAUGAG X CGAA AGAGUICU 2883 1676 TTGGACTT T CAGCAAT 375 AUUNCUGA CUGAUGAG X CGAA AGAGUICCAA 2884 1676 TTGGACTT C CAGCAATG 376 CAUUNCUG CUGAUGAG X CGAA AAGUICCAA 2885 1677 TGGACTT C CAGCAATG 376 CAUUNCUG CUGAUGAG X CGAA AAGUICCAA 2885 1678 TGGACTT C GAGCATG 377 CACUUNCU CUGAUGAG X CGAA AAGUICCAA 2885 1686 AGCANTOT C AAGCACCG 378 CAGUICCUU CUGAUGAG X CGAA AAGUICCA 2887 1699 ACCGACCT T GAGCATT 379 UNUNCCUG CUGAUGAG X CGAA AAGUICGU CUGAUGAG X CGAA AAGUICGU CUGAUGAG X CGAA AAGACACA 2891 1743 CTOTOTTT T AATGGACT 383 ACUCAUUC CUGAUGAG X CGAA AACACACA 2891 1743 CTOTOTTT T AATGGACT 384 CACUCAUU CUGAUGAG X CGAA AACACACA 2894 1743 CGAGCACT T ATGGACT 386 CACUCCCC CUGAUGAG X CGAA AACACACAC 2895 1743 CGAGCACT T AAGGGCT 386 CACUCCCC CUGAUGAG X CGAA AACACACAC 2895 1743 CGAGCACT T AAGGGCT 386 CACUCCCC CUGAUGAG X CGAA AACACACAC 2895 1743 CGAGCACT T AAGGGCT 386 CACUCCCC CUGAUGAG X CGAA AACACACAC 2895 1743 CGAGCACT T AAGGGCT 386 CACUCCCCC CUGAUGAG X CGAA AACACCACAC 2895 1743 CGAGCACTT T AATGG	1607		369		
1658 TOTTOPONT A GARGACTT 372 AGUICCIGU CUGAUGAG X CGAA AUGCAAGA 2881 1667 AGAGGACT C TTGGACTT 373 AGUICCAA CUGAUGAG X CGAA AUGCAAGA 2881 1669 AGACTCT T GAGCATT 374 GAAAGUCC CUGAUGAG X CGAA AGAGUCCU 2882 1675 CTGGACT T TCACCAAT 375 AUUGCUGA CUGAUGAG X CGAA AGAGUCCU 2883 1676 TTGGACTT T CACCAAT 375 AUUGCUGA CUGAUGAG X CGAA AGAGUCCA 2884 1677 TGGACTT C AGACACG 378 CACUUCCU CUGAUGAG X CGAA AGAGUCCA 2885 1688 AGCANTOT C AACGACCG 378 CACUUCCU CUGAUGAG X CGAA AAGUCCA 2885 1689 ACCACCT GAGCCATA 379 UNUGCUC CUGAUGAG X CGAA AAGUCCA 2887 1699 ACCACCT GAGCCATA 379 UNUGCUC CUGAUGAG X CGAA AAGUCCC 2887 1700 TGAGGCAT A CTTCAAAG 380 CUUUGAG CUGAUGAG X CGAA AGGUCGU 2888 1710 GACTACTT C AAAGACCT 381 AGUCUUU CUGAUGAG X CGAA AGUUGCC 2889 1711 GCATACTT C AAAGACT 381 AGUCUUU CUGAUGAG X CGAA AAGUUGC 2889 1726 TOTCTOTT T TAATGAGT 382 CAGUUUU CUGAUGAG X CGAA AAGUUGC 2891 1726 TOTCTOTT T AATGAGT 384 CACUCAUU CUGAUGAG X CGAA AACACACA 2892 1727 GTCTOTTT T AATGAGT 385 CACUCCCC CUGAUGAG X CGAA AACACACA 2891 1728 CACCACTACT C GAGCAGG 386 CCUCCCCC CUGAUGAG X CGAA AACACACA 2891 1729 CACCACTT T C AAAGACT 381 CACUCAUU CUGAUGAG X CGAA AACACACA 2891 1726 TOTCTOTT T AATGAGT 385 CACUCCCC CUGAUGAG X CGAA AACACACAC 2891 1727 GAGCAGAT T GGGGGAGG 386 CCUCCCCC CUGAUGAG X CGAA AACACACAC 2891 1728 CACCACCAC CUGAUGAG X CGAA AACACACAC 2891 1729 CACCACCACCAC CACCACCAC 2891 1720 CACCACCACCACCAC 2892 2892 2893 289	1651		370		
1658 TCTTGCAT A AGRICUACU 372 AGRICCAGU CARRAGAG X CORA GAUCCUCU 2882 1667 AGRIGGACT C TOGACTT TO 374 AGRICCAGU CUGAUGAG X CORA AGRICCUCU 2883 1669 AGRICCAT T GACTTTC 374 GARAGUCC CUGAUGAG X CORA AGRICCAGA 2884 1676 TOGACTT T CAGCART 375 AUUGCUGA CUGAUGAG X CORA AGRICCAA 2884 1676 TOGACTT T CAGCARTO 376 CALIJUCUG CUGAUGAG X CORA AGRUCCA 2885 1677 TGGACTT C AGCARTO 377 ACAJUGCU CUGAUGAG X CORA AGUUCCA 2885 1686 ACCARCOT T GAGCACTA 379 COGUCCUU CUGAUGAG X CORA AGUUCGU 2887 1707 TGAGGATT C TOTAJAG 380 CUULUGAG CUGAUGAG X CORA AGUUCGCU 2889 1710 GROCATACT T CARAGACT 381 AGUCUUUG CUGAUGAG X CORA AGUUGCC 2890 1711 GROCATACT C ARAGACT 381 AGUCUUUG CUGAUGAG X CORA AGUUGCC 2891 1711 GROCATACT C ARAGACT 381 AGUCUUUG CUGAUGAG X CORA AGACACA 2891 1726 TCTOTOTT T ARAGACT 382 ACUCAUUA CUGAUGAG X CORA AGACACA 2891	1653				
1669 AGGACTET C GACCATTC 373					
1659	1667		1		
1675 CTTGGGCTT T CAGCANT 373 ACCICCOS CONCREGAS X CGAA ANGUCCA 2885 1676 TTGGACTTT C AGCCANTG 376 CAUUGCUG CUGAUGAG X CGAA ANGUCCA 2885 1677 TGGACTTT C AGCCANTG 377 ACAUUGCUG CUGAUGAG X CGAA ANGUCCA 2886 1686 ACCANCTG C AAGCACCG 378 CGGUCCUU CUGAUGAG X CGAA ANGUCCA 2886 1699 ACCGACCT T GAGGCATA 379 UNUGCCUG CUGAUGAG X CGAA ANGUCGU 2887 1707 TGAGGCAT A CTTCANAG 380 CUUUGAGAG CUGAUGAG X CGAA ANGUCGU 2889 1710 GGCATACTT C ANAGACTG 381 AGUCUUUG CUGAUGAG X CGAA AGUAUGCC 2899 1711 GCATACTT C ANAGACTG 382 AGUCUUU CUGAUGAG X CGAA AGUAUGCC 2891 1713 CTCTGTGT T TATGGGT 383 ACUCAUUA CUGAUGAG X CGAA AAGCACA 2891 1726 TGTGTGTT T ANTGAGTG 384 ACUCCUG UCGAUGAG X CGAA AACACACA 2891 1727 GTGTGTT T ANTGAGTG 384 CACUCAUU CUGAUGAG X CGAA AACACACA 2891 1727 GTGTGTT T ANTGAGTG 384 CACUCAUU CUGAUGAG X CGAA AACACACA 2891 1727 GTGTGTT T ANTGAGTG 385 CACUCCUG CUGAUGAG X CGAA AACACACA 2891 1727 GTGTGTT T ANTGAGTG 385 CACUCCUG CUGAUGAG X CGAA AACACACA 2891 1727 GTGTGTT T ANTGAGTGG 385 CACUCCUCC CUGAUGAG X CGAA AACACACA 2891 1727 GTGTGTT T ANTGAGTGG 386 CCCUCCCC CUGAUGAG X CGAA AACACACA 2891 1728 GGAGGAGT T GGGGGAGG 386 CCCUCCCC CUGAUGAG X CGAA AACACACA 2891	1669				
1676 TIGOROTT T CAGCARIG 376 ACQUIGCU CUGAUGAG X CGAA ARAGUCCA 2886 1677 TGGACTT C ARCCARIG 377 ACQUIGCU CUGAUGAG X CGAA ARAGUCCA 2887 1698 ACCARCT C ARCCARICA 378 COGUICQUU CUGAUGAG X CGAA ARAGUCCA 2887 1699 ACCGACT T GAGGCATA 379 UNIGCCUC CUGAUGAG X CGAA ARAGUCCGA 2888 1707 TGAGGCAT A CTTCARAG 380 CUUUGAG CUGAUGAG X CGAA ARUGCCUCA 2889 1710 GECATACT T CARAGACT 381 AGUUCUUG CUGAUGAG X CGAA ARUGCUCA 2891 1711 GCATACTT C ARAGACT 382 CAGLUUUU CUGAUGAG X CGAA ARGAUGCC 2891 1725 CTGTGTGT T TAATGAGTG 383 ACUCAUUA CUGAUGAG X CGAA ARCACACA 2893 1726 TGTGTGTT T ARTGAGTG 384 CACUCAUU CUGAUGAG X CGAA ARCACACA 2893 1727 CTGTGTTT A ATGAGTGG 384 CACUCAUU CUGAUGAG X CGAA ARCACACA 2894 1728 TGTGTGTT T GAGGTGG 385 CCACUCCUC UCGAUGAG X CGAA ARCUCCUC 2894 1729 GGGGGAGG 386 CCUCCCCC CUGAUGAG X CGAA ACUCCUCC 2894 1729 GGGGGAGG 386 CCUCCCCC CUGAUGAG X CGAA ACUCCUCC 2895 1729 CGGGGGAGG 386 CCUCCCCC CUGAUGAG X CGAA ACUCCUCC 2895 1729 TGGGGGAGG 386 CCUCCCCC CUGAUGAG X CGAA ACUCCUCC 2895 1720 TGGGGGAGG 386 CCUCCCCC CUGAUGAG X CGAA ACUCCUCC 2895 1720 TGGGGGAGG 386 CCUCCCCC CUGAUGAG X CGAA ACUCCUCC 2895 1720 TGGGGGAGG 386 CCUCCCCC CUGAUGAG X CGAA ACUCCUCC 2895 1720 TGGGGGAGG 386 CCUCCCCC CUGAUGAG X CGAA ACUCCUCC 2895 1721 TGGGGGAGG 386 CCUCCCC CUGAUGAG X CGAA ACUCCUCC 2895 1722 TGGGGGAGG 386 CCUCCCC CUGAUGAG X CGAA ACUCCUCC 2895 1723 TGGGGGAGG 386 CCUCCCC CUGAUGAG X CGAA ACUCCUCCC 2895 1724 TGGGGGAGG 386 CCUCCCC CUGAUGAG X CGAA ACUCCUCCC 2895 1725 TGGGGGAGG 386 CCUCCCC CUGAUGAG X CGAA ACUCCUCCC 2895	1675				
1677 TORACTIT C AUCANTOL 377 CANDESCE CONCARGAS X CORA NATURCU 2887 1686 ACCANTOC T AGAGACCO 378 CANDECUCU CUGAUGAG X CORA AGAUUCCU 2887 1599 ACCGACCT T GAGGCATA 379 UNIOCCUC CUGAUGAG X CORA AGCUCGU 2888 1700 TORAGCAT A CITTONAG 380 CUUUCAGA CUGAUGAG X CORA AGCUCUCA 2889 1710 GGCATACT T CANAGACT 381 AGUCUUUG CUGAUGAG X CORA AGUAUGCC 2890 1711 GCATACTT C ARAGACTG 382 CAGUCUU CUGAUGAG X CORA AGUAUGCC 2891 1725 CITCOTOTT T ARAGAGTG 383 ACUCAUUA CUGAUGAG X CORA AACACACA 2891 1726 TOTGTOTT T ARTGAGTG 384 CACUCAUU CUGAUGAG X CORA AACACACA 2891 1727 CITCOTOTT T ARTGAGTG 385 CACUCCUCC UCGAUGAG X CORA AACACACA 2891 1728 CACUCAUGA CUGAUGAG X CORA AACACACA 2894 1729 CITCOTOTT A ARTGAGTGG 385 CACUCCUCC UCGAUGAG X CORA AACACACA 2894 1733 GGAGGAGT T GGGGGAGG 386 CCUCCCCC CUGAUGAG X CORA AACACCAC 2895 1743 GGAGGAGT T GGGGGAGG 386 CCUCCCCC CUGAUGAG X CORA AACACCAC 2895 1743 GGAGGAGT T GGGGGAGG 386 CCUCCCCC CUGAUGAG X CORA AACACCAC 2895 1743 GGAGGAGT T GGGGGAGG 386 CCUCCCCC CUGAUGAG X CORA AACACCAC 2895 1744 CACUCAUCAUCAUGAG X CORA AACACCAC 2895 1745 CACUCAUCAUCAUCAUCAUCAUCAUCAUCAUCAUCAUCAU	1676				
1886 ASCANCIO C ARGORCATA 379 UNIOCCUIC CUGAUGAG X CGRA AGGUCGGU 2888	1677				
1699 ACCUARCH T GROUGHT 379 CHURCHOS CHEARAGH X CORA MUSCCUCA 2889					
1707 TOAGGCAT A CITCHANGA 380 COUCUMUS CUGANAGAS X CORA AGUIUGCC 2890					
1710 GECATACTT C ANAGACTO 381 AGUCUSUU CUGAUGAG X CORA ARGUMUSC 2891					
1711 GEATACTI C ADMINICTO 302 CROSCOSO CHARAGE I CODA ACACACAG 2892 1725 CTOTOTOT T TATACAGT 383 ACUCAJUA CUCAJUAGA X CODA ACACACAG 2893 1726 TOTOTOTT T ANTOATOT 384 CACUCAJU CUCAJUAG X CODA AACACACA 2894 1727 GTOTOTT A ATGAGTGG 385 CACACACA UCAJUAGA X CODA AACACAC 2894 1743 GGAGGAOT T GGGGGAGG 386 CCUCCCC CUGAJUAGA X CODA ACUCCUCC 2895 1743 CACACACACACAC 2895 1743 CACACACACACACACACACACACACACACACACACAC					
1725 CITCHENT T TANIGART 383 CACUCADU CUGAUGAG X CGAA AACACACA 2893 1727 CITCHENT A ATGASTG 384 CACUCADU CUGAUGAG X CGAA AACACACA 2894 1727 CITCHENT A ATGASTG 385 CCACUCAU CUGAUGAG X CGAA AACACCC 2894 1743 OGAGGAGT T GGGGGAGG 386 CCUCCCC CUGAUGAG X CGAA AACUCCUCC 2895 1743 CACUCADU CUGAUGAG X CGAA ACUCCUCC 2895 1743 1744					
1726 TGTGTGTT F ATGAGTGG 385 CCACUCAU CUGAUGAG X CGAA AAACACAC 2894 1727 GTGTGTT A ATGAGTGG 385 CCUCCCCC CUGAUGAG X CGAA AAACACAC 2894 1743 GGAGGGT T GGGGGAGG 386 CCUCCCCC CUGAUGAG X CGAA ACUCCUCC 2895	1725				
1727 GTGTGTTT A ATGASTGG 385 CCACCGAC CUGAUGAG X CGAA ACUCCUCC 2895 1743 GGAGGAGT T GGGGGAGG 386 CCUCCCCC CUGAUGAG X CGAA ACUCCUCC 2895					
1743 GGAGGAGT T GGGGGAGG 380 CCCCCCCC CCCCCCCC 2000					
1756 GAGGAGGT T AGGTTAAA 387 UUUAACCU CUGAUGAG X CGAA ACCUCCUC 2896					
	1756	GAGGAGGT T AGGTTAAA	387	UUUAACCU CUGAUGAG X CGAA ACCUCCUC	2090

Table 37

			CUUUAACC CUGAUGAG X CGAA AACCUCCU	2897
1757	AGGAGGTT A GGTTAAAG	388	AGACCUUU CUGAUGAG X CGAA ACCUAACC	2898
1761	GGTTAGGT T AAAGGTCT	389	AAGACCUU CUGAUGAG X CGAA AACCUAAC	2899
1762	GTTAGGTT A AAGGTCTT	390		2900
1768	TTAAAGGT C TTTGTACT	391	AGUACAAA CUGAUGAG X CGAA ACCUUUAA	2901
1770	AAAGGTCT T TGTACTAG	392	CUAGUACA CUGAUGAG X CGAA AGACCUUU	2902
1771	AAGGTCTT T GTACTAGG	393	CCUAGUAC CUGAUGAG X CGAA AAGACCUU	2902
1774	GTCTTTGT A CTAGGAGG	394	CCUCCUAG CUGAUGAG X CGAA ACAAAGAC	
1777	TTTGTACT A GGAGGCTG	395	CAGCCUCC CUGAUGAG X CGAA AGUACAAA	2904
1787	GAGGCTGT A GGCATAAA	396	UUUAUGCC CUGAUGAG X CGAA ACAGCCUC	
1793	GTAGGCAT A AATTGGTG	397	CACCAAUU CUGAUGAG X CGAA AUGCCUAC	2906
1797	GCATAAAT T GGTGTGTT	398	AACACACC CUGAUGAG X CGAA AUUUAUGC	2907
1805	TGGTGTGT T CACCAGCA	399	UGCUGGUG CUGAUGAG X CGAA ACACACCA	2908
1806	GGTGTGTT C ACCAGCAC	400	GUGCUGGU CUGAUGAG X CGAA AACACACC	2909
1824	ATGCAACT T TTTCACCT	401	AGGUGAAA CUGAUGAG X CGAA AGUUGCAU	2910
1825	TGCAACTT T TTCACCTC	402	GAGGUGAA CUGAUGAG X CGAA AAGUUGCA	2911
1826	GCAACTIT T TCACCTCT	403	AGAGGUGA CUGAUGAG X CGAA AAAGUUGC	2912
1827	CAACTTTT T CACCTCTG	404	CAGAGGUG CUGAUGAG X CGAA AAAAGUUG	2913
1828	AACTTTTT C ACCTCTGC	405	GCAGAGGU CUGAUGAG X CGAA AAAAAGUU	2914
1833	TTTCACCT C TGCCTAAT	406	AUUAGGCA CUGAUGAG X CGAA AGGUGAAA	2915
1839	CTCTGCCT A ATCATCTC	407	GAGAUGAU CUGAUGAG X CGAA AGGCAGAG	2916
1842	TGCCTAAT C ATCTCATG	408	CAUGAGAU CUGAUGAG X CGAA AUUAGGCA	2917
1845	CTAATCAT C TCATGTTC	409	GAACAUGA CUGAUGAG X CGAA AUGAUUAG	2918
1847	AATCATCT C ATGTTCAT	410	AUGAACAU CUGAUGAG X CGAA AGAUGAUU	2919
1852	TCTCATGT T CATGTCCT	411	AGGACAUG CUGAUGAG X CGAA ACAUGAGA	2920
1853	CTCATGTT C ATGTCCTA	412	UAGGACAU CUGAUGAG X CGAA AACAUGAG	2921
1858	GTTCATGT C CTACTGTT	413	AACAGUAG CUGAUGAG X CGAA ACAUGAAC	2922
1861	CATGTCCT A CTGTTCAA	414	UUGAACAG CUGAUGAG X CGAA AGGACAUG	2923
1866	CCTACTGT T CAAGCCTC	415	GAGGCUUG CUGAUGAG X CGAA ACAGUAGG	2924
1867	CTACTGTT C AAGCCTCC	416	GGAGGCUU CUGAUGAG X CGAA AACAGUAG	2925
1874	TCAAGCCT C CAAGCTGT	417	ACAGCUUG CUGAUGAG X CGAA AGGCUUGA	2926
1887	CTGTGCCT T GGGTGGCT	418	AGCCACCC CUGAUGAG X CGAA AGGCACAG	2927
1896	GGGTGGCT T TGGGGCAT	419	AUGCCCCA CUGAUGAG X CGAA AGCCACCC	2928
1897	GGTGGCTT T GGGGCATG	420	CAUGCCCC CUGAUGAG X CGAA AAGCCACC	2929
1911	ATGGACAT T GACCCGTA	421	UACGGGUC CUGAUGAG X CGAA AUGUCCAU	2930
1919	TGACCCGT A TAAAGAAT	422	AUUCUUUA CUGAUGAG X CGAA ACGGGUCA	2931
1921	ACCCGTAT A AAGAATTT	423	AAAUUCUU CUGAUGAG X CGAA AUACGGGU	2932
1928	TAAAGAAT T TGGAGCTT	424	AAGCUCCA CUGAUGAG X CGAA AUUCUUUA	2933
1929	AAAGAATT T GGAGCTTC	425	GAAGCUCC CUGAUGAG X CGAA AAUUCUUU	2934
1936	TTGGAGCT T CTGTGGAG	426	CUCCACAG CUGAUGAG X CGAA AGCUCCAA	2935
1937	TGGAGCTT C TGTGGAGT	427	ACUCCACA CUGAUGAG X CGAA AAGCUCCA	2936
1946	TGTGGAGT T ACTCTCTT	428	AAGAGAGU CUGAUGAG X CGAA ACUCCACA	2937
1947	GTGGAGTT A CTCTCTTT	429	AAAGAGAG CUGAUGAG X CGAA AACUCCAC	2938
1950	GAGTTACT C TCTTTTT	430	AAAAAAGA CUGAUGAG X CGAA AGUAACUC	2939
1952	GTTACTCT C TTTTTTGC	431	GCAAAAA CUGAUGAG X CGAA AGAGUAAC	2940
1954	TACTOTOT T TTTTGCCT	432	AGGCAAAA CUGAUGAG X CGAA AGAGAGUA	2941
1955	ACTOTOTT T TTTGCCTT	433	AAGGCAAA CUGAUGAG X CGAA AAGAGAGU	2942
1956	CTCTCTTT T TTGCCTTC	434	GAAGGCAA CUGAUGAG X CGAA AAAGAGAG	2943
1957	TCTCTTTT T TGCCTTCT	435	AGAAGGCA CUGAUGAG X CGAA AAAAGAGA	2944
1958	CTCTTTTT T GCCTTCTG	436	CAGAAGGC CUGAUGAG X CGAA AAAAAGAG	2945
1963	TTTTGCCT T CTGACTTC	437	GAAGUCAG CUGAUGAG X CGAA AGGCAAAA	2946
1964	TTTGCCTT C TGACTTCT	438	AGAAGUCA CUGAUGAG X CGAA AAGGCAAA	2947
1704	11100011 0 1111111			

Table 37

1970	TTCTGACT T CTTTCCTT	439	AAGGAAAG CUGAUGAG X CGAA AGUCAGAA	2948
1971	TCTGACTT C TTTCCTTC	440	GAAGGAAA CUGAUGAG X CGAA AAGUCAGA	2949
1973	TGACTTCT T TCCTTCTA	441	UAGAAGGA CUGAUGAG X CGAA AGAAGUCA	2950
1974	GACTTCTT T CCTTCTAT	442	AUAGAAGG CUGAUGAG X CGAA AAGAAGUC	2951
1975	ACTTCTTT C CTTCTATT	443	AAUAGAAG CUGAUGAG X CGAA AAAGAAGU	
1978	TCTTTCCT T CTATTCGA	444	UCGAAUAG CUGAUGAG X CGAA AGGAAAGA	2953
1979	CTTTCCTT C TATTCGAG	445	CUCGAAUA CUGAUGAG X CGAA AAGGAAAG	2954
1981	TTCCTTCT A TTCGAGAT	446	AUCUCGAA CUGAUGAG X CGAA AGAAGGAA	2955
1983	CCTTCTAT T CGAGATCT	447	AGAUCUCG CUGAUGAG X CGAA AUAGAAGG	2956
1984	CTTCTATT C GAGATCTC	448	GAGAUCUC CUGAUGAG X CGAA AAUAGAAG	2957
1990	TTCGAGAT C TCCTCGAC	449	GUCGAGGA CUGAUGAG X CGAA AUCUCGAA	2958
1992	CGAGATCT C CTCGACAC	450	GUGUCGAG CUGAUGAG X CGAA AGAUCUCG	2959
1995	GATCTCCT C GACACCGC	451	GCGGUGUC CUGAUGAG X CGAA AGGAGAUC	2960
2006	CACCGCCT C TGCTCTGT	452	ACAGAGCA CUGAUGAG X CGAA AGGCGGUG	2961
2011	CCTCTGCT C TGTATCGG	453	CCGAUACA CUGAUGAG X CGAA AGCAGAGG	2962
2015	TGCTCTGT A TCGGGGGG	454	CCCCCCGA CUGAUGAG X CGAA ACAGAGCA	2963
2017	CTCTGTAT C GGGGGGCC	455	GGCCCCC CUGAUGAG X CGAA AUACAGAG	2964
2027	GGGGGCCT T AGAGTCTC	456	GAGACUCU CUGAUGAG X CGAA AGGCCCCC	2965
2028	GGGGCCTT A GAGTCTCC	457	GGAGACUC CUGAUGAG X CGAA AAGGCCCC	2966
2033	CTTAGAGT C TCCGGAAC	458	GUUCCGGA CUGAUGAG X CGAA ACUCUAAG	2967
2035	TAGAGTCT C CGGAACAT	459	AUGUUCCG CUGAUGAG X CGAA AGACUCUA	2968
2044	CGGAACAT T GTTCACCT	460	AGGUGAAC CUGAUGAG X CGAA AUGUUCCG	2969
2047	AACATTGT T CACCTCAC	461	GUGAGGUG CUGAUGAG X CGAA ACAAUGUU	2970
2048	ACATTGTT C ACCTCACC	462	GGUGAGGU CUGAUGAG X CGAA AACAAUGU	2971
2053	GTTCACCT C ACCATACG	463	CGUAUGGU CUGAUGAG X CGAA AGGUGAAC	2972
2059	CTCACCAT A CGGCACTC	464	GAGUGCCG CUGAUGAG X CGAA AUGGUGAG	2973
2067	ACGGCACT C AGGCAAGC	465	GCUUGCCU CUGAUGAG X CGAA AGUGCCGU	2974
2077	GGCAAGCT A TTCTGTGT	466	ACACAGAA CUGAUGAG X CGAA AGCUUGCC	2975
2079	CAAGCTAT T CTGTGTTG	467	CAACACAG CUGAUGAG X CGAA AUAGCUUG	2976
2080	AAGCTATT C TGTGTTGG	468	CCAACACA CUGAUGAG X CGAA AAUAGCUU	2977
2086	TTCTGTGT T GGGGTGAG	469	CUCACCCC CUGAUGAG X CGAA ACACAGAA	
2096	GGGTGAGT T GATGAATC	470	GAUUCAUC CUGAUGAG X CGAA ACUCACCC	2979
2104	TGATGAAT C TAGCCACC	471	GGUGGCUA CUGAUGAG X CGAA AUUCAUCA	2980
2106	ATGAATCT A GCCACCTG	472	CAGGUGGC CUGAUGAG X CGAA AGAUUCAU	2982
2125	TGGGAAGT A ATTTGGAA	473	UUCCAAAU CUGAUGAG X CGAA ACUUCCCA	1
2128	GAAGTAAT T TGGAAGAT	474	AUCUUCCA CUGAUGAG X CGAA AUUACUUC	2983
2129	AAGTAATT T GGAAGATC	475	GAUCUUCC CUGAUGAG X CGAA AAUUACUU	2984
2137	TGGAAGAT C CAGCATCC	476	GGAUGCUG CUGAUGAG X CGAA AUCUUCCA	2985
2144	TCCAGCAT C CAGGGAAT	477	AUUCCCUG CUGAUGAG X CGAA AUGCUGGA	2986
2153	CAGGGAAT T AGTAGTCA	478	UGACUACU CUGAUGAG X CGAA AUUCCCUG	2987
2154	AGGGAATT A GTAGTCAG	479	CUGACUAC CUGAUGAG X CGAA AAUUCCCU	2988
2157	GAATTAGT A GTCAGCTA	480	UAGCUGAC CUGAUGAG X CGAA ACUAAUUC	2989
2160	TTAGTAGT C AGCTATGT	481	ACAUAGCU CUGAUGAG X CGAA ACUACUAA	2990
2165	AGTCAGCT A TGTCAACG	482	CGUUGACA CUGAUGAG X CGAA AGCUGACU	2991
2169	AGCTATGT C AACGTTAA	483	UUAACGUU CUGAUGAG X CGAA ACAUAGCU	2992
2175	· GTCAACGT T AATATGGG	484	CCCAUAUU CUGAUGAG X CGAA ACGUUGAC	2993
2176	TCAACGTT A ATATGGGC	485	GCCCAUAU CUGAUGAG X CGAA AACGUUGA	2994
2179	ACGTTAAT A TGGGCCTA	486	UAGGCCCA CUGAUGAG X CGAA AUUAACGU	2995
2187	ATGGGCCT A AAAATCAG	487	CUGAUUUU CUGAUGAG X CGAA AGGCCCAU	2996
2193	CTAAAAAT C AGACAACT	488	AGUUGUCU CUGAUGAG X CGAA AUUUUUAG	2997
2202	AGACAACT A TTGTGGTT.	489	AACCACAA CUGAUGAG X CGAA AGUUGUCU	2998

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2204	ACAACTAT T GTGGTTTC	490	GAAACCAC CUGAUGAG X CGAA AUAGUUGU	2999
2210	ATTGTGGT T TCACATTT	491	AAAUGUGA CUGAUGAG X CGAA ACCACAAU	3000
2211	TTGTGGTT T CACATTTC	492	GAAAUGUG CUGAUGAG X CGAA AACCACAA	3001
2212	TGTGGTTT C ACATTTCC	493	GGAAAUGU CUGAUGAG X CGAA AAACCACA	3002
2217	TTTCACAT T TCCTGTCT	494	AGACAGGA CUGAUGAG X CGAA AUGUGAAA	3003
2218	TTCACATT T CCTGTCTT	495	AAGACAGG CUGAUGAG X CGAA AAUGUGAA	3004
2219	TCACATTT C CTGTCTTA	496	UAAGACAG CUGAUGAG X CGAA AAAUGUGA	3005
2224	TTTCCTGT C TTACTTTT	497	AAAAGUAA CUGAUGAG X CGAA ACAGGAAA	3006
2226	TCCTGTCT T ACTTTTGG	498	CCAAAAGU CUGAUGAG X CGAA AGACAGGA	3007
2227	CCTGTCTT A CTTTTGGG	499	CCCAAAAG CUGAUGAG X CGAA AAGACAGG	3008
2230	GTCTTACT T TTGGGCGA	500	UCGCCCAA CUGAUGAG X CGAA AGUAAGAC	3009
2231	TCTTACTT T TGGGCGAG	501	CUCGCCCA CUGAUGAG X CGAA AAGUAAGA	3010
2232	CTTACTTT T GGGCGAGA	502	UCUCGCCC CUGAUGAG X CGAA AAAGUAAG	3011
2247	GAAACTGT T CTTGAATA	503	UAUUCAAG CUGAUGAG X CGAA ACAGUUUC	3012
2248	AAACTGTT C TTGAATAT	504	AUAUUCAA CUGAUGAG X CGAA AACAGUUU	3013
2250	ACTGTTCT T GAATATTT	505	AAAUAUUC CUGAUGAG X CGAA AGAACAGU	3014
2255	TCTTGAAT A TTTGGTGT	506	ACACCAAA CUGAUGAG X CGAA AUUCAAGA	3015
2257	TTGAATAT T TGGTGTCT	507	AGACACCA CUGAUGAG X CGAA AUAUUCAA	3016
2258	TGAATATT T GGTGTCTT	508	AAGACACC CUGAUGAG X CGAA AAUAUUCA	3017
2264	TTTGGTGT C TTTTGGAG	509	CUCCAAAA CUGAUGAG X CGAA ACACCAAA	3018
2266	TGGTGTCT T TTGGAGTG	510	CACUCCAA CUGAUGAG X CGAA AGACACCA	3019
2267	GGTGTCTT T TGGAGTGT	511	ACACUCCA CUGAUGAG X CGAA AAGACACC	3020
2268	GTGTCTTT T GGAGTGTG	512	CACACUCC CUGAUGAG X CGAA AAAGACAC	3021
2280	GTGTGGAT T CGCACTCC	513	GGAGUGCG CUGAUGAG X CGAA AUCCACAC	3022
2281	TGTGGATT C GCACTCCT	514	AGGAGUGC CUGAUGAG X CGAA AAUCCACA	3023
2287	TTCGCACT C CTCCTGCA	515	UGCAGGAG CUGAUGAG X CGAA AGUGCGAA	3024
2290	GCACTCCT C CTGCATAT	516	AUAUGCAG CUGAUGAG X CGAA AGGAGUGC	3025
2297	TCCTGCAT A TAGACCAC	517	GUGGUCUA CUGAUGAG X CGAA AUGCAGGA	3026
2299	CTGCATAT A GACCACCA	518	UGGUGGUC CUGAUGAG X CGAA AUAUGCAG	3027
2317	ATGCCCCT A TCTTATCA	519	UGAUAAGA CUGAUGAG X CGAA AGGGGCAU	3028
2319	GCCCCTAT C TTATCAAC	520	GUUGAUAA CUGAUGAG X CGAA AUAGGGGC	3029
2321	CCCTATCT T ATCAACAC	521	GUGUUGAU CUGAUGAG X CGAA AGAUAGGG	3030
2322	CCTATCTT A TCAACACT	522	AGUGUUGA CUGAUGAG X CGAA AAGAUAGG	3031
2324	TATCTTAT C AACACTTC	523	GAAGUGUU CUGAUGAG X CGAA AUAAGAUA	3032
2331	TCAACACT T CCGGAAAC	524	GUUUCCGG CUGAUGAG X CGAA AGUGUUGA	3033
2332	CAACACTT C CGGAAACT	525	AGUUUCCG CUGAUGAG X CGAA AAGUGUUG	3034
2341	CGGAAACT A CTGTTGTT	526	AACAACAG CUGAUGAG X CGAA AGUUUCCG	3035
2346	ACTACTGT T GTTAGACG	527	CGUCUAAC CUGAUGAG X CGAA ACAGUAGU	3036
2349	ACTGTTGT T AGACGAAG	528	CUUCGUCU CUGAUGAG X CGAA ACAACAGU	3037
2350	CTGTTGTT A GACGAAGA	529	UCUUCGUC CUGAUGAG X CGAA AACAACAG	3038
2366	AGGCAGGT C CCCTAGAA	530	UUCUAGGG CUGAUGAG X CGAA ACCUGCCU	3039
2371	GGTCCCCT A GAAGAAGA	531	UCUUCUUC CUGAUGAG X CGAA AGGGGACC	3040
2383	GAAGAACT C CCTCGCCT	532	AGGCGAGG CUGAUGAG X CGAA AGUUCUUC	3041
2387	AACTCCCT C GCCTCGCA	533	UGCGAGGC CUGAUGAG X CGAA AGGGAGUU	3042
2392	CCTCGCCT C GCAGACGA	534	UCGUCUGC CUGAUGAG X CGAA AGGCGAGG	3043
2405	ACGAAGGT C TCAATCGC	535	GCGAUUGA CUGAUGAG X CGAA ACCUUCGU	3044
2407	GAAGGTCT C AATCGCCG	536	CGGCGAUU CUGAUGAG X CGAA AGACCUUC	3045
2411	GTCTCAAT C GCCGCGTC	537	GACGCGGC CUGAUGAG X CGAA AUUGAGAC	3046
2419	CGCCGCGT C GCAGAAGA	538	UCUUCUGC CUGAUGAG X CGAA ACGCGGCG	3047
2429	CAGAAGAT C TCAATCTC	539	GAGAUUGA CUGAUGAG X CGAA AUCUUCUG	3048
2431	GAAGATCT C AATCTCGG	540	CCGAGAUU CUGAUGAG X CGAA AGAUCUUC	3049

Table 37

2415 ATCTCANT C TOGGGAATT 542 AGUIUCCC CUGAUGAG X GGAA AGUIGAGAU 3050 2444 TOGGGAAT C TOARTOTT 542 AGUIUCCC CUGAUGAG X GGAA AGUIUCCC 3051 2446 GGRAATCT C ATGTTED 545 AACAUUCC CUGAUGAG X GGAA AGUIUCCC 3052 2452 CTCAATGT T AGTATTCC 546 GGRAAUCC CUGAUGAG X GGAA AGUIUCCC 3052 2452 CTCAATGT T AGTATTCC 546 AGGAUGAC CUGAUGAG X CGAA ACAUUCCC 3053 2452 CTCAATGT T AGTATTCC 546 AGGAUGAC CUGAUGAG X CGAA ACAUUCCC 3053 2455 TOCAATGT T AGTATTCC 546 AGGAUGAC CUGAUGAG X CGAA ACAUUCCC 3054 2455 TOCAATGT T AGTATTCC 546 AGGAUGAC CUGAUGAG X CGAA ACAUUCAG 3054 2455 TOCAATGT T CCTTGGAC 548 GUCCAAG CUGAUGAG X CGAA ACAUUCAC 3056 2458 GTTAGTAT T CCTTGGAC 549 CUCCAAG CUGAUGAG X CGAA ACAUUCAC 3057 2459 TTAGTAT T CCTTGGAC 549 CUCCAAG CUGAUGAG X CGAA AGUACACA 3057 2469 TTAGTAT T CCTTGGAC 549 CUCCAAG CUGAUGAG X CGAA AGUACACA 3058 2461 GTTAGTAT T CCTTGGAC 549 CUCCAAG CUGAUGAG X CGAA AGUACACA 3058 2461 GGACACT T AGGGGCC 552 GCCCCGU CUGAUGAG X CGAA AGUACACA 3058 2461 GGAAACTT T AGGGGCC 552 GCCCCGU CUGAUGAG X CGAA AGUUUCC 3061 2484 GGAAACTT T AGGGGC 552 GCCCCGU CUGAUGAG X CGAA AGUUUCC 3061 2486 GGAAACTT T AGGGGCT 553 AGGCCCCO CUGAUGAG X CGAA AGUUUCC 3061 2486 GAAACTT T AGGGGCT 554 AGCCCCG CUGAUGAG X CGAA AGUUUCC 3061 2486 GAAACTT T AGGGGCT 554 AGCCCCG CUGAUGAG X CGAA AAGUUUC 3062 2486 GAACTT A TCTCTC 556 AGAGAAUA CUGAUGAG X CGAA AAGUUUC 3062 2486 GACCTTA TTCTCTC 556 AGAGAAUA CUGAUGAG X CGAA AAGUUUC 3062 2486 GACCTTA T TCTTCTC 556 AGAGAAUA CUGAUGAG X CGAA AAACCCCC 3066 2489 GCCTTTAT TCTTCTC 556 AGAGAAUA CUGAUGAG X CGAA AAACCCCC 3066 2489 GCCTTTAT T TCTTCTC 557 AGCCCCG CUGAUGAG X CGAA AAACCCCC 3066 2489 GCCTTTAT T TCTTCTC 558 AGAGAAUA CUGAUGAG X CGAA AAACCCCC 3066 2489 GCCTTTAT T TCTTCTC 558 AGAGAAUA CUGAUGAG X CGAA AAACCCCC 3066 2489 GCCTTTAT T TCTTCTC 558 AGAGAAUA CUGAUGAG X CGAA AAACCCCC 3066 2489 GCCTTTAT T TCTTCTC 558 AGAGAAUA CUGAUGAG X CGAA AAAACCCC 3066 2489 GCCTTTAT T TCTTCTC 558 AGAGAAUA CUGAUGAG X CGAA AAAACCCC 3066 2489 AGCTTTAT T TCTTCAG 558 CCCGAACA CUGAUGAG X CGAA AAAAACCC 3066 2580 AGCCCT T ACATCT T TCTTCAG 558 CCCGAAC CUGAUGAG X C					
2448			541	AUUCCCGA CUGAUGAG X CGAA AUUGAGAU	3050
2446 GOGANTCT C NATGTTAG	2437				
2452 CTCAATGT T AGTATTCC 545 GGANUAGU CUGARDAG X CGAA ACADUCAG 3054 2455 TCCATGT A GTATTCCT 546 AGGANUAG CUGARDAG X CGAA ACADUCAG 3054 2455 TCTATGT A GTATTCCT 547 CCAAGGAA CUGARDAG X CGAA ACUAACAU 3056 2458 GTTAGTAT T CCTTGGAC 548 GUCCAAGG CUGARDAG X CGAA ACUAACAU 3056 2458 GTTAGTAT T CCTTGGAC 549 GUCCAAGG CUGARDAG X CGAA AGUAACAU 3058 2452 GTTAGTAT T CCTTGGAC 549 GUCCAAGG CUGARDAG X CGAA AGUAACAU 3058 2462 GTTATCCT T GGACACAT 550 AUGUCACAG CUGARDAG X CGAA AGUARCAU 3058 2462 GTTATCCT T GGACACAT 550 AUGUCACAC CUGARDAG X CGAA AGGARDAC 3059 2471 GGACACAT AGGGGCT 551 GUCCACCC UCARDAGA X CGAA AGUARDAC 3059 2485 GGAAAACT T TACGGGGC 552 GCCCCGU CUGARDAG X CGAA AGUARDAC 3061 2485 GGAAAACT T ACGGGGCT 554 AAGCCCC UCARDAGA X CGAA AGUARDAC 3061 2486 GGAAAACT T ACGGGGCT 554 AAGCCCC UCARDAGA X CGAA AAGURUCC 3061 2486 GGAAAACT T ACGGGGCT 554 AAGCCCCC UCARDAGA X CGAA AAAGURUCC 3062 2486 GGAAAACT T ACGGGGCT 554 AAGCCCCC UCARDAGA X CGAA AAAGURUCC 3062 2486 GGAACAT A AGGCCCC 555 AGAGAARA CUGARDAG X CGAA AAAAGURUC 3063 2486 GGACAT A TATCTTCT 555 GAAGAARA CUGARDAG X CGAA AAAACCCC 3064 2486 GGACTTAT T CTTCTCTA 557 AAAAGCCCC GUARDAG X CGAA AAAACCCC 3064 2486 GCGCCTTAT T ATCTTCTA 557 AAAAGAA CUGARDAG X CGAA AAAAACCC 3065 2489 GCTTTAT C TTCTAGG 558 CCUAGAAA CUGARDAG X CGAA AAAACCCC 3066 2489 GCTTATT C TTCTAGG 558 CCUAGAAA CUGARDAG X CGAA AAAAACCC 3067 2500 TTATCTCT C TACGGTAC 561 GUACCGUA CUGARDAG X CGAA AAAAACCC 3067 2500 TTATCTCT C TACGGTAC 561 GUACCGUA CUGARDAG X CGAA AAAAACCC 3067 2500 TTATCTCT C TACGGTAC 561 GUACCGUA CUGARDAG X CGAA AAAAAAACC 3067 2500 TTCTACCGTA 560 UACCGUA CUGARDAG X CGAA AAAAAAAAA 3071 3511 ACCTTCCTT ACCTTATAT 564 AAGGACCC CUGARDAG X CGAA AAAGAARAA 3071 3511 ACCTTCCTT T ATCTCTAC 561 AGGACCCC CUGARDAG X CGAA AAAGAARAA 3071 3511 AACTCCTT C GCTTTATT	2444				
2455 TOANTOTT A GTATTECT 546 AGGARIAC CUGAUGAG X CGAA AACAULIGA 3055 (2456 ATGTTAGT A TTCCTTGG 547 CCAAGGAA CUGAUGAG X CGAA ACAULIGA 3055 (2459) TTAGTATT C CTTGGAC 548 GUCCAAG CUGAUGAG X CGAA ALGULACAU 3057 (2459) TTAGTATT C CTTGGAC 548 GUCCAAG CUGAUGAG X CGAA ALGULACAU 3057 (2459) TTAGTATT C CTTGGACA 549 UGUCCAAG CUGAUGAG X CGAA ALGULACAU 3058 (2462) GTATTCCTT G GACACAT 550 AUGUGUCC CUGAUGAG X CGAA AUGULACA 3058 (2471) GGACACAT A AGGTGGAG 551 UGUCCAAG CUGAUGAG X CGAA AUGULACA 3058 (2471) GGACACAT A AGGTGGGA 551 UGCCACCU CUGAUGAG X CGAA AUGULACC 3060 (2486 GGAAACTT TAGGGGC 552 GCCCCGAU CUGAUGAG X CGAA AUGULACC 3061 (2486 GGAAACTT A CGGGGCT 553 AGGCCCCG CUGAUGAG X CGAA AUGULACC 3061 (2486 GGAAACTT A CGGGGCT 553 AGGCCCCG CUGAUGAG X CGAA AUGULACC 3062 (2486 GGAAACTT A CGGGGCT 554 AGGCCCCG CUGAUGAG X CGAA AAGULUCC 3062 (2494 ACGGGCTT ATTCTTC 555 GAAGAAU CUGAUGAG X CGAA AAGULUCC 3062 (2494 ACGGGCTT ATTCTTC 555 GAAGAAU CUGAUGAG X CGAA AAGUCCCG 3064 (2494 ACGGCCTT ATTCTTC 557 UAGAGAGA CUGAUGAG X CGAA AAGCCCCG 3065 (2496 GCCTTTAT T CTTCTACG 558 CGUAGAGA CUGAUGAG X CGAA AAACCCCC 3065 (2496 GCTTTAT C TTCTACG 558 CCUGAGAA CUGAUGAG X CGAA AAACCCC 3065 (2496 GCTTTAT C TTCTACG 558 CCUGAGAA CUGAUGAG X CGAA AAAACCCC 3065 (2496 GCTTTAT C TTCTACG 558 CCUGAGAA CUGAUGAG X CGAA AAAACCCC 3065 (2496 GCTTTAT C TTCTACG 558 CCUGAGAA CUGAUGAG X CGAA AAAACCC 3067 (2496 CCTTATT C TTCTACG 558 CCUGAGAA CUGAUGAG X CGAA AAAACCC 3067 (2496 CCTTATT C TTCTACG 558 CCUGAGAC CUGAUGAG X CGAA AAAAACC 3067 (2496 CCTTATTCTT C TACCGTTA 560 UACCGUA CUGAUGAG X CGAA AAAAACC 3067 (2506 CTTATTCTT C TACCGTTA 561 UACCGUA CUGAUGAG X CGAA AAAAACC 3067 (2506 CTTATTCTT C TACCGTTAC 562 AGGGACCG CUGAUGAG X CGAA AAGAAGAA 3070 (2506 CTTATTCTT C TACCGTTAC 562 AGGAACCG CUGAUGAG X CGAA AAGAAGAA 3070 (2506 CTTATAT 564 AUGACGA CUGAUGAG X CGAA AAGAAGAA 3071 (2506 CTTATTCTT A ATCCTAA 566 UACCGUA CUGAUGAG X CGAA AAGAAGAA 3071 (2506 CTTCTTT T AATCCTAA 566 UACCGUA CUGAUGAG X CGAA AAGAAGA 3071 (2506 CTTCTTT T AATCCTAA 567 UUAGGAA CUGAUGAG X CGAA AAGAAGA 3071 (2506 CTTCTTTT T CTTC	2446				
2456 ATOTTAGT A TTCCTTGG	2452				
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2491 GARACATT A AGGTGGGA 550	2458				
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2486	2484				
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2501 TITATTCT T CTACGOTA 550	2498				
TRATECT C TAGGGTAC 561	2499	GCTTTATT C TTCTACGG	559		
2504 ATTCTTCT A COGTACCT	2501	TTTATTCT T CTACGGTA	560		
TCTACGGT A CCTTGCTT 563	2502		561		
2511 CORTACT T GETTTANT	2504	ATTCTTCT A CGGTACCT	562		
2517 ACCTTOCT T TARTCCTA	2509	TCTACGGT A CCTTGCTT	563		
2518 CCTTGCTT T AATCCTAA 566	2513	CGGTACCT T GCTTTAAT	564		
2519 CTTOCTIT A ATCCTANA 567 UUURGGAU CUGAUGRA X CGAA ANAGCANG 3076 2522 GCTTHART C CTAAATGG 568 CCAUUURA CUGAUGRA X CGAA ANAGCANG 3077 2525 TATACTCT A ANTGCAA 569 UUGCCAUUU CUGAUGRG X CGAA AGGAUUTA 3078 2537 GGCANACT C CTTCTTT 570 AAAAGAAA CUGAUGRA X CGAA AGGAUUTA 3078 2540 AAAACCCT T CTTTTCCT 571 AAGACAAA CUGAUGRA X CGAA AGGAUUTA 3080 2541 AACTCCTT C TTTTCCTG 572 CAGGANAA CUGAUGRA X CGAA AAGGAGUU 3081 2543 CTCCTTCTT T TCCTGACA 574 UUGLCAGGA CUGAUGRA X CGAA AAGAGAGU 3082 2544 TCCTTCTT T TCCTGACA 574 UUGLCAGGA CUGAUGRA X CGAA AAAGAAGGA 3082 2544 TCCTTCTT T TCCTGACA 575 AUGUCAGG CUGAUGRA X CGAA AAAAGAGGA 3082 2545 CTCTCTTT T CCTGACAT 576 AUGUCAGG CUGAUGRA X CGAA AAAAGAGGA 3084 2546 CTCTTCTT T TCCTGACAT 576 AUGUCAGG CUGAUGRA X CGAA AAAAGAGGA 3085 2555 CCTGACAT T CATTGCAG 577 UCCAAAUU CUGAUGRA X CGAA AAAGGAGG 3086 2555 CCTGACAT T CATTGCAG 578 CUGCAAAU CUGAUGRA X CGAA AUGUCAGG 3086 2555 CATCATT T TCCAGGAG 579 CUCCUGAC CUGAUGRA X CGAA AUGUCAGG 3086 2555 CATCATT T TCCAGGAG 580 CUCCUGCA CUGAUGRA X CGAA AUGUCAGG 3086 2559 CATTCATT T TGCAGGAG 580 CUCCUGCA CUGAUGRA X CGAA AUGUCAGG 3086 2559 CATTCATT T TGCAGGAG 580 CUCCUGCA CUGAUGRA X CGAA AUGUCAGG 3086 2559 CATTCATT T TGCAGGAG 580 CUCCUGCA CUGAUGRA X CGAA AUGUCAGG 3087 2555 CATCATTCT T TGCAGGAG 580 CUCCUGCA CUGAUGRA X CGAA AUGUCAG 3089 2572 GAGACATT T GATGAGTG 581 CUUCAGUC CUGAUGRA X CGAA AUGUCAG 3091 2573 TGTTGTTAT A GCCATT 584 AAAUUCCU CUGAUGRA X CGAA AUGUCAG 3092 2575 CATCATT T TGCAGGAG 589 CUCCUGCA CUGAUGRA X CGAA AUGUCAG 3092 2575 CATCATT T TGCAGGAG 580 CUCCUGCA CUGAUGRA X CGAA AUGUCAG 3091 2575 GACATTTAT T TGCAGGAG 580 CUCCUGCA CUGAUGRA X CGAA AUGUCAU 3092 2575 CATCATTAT A AGCAATT 584 AAAUUCCU CUGAUGRA X CGAA AUGUCAU 3093 2575 TGTTGTTAT A GCAATTAT 586 CUCCCACA CUGAUGRA X CGAA AUGUCAU 3093 2575 TGTTGTTAT A	2517	ACCTTGCT T TAATCCTA	565		
2522 CITCHTART C CTRAATUG 568 CCAUUURG CUGAUGAG X CGAA AUUAAAGC 3077	2518				
2525 TEANTOCT A ANTOGCAA 559 UUGGCAUU CUGAUGAG X CCBA AGGAUUAA 3078 2537 GOCANACT C CITCTITT 570 AANAGAMG CUGAUGAG X CCBA AGGUUGA 2540 AAACTCCTT C TITTTCCT 571 AAGGAAAG CUGAUGAG X CCBA AGGUUGU 3080 2541 AACTCCTT C TITTCCTG 572 CAGGAAAA CUGAUGAG X CCBA AGGAUGU 3081 2543 ACTCCTT C TITTCCTG 573 GUCAGAGA CUGAUGAG X CCBA AGGAGGA 3082 2544 TCCTTCTT T TCCTGACA 574 UUGCAGGA CUGAUGAG X CCBA AGGAGGA 3082 2545 CCTTCTTT T CCTGACA 575 AUGUCAGGA CUGAUGAG X CCBA AAAAGAGGA 3082 2546 CCTTCTTT T CCTGACAT 576 AAUGUCAG CUGAUGAG X CCBA AAAAGAGGA 3084 2546 CCTTCTTT T CCTGACAT 577 AUGUCAGG CUGAUGAG X CCBA AAAAGAGG 3084 2547 CCTGACAT T CATTTGCA 577 UUCAAAUU CUGAUGAG X CCBA AAAAGAGG 3084 2558 CCTGACAT T CATTTGCA 577 UUCAAAUU CUGAUGAG X CCBA AAAUGACG 3086 2559 CATTCAT T TCCAGGAG 578 CUGCAAAU CUGAUGAG X CCBA AAUGUCAG 3086 2559 CATTCAT T TCCAGGAG 578 CUGCAAAU CUGAUGAG X CCBA AAUGUCAG 3086 2559 CATTCAT T TGCAGGAG 580 CUCCUGC CUGAUGAG X CCBA AAUGUCAG 3089 2572 GAGACAT T GTTGATAG 581 CUGACAUC CUGAUGAG X CCBA AAUGUCAG 3099 2573 TTGTTCAT A GATGATAG 582 CAUCAUCAC CUGAUGAG X CCBA AUGUCAC 3090 2585 TATCATTT A GATGATAG 581 CUGACAUC CUGAUGAG X CCBA AUGUCAC 3090 2585 TATCATTT A GATGATAG 581 CUUACAUC CUGAUGAG X CCBA AUGUCAC 3091 2585 TATCATTT A GATGATAG 581 CUUACAUC CUGAUGAG X CCBA AUGUCAC 3091 2587 TTGTTCAT A GATGATAG 581 CUUACAUC CUGAUGAG X CCBA AUGUCAC 3092 2589 TATCATTT A GATGATAG 581 CUUACAUC CUGAUGAG X CCBA AUGUCAC 3092 2589 TATCATTT T GATGAGG 586 GCCCCC CUGAUGAG X CCBA AUGCAUCA 3093 2580 GGCCCCT T ACAGTTAA 588 MUUACAUC CUGAUGAG X CCBA AUGCAUCA 3093 2606 GGCCCCTT A CAGTTAAA 588 MUUACAUC CUGAUGAG X CCBA AUGCAUCA 3095 2607 GAGGACTT T ACAGTTAA 588 MUUACAUC CUGAUGAG X CCBA AUGCAUCA 3096 2607 GGCCCCTT A CAGTTAAA 588 MUUACAUC CUGAUGAG X CCBA AUGCAUCA 3097 2608 GGCCCCTT A CAGTTAAA 588 MUUAC	2519	CTTGCTTT A ATCCTAAA	567		
2537 GOCAMACT C CITICTITT 570 AANAGAMG CUGAUGAG X CGAA AGUUUGCC 3079 2540 AAACCACT T CITITECT 571 AGGAAAAG CUGAUGAG X CGAA AGGAGUU 3080 2541 AAACCACT T CITITECT 572 AGGAAAAA CUGAUGAG X CGAA AAGGAGUU 3081 2543 CITACTOTT T TITECTG 572 AGGAAAAA CUGAUGAG X CGAA AAGGAGUU 3081 2544 CITCTITT T CCTGACAT 573 GUCAGGAA CUGAUGAG X CGAA AAGGAGGA 3082 2545 CITCTITT T CCTGACAT 574 UUUCAGAG CUGAUGAG X CGAA AAGAAGGA 3083 2546 COTTCITT T CCTGACAT 575 AUGUCAGG CUGAUGAG X CGAA AAAGAAGG 3083 2546 COTTCITT T CCTGACAT 576 AUGUCAGG CUGAUGAG X CGAA AAAGAAGG 3084 2546 CTTCTTTT T CCTGACAT 576 AUGUCAGG CUGAUGAG X CGAA AAAGAAGG 3084 2547 CTGACAT T CATTTGCA 577 UUCAAAUG CUGAUGAG X CGAA AAAGAAG 3084 2558 CTGACATT T CATTTGCAG 578 CUCCAGAU CUGAUGAG X CGAA AAAGAAGG 3086 2559 CATTCATT T GCAGGAGG 578 CUCCAGAA CUGAUGAG X CGAA AAAGAAGG 3086 2559 CATTCATT T GCAGGAGG 580 CUUCAUGA CUGAUGAG X CGAA AAUGAUG 3088 2570 GAGGACAT T GATTGATAG 581 CUAUCAGA CUGAUGAG X CGAA AAUGAUG 3089 2571 GAGGACAT T GATGATAG 581 CUAUCAGA CUGAUGAG X CGAA AAGAACG 3092 2572 GAGGACAT T GATGATAG 582 CUAUCAGC CUGAUGAG X CGAA AAUGACC 3090 2573 TOTTCATT A GATGATAG 582 CUAUCAGC CUGAUGAG X CGAA AAUGUCC 3090 2574 CATTCATT T GATGAGTG 582 CUAUCAGC CUGAUGAG X CGAA AAUGUCC 3091 2575 TATACATT T GATGAGTG 582 CUAUCAGC CUGAUGAG X CGAA AACAUCUA 3092 2576 TATACATT T GATGAGAC 583 CUUCACAC CUGAUGAG X CGAA AACAUCUA 3093 2586 ATACATTT T GATGAGC 586 GCCCCCAC CUGAUGAG X CGAA AACAUCUA 3093 2587 TATACATT T AACCAATT 584 AAAUUCCU CUGAUGAG X CGAA AACAUCUA 3093 2588 ATACATTT T GATGAGCC 586 GCCCCCAC CUGAUGAG X CGAA AACAUCUA 3093 2589 AAGCAATT T GATGAGGC 586 GCCCCCAC CUGAUGAG X CGAA AACAUCUA 3093 2580 GGCCCCTT A CACTTAAA 587 UUUACAU CUGAUGAG X CGAA AACAUCUA 3093 2606 GGCCCCTT A CACTTAAA 588 UUUACAU CUGAUGAG X CGAA AAUGGCC 3097 2607 GGCCCCT A CACTTAAA	2522	GCTTTAAT C CTAAATGG			
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2541 AACTICOTT C TITTICCTG 572 CAGGAAAA CUGAUGAG X CGAA AAGGAGUU 3081 2543 CTCCTTCT T TTCCTGAC 573 GICLAGGAG UCGAUGAG X CGAA AAGGAGGAG 3082 2544 TCCTTCTT T TCCTGACAT 574 UGUICAGGA CUGAUGAG X CGAA AAGGAAGGA 3083 2548 CCTTCTTT T CCTGACAT 575 AUGUICAGG CUGAUGAG X CGAA AAAGGAAG 3084 2546 CTTCTTT C CTGACAT 576 AUGUICAGG CUGAUGAG X CGAA AAAGGAAG 3085 2554 CCTGACAT T CATTGCAG 577 UGCAAAUG CUGAUGAG X CGAA AAUGUICAGG 3086 2555 CTGACAT T CATTGCAG 577 UGCAAAUG CUGAUGAG X CGAA AUGUICAGG 3086 2555 CTGACAT T CATTGCAG 578 CUGCUACA CUGAUGAG X CGAA AUGUICAGG 3087 2558 CATTCAT T GCAGGAG 579 CUCCUGCA CUGAUGAG X CGAA AUGUICAG 3089 2557 CATTCATT T GCAGGAG 579 CUCCUGCA CUGAUGAG X CGAA AUGUICAG 3089 2572 GAGGACAT T GATGATG 581 CUUAUCAAC CUGAUGAG X CGAA AUGUICAG 3099 2575 GACATTGT T GATGAGTG 581 CUUAUCAAC CUGAUGAG X CGAA AUGUICAG 3092 2575 TGTGTTGT GATGAGTG 582 CUUAUCAAC CUGAUGAG X CGAA AUGUICAG 3092 2575 TGTGTTGT AAGCAATT 584 AAAUUCAC CUGAUGAG X CGAA AUGUICAG 3092 2585 ATAGCAATT A AGCAATT 584 AAAUUCAC CUGAUGAG X CGAA AUGUICAG 3092 2592 TAAACGAAT T GATGGGGC 585 CCCCCACA CUGAUGAG X CGAA AUGUICAG 3094 2595 AACCAATT T GCAGGAC 586 GGCCCCCAC CUGAUGAG X CGAA AUGUICAU 3093 2595 AACCAATT T GCAGGAC 586 GGCCCCCAC CUGAUGAG X CGAA AUGUICAU 3094 2605 GGGCCCCT T A CAGTAAAT 588 AUUUACUG CUGAUGAG X CGAA AUGUICAU 3095 2606 GGCCCCTT A CAGTAAAT 588 AUUUACUG CUGAUGAG X CGAA AUGUICAU 3095 2606 GGCCCCTT A CAGTAAAT 588 AUUUACUG CUGAUGAG X CGAA AUGUICAU 3095 2606 GGCCCCTT A CAGTAAAT 588 AUUUACUG CUGAUGAG X CGAA AUGUICAU 3095 2606 GGCCCCTT A CAGTAAAT 588 AUUUACUG CUGAUGAG X CGAA AUGUICAU 3095 2606 GGCCCCTT A CAGTAAAT 588 AUUUACUG CUGAUGAG X CGAA AUGUICAU 3095 2606 GGCCCCTT A CAGTAAAT 588 AUUUACUG CUGAUGAG X CGAA AUGUICAU 3095 2606 GGCCCCTT A CAGTAAAT 588 AUUUACUG CUGAUGAG X CGAA AUGUICAU 3095 2606 GG	2537	GGCAAACT C CTTCTTTT			
2543 CTCCTTCT T TTCCTGAC	2540				
2844 TCCTTCTT T TCCTGACA 574 UGUCAGGA CUGAUGAG X CGAA AAGAAGGA 3083 2845 CCTTCTTT T CCTGACAT 575 AUGUCAGG CUGAUGAG X CGAA AAGAAGGA 3083 2856 CCTTCTTT T CCTGACAT 575 AUGUCAGG CUGAUGAG X CGAA AAGAAGGA 3085 2854 CCTGACAT T CATTGCAG 577 UGCAAAUG CUGAUGAG X CGAA AAGGAAG 3085 2855 CCTGACAT T CATTGCAG 578 CUGCAAAU CUGAUGAG X CGAA AUGUCAGG 3086 2855 CCTGACAT T TCCAGGAG 579 CUGCUGAC CUGAUGAG X CGAA AUGUCAGG 3086 2859 CATTCAT T TCCAGGAG 580 CUCCUGA CUGAUGAG X CGAA AUGUCAGG 3089 2552 GAGGACAT T GTTGATAG 581 CUGACAC CUGAUGAG X CGAA AUGUCAG 3099 2572 GAGGACT T GTTGATAG 581 CUGACAC CUGAUGAG X CGAA AUGUCAUG 3090 2579 TGTTGATAG 581 CUGACAC CUGAUGAG X CGAA AUGUCCUC 3090 2579 TGTTGATA AGCAATT 584 AAGUCACU CUGAUGAG X CGAA AUCANGUC 3091 2589 TAGAATGT A AGCAATT 584 AAGUCACU CUGAUGAG X CGAA AUCANGUC 3092 2593 AAGCAATT T GTGGGGC 585 CCCCCAC, CUGAUGAG X CGAA ACANGUU 3093 2593 AAGCAATT T GTGGGGC 586 GGCCCCC CUGAUGAG X CGAA AUCANGUC 3093 2593 AAGCAATT T GTGGGGC 586 GGCCCCCAC CUGAUGAG X CGAA AUCANGUC 3095 2605 GGCCCCT A CAGTAAAA 587 UUUACUGU CUGAUGAG X CGAA AUCANGUC 3096 2606 GGCCCCT A CAGTAAAA 588 UUUACUGU CUGAUGAG X CGAA AUGCGCC 3097 2606 GGCCCCT A CAGTAAAA 588 UUUACUGU CUGAUGAG X CGAA AAGGGGCC 3097 2606 GGCCCCT A CAGTAAAA 588 UUUACUGU CUGAUGAG X CGAA AAGGGGCC 3097 260	2541		-		
2545 COTTCTTT T CCTGACATT 575 AUGUCAGG CUGAUGAG X CGAA AAAGAAGG 3084	2543				
2546 CTICTITT C CTGRCATT 576 AMUGUCAG CUCANGAG X CGAA ANAGAAG 3085 2554 CCTGACAT T CATTTGCA 577 UGCAAAUG CUCANGAG X CGAA ANAGAAG 3086 2555 CTGACAT T CATTTGCAG 578 CUGCAAUG CUGANGAG X CGAA ANGGCAG 3086 2558 CACATCAT T TGCAGGAG 579 CUCCUGAC CUGANGAG X CGAA ANGGACG 3087 2559 CATTCATT T GCAGGAGG 580 CUCCUGC CUGANGAG X CGAA ANGGANG 3089 2572 GAGSACAT T GTTGATAG 581 CUGACAGC CUGANGAG X CGAA ANGGANG 3089 2575 GACATTGT T GATGAGTG 582 CAUCAGAC CUGANGAG X CGAA ANGGANG 3091 2576 TTGTTGAT A GATGTAAG 581 CUURCAUC CUGANGAG X CGAA ANGGANG 3092 2585 ATRGATGT A AGCAATTT 584 AAAUGUCC CUGANGAG X CGAA ANGGANG 3092 2585 ATRGATGT A AGCAATTT 584 AAAUGUCC CUGANGAG X CGAA ANGGANG 3093 2585 ATRGATGT T A GGCACTC 585 CCCCCACA CUGANGAG X CGAA ANGGCAC 3094 2592 TAAGCAATT T GTGGGGC 586 GGCCCCC CUGANGAG X CGAA ANGCCULU 3095 2605 GGCCCCT T ACAGTAAA 587 UULACUGU CUGANGAG X CGAA ANGCCULU 3095 2606 GGCCCCTT A CAGTAAAA 588 INUURCUG CUGANGAG X CGAA ANGGGCC 3097 2611 CTTACAGT A ARTGAAAA 588 INUURCUG CUGANGAG X CGAA ANGGGCC 3097 2629 AGGGACT T A ARTGAAAA 589 INUURCUGU CUGANGAG X CGAA ANGGGCC 3097 2629 CAGGAGCCT T ACAGTAAAA 589 INUURCUGAGG X CGAA ANGGGCC 3097 2629 CAGGAGCCT T ACAGTAAAA 589 INUURCUGAGG X CGAA ANGGGCC 3097 2629 CAGGAGCCT T ACAGTAAAA 589 INUURCUGAGG X CGAA ANGGGCC 3097 2629 CAGGAGCT T ACAGTAAA 589 INUURCUGAGG X CGAA ANGGGCC 3097 2629 CAGGAGCT T ACAGTAAA 589 INUURCUGAGG X CGAA AGCUGAAG X CGAA AGCUCCU 3098 2629 CAGGAGCT T ACAGTAAA 589 INUURCUGAGG X CGAA AGCUCCU 3098 2629 CAGGAGCT T ACAGTAAA 589 INUURCUGAGG X CGAA AGCUCCU 3098 2629 CAGGAGCT T ACAGTAAA 589 INUURCUGAGG X CGAA ACCUCCU 3098 2629 CAGGAGCT T ACAGTAAA 589 INUURCUGAGG X CGAA ACCUCCU 3098	2544	TCCTTCTT T TCCTGACA			
2554 COTGACAT T CATTTGCA 577 UGCAAAUG CUGAUGAG X CGAA AUGUCAGG 3086	2545				
2555	2546				
2558 ACATTCAT T TOCAGGAG 579 CUCCUGEA CUCAJUGAG X CGAA AJUGANUGU 3088 2559 CATTCATT T GCAGGAGG 580 COULCUIGE CUGAJUGAG X CGAA AJUGANUGU 3088 2575 GAGGACAT T GTTGATAG 581 CUAUCAGA CUGAJUGAG X CGAA AJUGCUC 3090 2575 GAGCATTGT T GATAGATG 582 CAUCUAUC CUGAJUGAG X CGAA AGAGGUC 3091 2579 TOTTGTGAT A GATGAAAG 583 CUUACAGC CUGAJUGAG X CGAA AGAGGUC 3092 2588 ATRAGAGAT T AGTGAGAG 583 CUUACAGC CUGAJUGAG X CGAA AJUGACAGA 3092 2588 ATRAGAGAT T AGTGAGGC 584 AAAJUJGCU CUGAJUGAG X CGAA AJUGACUJAU 3093 2592 TAAGCAATT T GTGGGGC 586 GGCCCCAC CUGAJUGAG X CGAA AJUGCUJU 3094 2593 AAGCAATT T GTGGGGC 586 GGCCCCAC CUGAJUGAG X CGAA AJUGCUJU 3094 2605 GGGCCCCT T ACAGTTAAA 587 JUJUACUJU CUGAJUGAG X CGAA AJUGGCC 3097 2606 GGCCCCTT A CAGTAAAT 588 JUJUACUJU CUGAJUGAG X CGAA AJUGGCC 3097 2611 CTTACAGGT A AATGAAAA 589 JUJUACUJU CUGAJUGAG X CGAA AJUGGCC 3097 2629 AGGGAGCT A AATGAAAA 589 JUJUACUJU CUGAJUGAG X CGAA AJUGGCC 3097 2629 AGGGAGCT A AATGAAAA 589 JUJUACUJU CUGAJUGAG X CGAA AJUGGCC 3097 3094					
2559 CATTCATT T GCAGGAGG 580 CCUCCUGC CUGANGAG X CGAA ADIGAAIG 3089 2572 GAGGACAT T GTTGATAG 581 CUANCAAC CUGANGAG X CGAA ANGUCCUC 3090 2575 GACATTGT T GATTGAGTG 582 CANCUANC CUGANGAG X CGAA ANGUCCUC 3091 2579 TIGTTGATA A GATGTAAG 583 CUNACANC CUGANGAG X CGAA ANCAACAA 3092 2585 ATAGGTATA A GATGTAAG 583 CUNACANC CUGANGAG X CGAA ANUCAACAA 3092 2585 ATAGGTAT A TOTGAGGGC 584 AAANUCUC CUGANGAG X CGAA ANUCAACAA 3093 2592 TAAGGCAT T TGTGGGGCC 585 GCCCCCA CUGANGAG X CGAA ANUCAUNU 3094 2593 AAGCAATT T GTGGGGCC 586 GCCCCCA CUGANGAG X CGAA ANUCAUNU 3094 2605 GGGCCCCT T ACAGTAAA 587 UUNACUG CUGANGAG X CGAA ANUGCCC 3096 2606 GGCCCCT A CAGTAAAT 588 AUNIACUG CUGANGAG X CGAA ANGGGCC 3097 2611 CTTACAGT A ANTGAAAA 589 UNUCAUU CUGANGAG X CGAA ANGGGCCC 3097 2629 AGGAGACT T AANTTAAC 590 GUUAANUU CUGANGAG X CGAA ANGCCAAC 3098 2629 AGGAGACT T AANTTAAC 590 GUUAANUU CUGANGAG X CGAA ANGCCAAC 3099 3098 3					
2572 GAGGACAT T OTTORTRG 581 CURICAL CUGALGAG X CGAA AUGUCCUC 3090 2575 GACATTOT T GATAGATG 582 CUULGAUC CUGALGAG X CGAA ACAUGUC 3091 2579 TOTTOTAT A GATTAGAT 583 CUULCAUC CUGALGAG X CGAA ACAUGUA 3092 2585 ATRAGATOT A AGCAATT 584 AAAUUCCU CUGALGAG X CGAA AUGACAA 3092 2592 TAAGCAAT T TOTGGGCC 585 GCCCCAC, CUGALGAG X CGAA AUGUCUA 3094 2593 AAGCAATT T OTGGGCC 586 GGCCCCAC CUGALGAG X CGAA AUGUCUA 3094 2605 GGGCCCCT A CAGTAAA 587 UULACUG CUGALGAG X CGAA AUGUCU 3095 2606 GGCCCCT A CAGTAAA 588 AUGUACU CUGALGAG X CGAA AAGGGCC 3097 2611 COTTACAGT A AATGAAAA 589 UULACUU CUGALGAG X CGAA AACUGLAAG 3098 2629 AGGGACT T A AATGAAAA 589 UULACUU CUGALGAG X CGAA AACUGLAAG 3098 2629 AGGGACT T AAATTAAC 590 GULAAUUU CUGALGAG X CGAA ACUGLAAG 3098 2629 AGGGACT T AAATTAAC 590 GULAAUUU CUGALGAG X CGAA ACUGLAAG 3098	2558				
2575 GACATIGI T GATAGATG 582 CAUCUAUC CUGAUGAG X CGAA ACANUGUC 3091 2579 TIGITGAT A GATGTAAG 583 CUUACAUC CUGAUGAG X CGAA ACCACCA 3092 2585 ATROAGGT A ACCACATT 584 AAAUUCCU CUGAUGAG X CGAA ACAUCUAU 3093 2592 TAAGCAAT T TGTGGGGCC 585 GCCCCAC CUGAUGAG X CGAA AAUUCCUU 3094 2593 AAGCAAT T TGTGGGGCC 586 GGCCCCCC CUGAUGAG X CGAA AAUUCCUU 3095 2605 GGGCCCCT T ACAGTAAA 587 UUUACUGU CUGAUGAG X CGAA AAUUGCUU 3096 2606 GGCCCCTT A CAGTAAAT 588 AUUUACUG CUGAUGAG X CGAA AAGGGGCC 3097 2611 CTTACAGT A AATGAAAA 589 UUUACUGU CUGAUGAG X CGAA AAGGGCCC 3098 2629 AGGAGACT T AAATTAAC 590 GUUAAUUU CUGAUGAG X CGAA AGUCCCU 3099					
2579 TROTTIGAT A GATUTANG 583 CUUNCNUC CUGAUGAG X CGAA AUCAACAA 3092 2585 ATROATIGT A NGCAATTT 584 ANAUDICUC CUGAUGAG X CGAA AUCAACAA 3093 2592 TAAGCAATT TOTGGGGC 585 CCCCCACA CUGAUGAG X CGAA AUUCGUUA 3094 2593 ANGCAATT TOTGGGGC 586 GGCCCCC CUGAUGAG X CGAA AUUCGUUA 3095 2605 GGGCCCCT TA CAGTANA 587 UUUNCAUG UCGAUGAG X CGAA AAUUGGUU 3095 2606 GGCCCCTT A CAGTANA 588 AUUUNCAUG CUGAUGAG X CGAA AAGGGGCC 3097 2611 CTTACAGT A AATGAAAA 589 UUUNCAUG CUGAUGAG X CGAA ACUGUAAG 3098 2629 AGGGACT TA AATGAAAA 589 UUUNCAUG CUGAUGAG X CGAA ACUGUAAG 3098 2629 AGGGACT TA AATGAAAA 589 UUUNCAUG CUGAUGAG X CGAA ACUGUAAG 3098					
2585					
2592 TARGART TA SOCIATION 585 GCCCCCACA CUGAUGAG X CCGA ADURCUU 3095					
2593 AAGCART T CTGGGGGC 586 GGCCCCCAC CUGAUGAG X CGAA AAUUGCUU 3095					
2695 GGGCCCCT T ACAGTANA 587 UUUACUGU CUGAUGAG X CGAA AGGGGCCC 3096					
2606 GGCCCCTT A CAGTANAT 588 AUUINCUG CUGANGAG X CGRA AAGGGGCC 3097 2611 CTTACAGT A NATGANAA 589 UUUUCAUU CUGANGAG X CGRA ACUGUNAAG 3098 2629 AGGAGACT T RAMTTANC 590 GUUNAUUU CUGANGAG X CGRA ACUGUNCU 3039					
2611 CTTACAGT A AATGAAAA 589 UUUUCAUU CUGAUGAG X CGAA ACUGUAAG 3098 2629 AGGAGACT T AAATTAAC 590 GUUAAUUU CUGAUGAG X CGAA AGUCUCCU 3099					
2629 AGGAGACT T AAATTAAC 590 GUUAAUUU CUGAUGAG X CGAA AGUCUCCU 3099	2606				
2629 AGGAGACT T AAATTAAC 550 GOULAGOO COGAGGACT TOTAL	2611				
2630 GGAGACTT A AATTAACT 591 AGUUAAUU CUGAUGAG X CGAA AAGUCUCC 3100					
	2630	GGAGACTT A AATTAACT	591	AGUUAAUU CUGAUGAG X CGAA AAGUCUCC	3100

Table 37

2634	ACTTAAAT T AACTATGC	592	GCAUAGUU CUGAUGAG X CGAA AUUUAAGU	3101
2635	CTTAAATT A ACTATGCC	593	GGCAUAGU CUGAUGAG X CGAA AAUUUAAG	3102
2639	AATTAACT A TGCCTGCT	594	AGCAGGCA CUGAUGAG X CGAA AGUUAAUU	3103
2648	TGCCTGCT A GGTTTTAT	595	AUAAAACC CUGAUGAG X CGAA AGCAGGCA	3104
2652	TGCTAGGT T TTATCCCA	596	UGGGAUAA CUGAUGAG X CGAA ACCUAGCA	3105
2653	GCTAGGTT T TATCCCAA	597	UUGGGAUA CUGAUGAG X CGAA AACCUAGC	3106
2654	CTAGGTTT T ATCCCAAT	598	AUUGGGAU CUGAUGAG X CGAA AAACCUAG	3107
2655	TAGGTTTT A TCCCAATG	599	CAUUGGGA CUGAUGAG X CGAA AAAACCUA	3108
2657	GGTTTTAT C CCAATGTT	600	AACAUUGG CUGAUGAG X CGAA AUAAAACC	3109
2665	CCCAATGT T ACTAAATA	601	UAUUUAGU CUGAUGAG X CGAA ACAUUGGG	3110
2666	CCAATGTT A CTAAATAT	602	AUAUUUAG CUGAUGAG X CGAA AACAUUGG	3111
2669	ATGTTACT A AATATTTG	603	CAAAUAUU CUGAUGAG X CGAA AGUAACAU	3112
2673	TACTAAAT A TTTGCCCT	604	AGGGCAAA CUGAUGAG X CGAA AUUUAGUA	3113
2675	CTAAATAT T TGCCCTTA	605	UAAGGGCA CUGAUGAG X CGAA AUAUUUAG	3114
2676	TAAATATT T GCCCTTAG	606	CUAAGGGC CUGAUGAG X CGAA AAUAUUUA	3115
2682	TTTGCCCT T AGATAAAG	607	CUUUAUCU CUGAUGAG X CGAA AGGGCAAA	3116
2683	TTGCCCTT A GATAAAGG	608	CCUUUAUC CUGAUGAG X CGAA AAGGGCAA	3117
2687	CCTTAGAT A AAGGGATC	609	GAUCCCUU CUGAUGAG X CGAA AUCUAAGG	3118
2695	AAAGGGAT C AAACCGTA	610	UACGGUUU CUGAUGAG X CGAA AUCCCUUU	3119
2703	CAAACCGT A TTATCCAG	611	CUGGAUAA CUGAUGAG X CGAA ACGGUUUG	3120
2705	AACCGTAT T ATCCAGAG	612	CUCUGGAU CUGAUGAG X CGAA AUACGGUU	3121
2706	ACCGTATT A TCCAGAGT	613	ACUCUGGA CUGAUGAG X CGAA AAUACGGU	3122
2708	CGTATTAT C CAGAGTAT	614	AUACUCUG CUGAUGAG X CGAA AUAAUACG	3123
2715	TCCAGAGT A TGTAGTTA	615	UAACUACA CUGAUGAG X CGAA ACUCUGGA	3124
2719	GAGTATGT A GTTAATCA	616	UGAUUAAC CUGAUGAG X CGAA ACAUACUC	3125
2722	TATGTAGT T AATCATTA	617	UAAUGAUU CUGAUGAG X CGAA ACUACAUA	3126
2723	ATGTAGTT A ATCATTAC	618	GUAAUGAU CUGAUGAG X CGAA AACUACAU	3127
2726	TAGTTAAT C ATTACTTC	619	GAAGUAAU CUGAUGAG X CGAA AUUAACUA	3128
2729	TTAATCAT T ACTTCCAG	620	CUGGAAGU CUGAUGAG X CGAA AUGAUUAA	3129
2730	TAATCATT A CTTCCAGA	621	UCUGGAAG CUGAUGAG X CGAA AAUGAUUA	3130
2733	TCATTACT T CCAGACGC	622	GCGUCUGG CUGAUGAG X CGAA AGUAAUGA	3131
2734	CATTACTT C CAGACGCG	623	CGCGUCUG CUGAUGAG X CGAA AAGUAAUG	3132
2747	CGCGACAT T ATTTACAC	624	GUGUAAAU CUGAUGAG X CGAA AUGUCGCG	3133
2748	GCGACATT A TTTACACA	625	UGUGUAAA CUGAUGAG X CGAA AAUGUCGC	3134
2750	GACATTAT T TACACACT	626	AGUGUGUA CUGAUGAG X CGAA AUAAUGUC	3135
2751	ACATTATT T ACACACTC	627	GAGUGUGU CUGAUGAG X CGAA AAUAAUGU	3136
2752	CATTATTT A CACACTCT	628	AGAGUGUG CUGAUGAG X CGAA AAAUAAUG	3137
2759	TACACACT C TTTGGAAG	629	CUUCCAAA CUGAUGAG X CGAA AGUGUGUA	3138
2761	CACACTCT T TGGAAGGC	630	GCCUUCCA CUGAUGAG X CGAA AGAGUGUG	3139
2762	ACACTCTT T GGAAGGCG	631 .	CGCCUUCC CUGAUGAG X CGAA AAGAGUGU	3140
2776	GCGGGGAT C TTATATAA	632	UUAUAUAA CUGAUGAG X CGAA AUCCCCGC	3141
2778	GGGGATCT T ATATAAAA	633	UUUUAUAU CUGAUGAG X CGAA AGAUCCCC	3142
2779	GGGATCTT A TATAAAAG	634	CUUUUAUA CUGAUGAG X CGAA AAGAUCCC	3143
2781	GATCTTAT A TAAAAGAG	635	CUCUUUUA CUGAUGAG X CGAA AUAAGAUC	3144
2783	TCTTATAT A AAAGAGAG	636	CUCUCUUU CUGAUGAG X CGAA AUAUAAGA	3145
2793	AAGAGAGT C CACACGTA	637	UACGUGUG CUGAUGAG X CGAA ACUCUCUU	3146
2801	CCACACGT A GCGCCTCA	638	UGAGGCGC CUGAUGAG X CGAA ACGUGUGG	3147
2808	TAGCGCCT C ATTTTGCG	639	CGCAAAAU CUGAUGAG X CGAA AGGCGCUA	3148
2811	CGCCTCAT T TTGCGGGT	640	ACCCGCAA CUGAUGAG X CGAA AUGAGGCG	3149
2812	GCCTCATT T TGCGGGTC	641	GACCCGCA CUGAUGAG X CGAA AAUGAGGC	3150
2813	CCTCATTT T GCGGGTCA	642	UGACCCGC CUGAUGAG X CGAA AAAUGAGG	3151

Table 37

				2152
2820	TTGCGGGT C ACCATATT	643	AAUAUGGU CUGAUGAG X CGAA ACCCGCAA	3152
2826	GTCACCAT A TTCTTGGG	644	CCCAAGAA CUGAUGAG X CGAA AUGGUGAC	3153
2828	CACCATAT T CTTGGGAA	645	UUCCCAAG CUGAUGAG X CGAA AUAUGGUG	3154
2829	ACCATATT C TTGGGAAC	646	GUUCCCAA CUGAUGAG X CGAA AAUAUGGU	3155
2831	CATATTCT T GGGAACAA	647	UUGUUCCC CUGAUGAG X CGAA AGAAUAUG	3156
2843	AACAAGAT C TACAGCAT	648	AUGCUGUA CUGAUGAG X CGAA AUCUUGUU	3157
2845	CAAGATCT A CAGCATGG	649	CCAUGCUG CUGAUGAG X CGAA AGAUCUUG	3158
2859	TGGGAGGT T GGTCTTCC	650	GGAAGACC CUGAUGAG X CGAA ACCUCCCA	3159
2863	AGGTTGGT C TTCCAAAC	651	GUUUGGAA CUGAUGAG X CGAA ACCAACCU	3160
2865	GTTGGTCT T CCAAACCT	652	AGGUUUGG CUGAUGAG X CGAA AGACCAAC	3161
2866	TTGGTCTT C CAAACCTC	653	GAGGUUUG CUGAUGAG X CGAA AAGACCAA	3162
2874	CCAAACCT C GAAAAGGC	654	GCCUUUUC CUGAUGAG X CGAA AGGUUUGG	3163
2895	GGACAAAT C TTTCTGTC	655	GACAGAAA CUGAUGAG X CGAA AUUUGUCC	3164
2897	ACAAATCT T TCTGTCCC	656	GGGACAGA CUGAUGAG X CGAA AGAUUUGU	3165
2898	CAAATCTT T CTGTCCCC	657	GGGGACAG CUGAUGAG X CGAA AAGAUUUG	3166
2899	AAATCTTT C TGTCCCCA	658	UGGGGACA CUGAUGAG X CGAA AAAGAUUU	3167
2903	CTTTCTGT C CCCAATCC	659	GGAUUGGG CUGAUGAG X CGAA ACAGAAAG	3168
2910	TCCCCAAT C CCCTGGGA	660	UCCCAGGG CUGAUGAG X CGAA AUUGGGGA	3169
2920	CCTGGGAT T CTTCCCCG	661	CGGGGAAG CUGAUGAG X CGAA AUCCCAGG	3170
2921	CTGGGATT C TTCCCCGA	662	UCGGGGAA CUGAUGAG X CGAA AAUCCCAG	3171
2923	GGGATTCT T CCCCGATC	663	GAUCGGGG CUGAUGAG X CGAA AGAAUCCC	3172
2924	GGATTCTT C CCCGATCA	664	UGAUCOGG CUGAUGAG X CGAA AAGAAUCC	. 3173
2931	TCCCCGAT C ATCAGTTG	665	CAACUGAU CUGAUGAG X CGAA AUCGGGGA	3174
2934	CCGATCAT C AGTTGGAC	666	GUCCAACU CUGAUGAG X CGAA AUGAUCGG	3175
2938	TCATCAGT T GGACCCTG	667	CAGGGUCC CUGAUGAG X CGAA ACUGAUGA	3176
2950	CCCTGCAT T CAAAGCCA	668	UGGCUUUG CUGAUGAG X CGAA AUGCAGGG	3177
2951	CCTGCATT C AAAGCCAA	669	UUGGCUUU CUGAUGAG X CGAA AAUGCAGG	3178
2962	AGCCAACT C AGTAAATC	670	GAUUUACU CUGAUGAG X CGAA AGUUGGCU	3179
2966	AACTCAGT A AATCCAGA	671	UCUGGAUU CUGAUGAG X CGAA ACUGAGUU	3180
2970	CAGTAAAT C CAGATTGG	672	CCAAUCUG CUGAUGAG X CGAA AUUUACUG	3181
2976	ATCCAGAT T GGGACCTC	673	GAGGUCCC CUGAUGAG X CGAA AUCUGGAU	3182
2984	TGGGACCT C AACCCGCA	674	UGCGGGUU CUGAUGAG X CGAA AGGUCCCA	3183
3037	GGGAGCAT T CGGGCCAG	675	CUGGCCCG CUGAUGAG X CGAA AUGCUCCC	3184
3038	GGAGCATT C GGGCCAGG	676	CCUGGCCC CUGAUGAG X CGAA AAUGCUCC	3185
3049	GCCAGGGT T CACCCCTC	677	GAGGGGUG CUGAUGAG X CGAA ACCCUGGC	3186
3050	CCAGGGTT C ACCCCTCC	678	GGAGGGU CUGAUGAG X CGAA AACCCUGG	3187
3057	TCACCCCT C CCCATGGG	679	CCCAUGGG CUGAUGAG X CGAA AGGGGUGA	3188
3073	GGGACTGT T GGGGTGGA	680	UCCACCCC CUGAUGAG X CGAA ACAGUCCC	3189
3087	GGAGCCCT C ACGCTCAG	681	CUGAGCGU CUGAUGAG X CGAA AGGGCUCC	3190
3093	CTCACGCT C AGGGCCTA	682	UAGGCCCU CUGAUGAG X CGAA AGCGUGAG	3191
3101	CAGGGCCT A CTCACAAC	683	GUUGUGAG CUGAUGAG X CGAA AGGCCCUG	3192
3104	GGCCTACT C ACAACTGT	684	ACAGUUGU CUGAUGAG X CGAA AGUAGGCC	3193
3123	CAGCAGCT C CTCCTCCT	685	AGGAGGAG CUGAUGAG X CGAA AGCUGCUG	3194
3126	CAGCTCCT C CTCCTGCC	686	GGCAGGAG CUGAUGAG X CGAA AGGAGCUG	3195
3129	CTCCTCCT C CTGCCTCC	687	GGAGGCAG CUGAUGAG X CGAA AGGAGGAG	3196
3136	TCCTGCCT C CACCAATC	688	GAUUGGUG CUGAUGAG X CGAA AGGCAGGA	3197
3144	CCACCAAT C GGCAGTCA	689	UGACUGCC CUGAUGAG X CGAA AUUGGUGG	3198
3151	TCGGCAGT C AGGAAGGC	690	GCCUUCCU CUGAUGAG X CGAA ACUGCCGA	3199
3165	GGCAGCCT A CTCCCTTA	691	UAAGGGAG CUGAUGAG X CGAA ACGCUGCC	3200
3168	AGCCTACT C CCTTATCT	692	AGAUAAGG CUGAUGAG X CGAA AGUAGGCU	3201
3172	TACTCCCT T ATCTCCAC	693	GUGGAGAU CUGAUGAG X CGAA AGGGAGUA	3202

Table 37

ACTCCCTT A TCTCCACC	694	GGUGGAGA CUGAUGAG X CGAA AAGGGAGU	3203
TCCCTTAT C TCCACCTC	695	GAGGUGGA CUGAUGAG X CGAA AUAAGGGA	3204
CCTTATCT C CACCTCTA	696	UAGAGGUG CUGAUGAG X CGAA AGAUAAGG	3205
CTCCACCT C TAAGGGAC	697	GUCCCUUA CUGAUGAG X CGAA AGGUGGAG	3206
CCACCTCT A AGGGACAC	698	GUGUCCCU CUGAUGAG X CGAA AGAGGUGG	3207
GGGACACT C ATCCTCAG	699	CUGAGGAU CUGAUGAG X CGAA AGUGUCCC	3208
ACACTCAT C CTCAGGCC	700	GGCCUGAG CUGAUGAG X CGAA AUGAGUGU	3209
CTCATCCT C AGGCCATG	701	CAUGGCCU CUGAUGAG X CGAA AGGAUGAG	3210
	TCCCTTAT C TCCACCTC CCTTATCT C CACCTCTA CTCCACCT C TAAGGGAC CCACCTCT A AGGGACAC GGGACACT C ATCCTCAG ACACTCAT C CTCAGGCC	TCCCTTAT C TCCACCTC 695 CCTTATCT C CACCTCTA 696 CCTCACCT C TAAGGGAC 697 CCACCTCT A AGGGACAC 699 AGGACACT C ATCCTCAG 699 ACACTCAT C CTCAGGCC 700	TECCETRAT C TECACCTC 695 GAGGUGGA CUGAUSAG X CGAA AUAANGGA CETCACATC C CACCTCTA 696 UAGAGSUG CUGAUSAG X CGAA AGAURAGO CETCACACT C TRAGGGAC 697 GUCCCULA CUGAUGAG X CGAA AGAUGAGO CECACCTC A AGGGACAC 698 GUGUCCUU CUGAUGAG X CGAA AGAGGUGG GOGACACT C ATCCTCAG 699 CUGAGGAU CUGAUSAG X CGAA AGAGGUGG AGGAACTC C TCAGGCC 700 GGCCUGAG CUGAUSAG X CGAA AUGUGUCC

Input Sequence = AF100308. Cut Site = UH/.
Stem Length = 8. Core Sequence = CUGAUGAG X CGAA (X = GCCGUUAGGC or other stem II)
AF100308 (Repatitis B virus strain 2-18, 3215 bp)

Table 38

Table 38: Human HBV Inozyme and Substrate Sequence

Pos	Substrate	Seq ID	Ribozyme	Rz Seq ID
	and a semanage	702	UGGAAAGU CUGAUGAG X CGAA IUGGAGUU	3211
9	AACTCCAC C ACTTTCCA	702	GUGGAAAG CUGAUGAG X CGAA IGUGGAGU	3212
10	ACTCCACC A CTTTCCAC	703	UGGUGGAA CUGAUGAG X CGAA IUGGUGGA	3213
12	TCCACCAC T TTCCACCA	705	AGUUUGGU CUGAUGAG X CGAA IAAAGUGG	3214
16	CCACTTTC C ACCAAACT	706	GAGUUUGG CUGAUGAG X CGAA IGAAAGUG	3215
17	CACTITCC A CCAAACTC	707	AAGAGUUU CUGAUGAG X CGAA TUGGAAAG	3216
19	CTTTCCAC C AAACTCTT	707	GAAGAGUU CUGAUGAG X CGAA IGUGGAAA	3217
20	TTTCCACC A AACTCTTC	709	UCUUGAAG CUGAUGAG X CGAA IUUUGGUG	3218
24	CACCAAAC T CTTCAAGA	710	GAUCUUGA CUGAUGAG X CGAA IAGUUUGG	3219
26	CCAAACTC T TCAAGATC	711	UGGGAUCU CUGAUGAG X CGAA IAAGAGUU	3220
29	AACTCTTC A AGATCCCA	711	UGACUCUG CUGAUGAG X CGAA IAUCUUGA	3221
35	TCAAGATC C CAGAGTCA	712	CUGACUCU CUGAUGAG X CGAA IGAUCUUG	3222
36	CAAGATCC C AGAGTCAG	713	CCUGACUC CUGAUGAG X CGAA IGGAUCUU	3223
37	AAGATCCC A GAGTCAGG		CAGGGCCC CUGAUGAG X CGAA IACUCUGG	3224
43	CCAGAGTC A GGGCCCTG	715	AAGUACAG CUGAUGAG X CGAA ICCCUGAC	3225
48	GTCAGGGC C CTGTACTT		AAAGUACA CUGAUGAG X CGAA IGCCCUGA	3226
49	TCAGGGCC C TGTACTTT	717	GAAAGUACA CUGAUGAG X CGAA IGGCCCUG	3227
50	CAGGGCCC T GTACTTTC	718	AGCAGGAA CUGAUGAG X CGAA IUACAGGG	3228
55	CCCTGTAC T TTCCTGCT	719	CACCAGGA CUGAUGAG X CGAA IAAAGUAC	3229
59	GTACTTTC C TGCTGGTG	720	CCACCAGC CUGAUGAG X CGAA IGAAAGUA	3230
60	TACTITCC T GCTGGTGG	721	GAGCCACC CUGAUGAG X CGAA ICAGGAAA	3231
63	TTTCCTGC T GGTGGCTC	722	UGAACUGG CUGAUGAG X CGAA ICCACCAG	3232
70	CTGGTGGC T CCAGTTCA	723	CCUGAACU CUGAUGAG X CGAA IAGCCACC	3233
72	GGTGGCTC C AGTTCAGG	724	UCCUGAAC CUGAUGAG X CGAA IGAGCCAC	3234
73	GTGGCTCC A GTTCAGGA	725	ACUGUUCC CUGAUGAG X CGAA IAACUGGA	3235
78	TCCAGTTC A GGAACAGT	726	GGGCUCAC CUGAUGAG X CGAA IUUCCUGA	3236
84	TCAGGAAC A GTGAGCCC	727	CUGAGCAG CUGAUGAG X CGAA ICUCACUG	3237
91	CAGTGAGC C CTGCTCAG	728	UCUGAGCA CUGAUGAG X CGAA IGCUCACU	3238
92	AGTGAGCC C TGCTCAGA	729	UUCUGAGCA CUGAUGAG X CGAA IGCCUCAC	3239
93	GTGAGCCC T GCTCAGAA	730	GUAUUCUG CUGAUGAG X CGAA ICAGGGCU	3240
96	AGCCCTGC T CAGAATAC	731	CAGUAUUC CUGAUGAG X CGAA TAGCAGGG	3241
98	CCCTGCTC A GAATACTG	732	GCAGAGAC CUGAUGAG X CGAA IUAUUCUG	3242
105	CAGAATAC T GTCTCTGC	733	UAUGGCAG CUGAUGAG X CGAA IACAGUAU	3243
109	ATACTGTC T CTGCCATA	734	GAUAUGGC CUGAUGAG X CGAA IAGACAGU	3244
111	ACTGTCTC T GCCATATC	735	GACGAUAU CUGAUGAG X CGAA ICAGAGAC	3245
114	GTCTCTGC C ATATCGTC	736	UGACGAUAU CUGAUGAG X CGAA ICAGAGA UGACGAUA CUGAUGAG X CGAA IGCAGAGA	3246
115	TCTCTGCC A TATCGTCA	737	GAUAAGAU CUGAUGAG X CGAA IACGAUAU	3247
123	ATATOGTO A ATOTTATO	738	CUUCGAUA CUGAUGAG X CGAA TACGAGAG	3248
127	CGTCAATC T TATCGAAG	739	GGGUCCC CUGAUGAG X CGAA IUCUUCGA	3249
138	TCGAAGAC T GGGGACCC	740	CGGUACAG CUGAUGAG X CGAA IUCCCCAG	3250
145	CTGGGGAC C CTGTACCG	741	UCGGUACA CUGAUGAG X CGAA IGUCCCCA	3251
146	TGGGGACC C TGTACCGA	742	UCGGUACA CUGAUGAG X CGAA IGUCCCCA UUCGGUAC CUGAUGAG X CGAA IGGUCCCC	3252
147	GGGGACCC T GTACCGAA	743	CCAUGUUC CUGAUGAG X CGAA IUACAGGG	3253
152	CCCTGTAC C GAACATGG	744		3254
157	TACCGAAC A TGGAGAAC	745	GUUCUCCA CUGAUGAG X CGAA IUUCGGUA	3255
166	TGGAGAAC A TCGCATCA	746	UGAUGCGA CUGAUGAG X CGAA IUUCUCCA	3256
171	AACATCGC A TCAGGACT		AGUCCUGA CUGAUGAG X CGAA ICGAUGUU	3257
174	ATCGCATC A GGACTCCT	748	AGGAGUCC CUGAUGAG X CGAA IAUGCGAU	3237

Table 38

179	ATCAGGAC T CCTAGGAC	749	GUCCUAGG CUGAUGAG X CGAA IUCCUGAU	3258
181	CAGGACTC C TAGGACCC	750	GGGUCCUA CUGAUGAG X CGAA IAGUCCUG	3259
182	AGGACTCC T AGGACCCC	751	GGGGUCCU CUGAUGAG X CGAA IGAGUCCU	3260
188	CCTAGGAC C CCTGCTCG	752	CGAGCAGG CUGAUGAG X CGAA IUCCUAGG	3261
189	CTAGGACC C CTGCTCGT	753	ACGAGCAG CUGAUGAG X CGAA IGUCCUAG	3262
190	TAGGACCC C TGCTCGTG	754	CACGAGCA CUGAUGAG X CGAA IGGUCCUA	3263
191	AGGACCCC T GCTCGTGT	755	ACACGAGC CUGAUGAG X CGAA IGGGUCCU	3264
194	ACCCCTGC T CGTGTTAC	756	GUAACACG CUGAUGAG X CGAA ICAGGGGU	3265
203	CGTGTTAC A GGCGGGGT	757	ACCCCGCC CUGAUGAG X CGAA IUAACACG	3266
217	GGTTTTTC T TGTTGACA	758	UGUCAACA CUGAUGAG X CGAA IAAAAACC	3267
225	TTGTTGAC A AAAATCCT	759	AGGAUUUU CUGAUGAG X CGAA IUCAACAA	3268
232	CAAAAATC C TCACAATA	760	UAUUGUGA CUGAUGAG X CGAA IAUUUUUG	3269
233	AAAAATCC T CACAATAC	761	GUAUUGUG CUGAUGAG X CGAA IGAUUUUU	3270
235	AAATCCTC A CAATACCA	762	UGGUAUUG CUGAUGAG X CGAA IAGGAUUU	3271
237	ATCCTCAC A ATACCACA	763	UGUGGUAU CUGAUGAG X CGAA IUGAGGAU	3272
242	CACAATAC C ACAGAGTC	764	GACUCUGU CUGAUGAG X CGAA IUAUUGUG	3273
243	ACAATACC A CAGAGTCT	765	AGACUCUG CUGAUGAG X CGAA IGUAUUGU	3274
245	AATACCAC A GAGTCTAG	766	CUAGACUC CUGAUGAG X CGAA IUGGUAUU	3275
251	ACAGAGTC T AGACTCGT	767	ACGAGUCU CUGAUGAG X CGAA IACUCUGU	3276
256	GTCTAGAC T CGTGGTGG	768	CCACCACG CUGAUGAG X CGAA IUCUAGAC	3277
267	TGGTGGAC T TCTCTCAA	769	UUGAGAGA CUGAUGAG X CGAA IUCCACCA	3278
270	TGGACTTC T CTCAATTT	770	AAAUUGAG CUGAUGAG X CGAA IAAGUCCA	3279
272	GACTTCTC T CAATTTTC	771	GAAAAUUG CUGAUGAG X CGAA IAGAAGUC	3280
274	CTTCTCTC A ATTTTCTA	772	UAGAAAAU CUGAUGAG X CGAA IAGAGAAG	3281
281	CAATTTC T AGGGGGAA	773	UUCCCCCU CUGAUGAG X CGAA IAAAAUUG	3282
291	GGGGGAAC A CCCGTGTG	774	CACACGGG CUGAUGAG X CGAA IUUCCCCC	3283
293	GGGAACAC C CGTGTGTC	775	GACACACG CUGAUGAG X CGAA IUGUUCCC	3284
294	GGAACACC C GTGTGTCT	776	AGACACAC CUGAUGAG X CGAA IGUGUUCC	3285
302	CGTGTGTC T TGGCCAAA	777	UUUGGCCA CUGAUGAG X CGAA IACACACG	3286
307	GTCTTGGC C AAAATTCG	778	CGAAUUUU CUGAUGAG X CGAA ICCAAGAC	3287
308	TCTTGGCC A AAATTCGC	779	GCGAAUUU CUGAUGAG X CGAA IGCCAAGA	3288
317	AAATTCGC A GTCCCAAA	780	UUUGGGAC CUGAUGAG X CGAA ICGAAUUU	3289
321	TCGCAGTC C CAAATCTC	781	GAGAUUUG CUGAUGAG X CGAA IACUGCGA	3290
322	- CGCAGTCC C AAATCTCC	782	GGAGAUUU CUGAUGAG X CGAA IGACUGCG	3291
323	GCAGTCCC A AATCTCCA	783	UGGAGAUU CUGAUGAG X CGAA IGGACUGC	3292
328	CCCAAATC T CCAGTCAC	784	GUGACUGG CUGAUGAG X CGAA IAUUUGGG	3293
330	CAAATCTC C AGTCACTC	785	GAGUGACU CUGAUGAG X CGAA IAGAUUUG	3294
331	AAATCTCC A GTCACTCA	786	UGAGUGAC CUGAUGAG X CGAA IGAGAUUU	3295
335	CTCCAGTC A CTCACCAA	787	UUGGUGAG CUGAUGAG X CGAA IACUGGAG	3296
337	CCAGTCAC T CACCAACC	788	GGUUGGUG CUGAUGAG X CGAA IUGACUGG	3297
339	AGTCACTC A CCAACCTG	789	CAGGUUGG CUGAUGAG X CGAA IAGUGACU	3298
341	TCACTCAC C AACCTGTT	790	AACAGGUU CUGAUGAG X CGAA IUGAGUGA	3299
342	CACTCACC A ACCTGTTG	791	CAACAGGU CUGAUGAG X CGAA IGUGAGUG	3300
345	TCACCAAC C TGTTGTCC	792	GGACAACA CUGAUGAG X CGAA IUUGGUGA	3301
346	CACCAACC T GTTGTCCT	793	AGGACAAC CUGAUGAG X CGAA IGUUGGUG	3302
353	CTGTTGTC C TCCAATTT	794	AAAUUGGA CUGAUGAG X CGAA IACAACAG	3303
354	TGTTGTCC T CCAATTTG	795	CAAAUUGG CUGAUGAG X CGAA IGACAACA	3304
356	TTGTCCTC C AATTTGTC	796	GACAAAUU CUGAUGAG X CGAA IAGGACAA	3305
357	TGTCCTCC A ATTTGTCC	797	GGACAAAU CUGAUGAG X CGAA IGAGGACA	3306
365	AATTTGTC C TGGTTATC	798	GAUAACCA CUGAUGAG X CGAA IACAAAUU	3307
366	ATTTGTCC T GGTTATCG	799	CGAUAACC CUGAUGAG X CGAA IGACAAAU	3308

Table 38

276	GTTATCGC T GGATGTGT	800	ACACAUCC CUGAUGAG X CGAA ICGAUAAC	3309
376 386	GATGTGTC T GCGGCGTT	801	AACGCCGC CUGAUGAG X CGAA IACACAUC	3310
400	GTTTTATC A TCTTCCTC	802	GAGGAAGA CUGAUGAG X CGAA IAUAAAAC	3311
400	TTATCATC T TCCTCTGC	803	GCAGAGGA CUGAUGAG X CGAA IAUGAUAA	3312
	TCATCTTC C TCTGCATC	804	GAUGCAGA CUGAUGAG X CGAA IAAGAUGA	3313
406	CATCTTCC T CTGCATCC	805	GGAUGCAG CUGAUGAG X CGAA IGAAGAUG	3314
407	TCTTCCTC T GCATCCTG	806	CAGGAUGC CUGAUGAG X CGAA IAGGAAGA	3315
409	TOUTOTEC A TOUTGOTG	807	CAGCAGGA CUGAUGAG X CGAA ICAGAGGA	3316
412	TCTGCATC C TGCTGCTA	808	UAGCAGCA CUGAUGAG X CGAA IAUGCAGA	3317
415	CTGCATCC T GCTGCTAT	809	AUAGCAGC CUGAUGAG X CGAA IGAUGCAG	3318
416	CATCCTGC T GCTATGCC	810	GGCAUAGC CUGAUGAG X CGAA ICAGGAUG	3319
419	CCTGCTGC T ATGCCTCA	811	UGAGGCAU CUGAUGAG X CGAA ICAGCAGG	3320
422	TGCTATGC C TCATCTTC	812	GAAGAUGA CUGAUGAG X CGAA ICAUAGCA	3321
427	GCTATGCC T CATCTTCT	813	AGAAGAUG CUGAUGAG X CGAA IGCAUAGC	3322
428	TATGCCTC A TCTTCTTG	814	CAAGAAGA CUGAUGAG X CGAA IAGGCAUA	3323
430	GCCTCATC T TCTTGTTG	815	CAACAAGA CUGAUGAG X CGAA IAUGAGGC	3324
433	TCATCTTC T TGTTGGTT	816	AACCAACA CUGAUGAG X CGAA IAAGAUGA	3325
436	GTTGGTTC T TCTGGACT	817	AGUCCAGA CUGAUGAG X CGAA IAACCAAC	3326
446	GGTTCTTC T GGACTATC	818	GAUAGUCC CUGAUGAG X CGAA IAAGAACC	3327
449	TTCTGGAC T ATCAAGGT	819	ACCUUGAU CUGAUGAG X CGAA IUCCAGAA	3328
454	GGACTATC A AGGTATGT	820	ACAUACCU CUGAUGAG X CGAA IAUAGUCC	3329
458	TATGTTGC C CGTTTGTC	821	GACAAACG CUGAUGAG X CGAA ICAACAUA	3330
470	ATGITGC C GTTTGTCC	822	GGACAAAC CUGAUGAG X CGAA IGCAACAU	3331
471	CGTTTGTC C TCTAATTC	823	GAAUUAGA CUGAUGAG X CGAA IACAAACG	3332
480	GTTTGTCC T CTAATTCC	824	GGAAUUAG CUGAUGAG X CGAA IGACAAAC	3333
482	TTGTCCTC T AATTCCAG	825	CUGGAAUU CUGAUGAG X CGAA IAGGACAA	3334
488	TCTAATTC C AGGATCAT	826	AUGAUCCU CUGAUGAG X CGAA IAAUUAGA	3335
489	CTAATIC & AGGATCATC	827	GAUGAUCC CUGAUGAG X CGAA IGAAUUAG	3336
495	CCAGGATC A TCAACAAC	828	GUUGUUGA CUGAUGAG X CGAA IAUCCUGG	3337
498	GGATCATC A ACAACCAG	829	CUGGUUGU CUGAUGAG X CGAA IAUGAUCC	3338
501	TCATCAAC A ACCAGCAC	830	GUGCUGGU CUGAUGAG X CGAA IUUGAUGA	3339
504	TCAACAAC C AGCACCGG	831	CCGGUGCU CUGAUGAG X CGAA IUUGUUGA	3340
505	CAACAACC A GCACCGGA	832	UCCGGUGC CUGAUGAG X CGAA IGUUGUUG	3341
508	CAACCAGC A CCGGACCA	833	UGGUCCGG CUGAUGAG X CGAA ICUGGUUG	3342
510	ACCAGCAC C GGACCATG	834	CAUGGUCC CUGAUGAG X CGAA IUGCUGGU	3343
515	CACCGGAC C ATGCAAAA	835	UUUUGCAU CUGAUGAG X CGAA IUCCGGUG	3344
516	ACCGGACC A TGCAAAAC	836	GUUUUGCA CUGAUGAG X CGAA IGUCCGGU	3345
520	GACCATGC A AAACCTGC	837	GCAGGUUU CUGAUGAG X CGAA ICAUGGUC	3346
525	TGCAAAAC C TGCACAAC	838	GUUGUGCA CUGAUGAG X CGAA 1UUUUGCA	3347
526	GCAAAACC T GCACAACT	839	AGUUGUGC CUGAUGAG X CGAA IGUUUUGC	3348
529	AAACCTGC A CAACTCCT	840	AGGAGUUG CUGAUGAG X CGAA ICAGGUUU	3349
531	ACCTGCAC A ACTCCTGC	841	GCAGGAGU CUGAUGAG X CGAA IUGCAGGU	3350
534	TGCACAAC T CCTGCTCA	842	UGAGCAGG CUGAUGAG X CGAA IUUGUGCA	3351
536	CACAACTC C TGCTCAAG	843	CUUGAGCA CUGAUGAG X CGAA IAGUUGUG	3352
537	ACAACTCC T GCTCAAGG	844	CCUUGAGC CUGAUGAG X CGAA IGAGUUGU	3353
540	ACTCCTGC T CAAGGAAC	845	GUUCCUUG CUGAUGAG X CGAA ICAGGAGU	3354
542	TCCTGCTC A AGGAACCT	846	AGGUUCCU CUGAUGAG X CGAA IAGCAGGA	3355
549	CAAGGAAC C TCTATGTT	847	AACAUAGA CUGAUGAG X CGAA IUUCCUUG	3356
550	AAGGAACC T CTATGTTT	848	AAACAUAG CUGAUGAG X CGAA IGUUCCUU	3357
552	GGAACCTC T ATGTTTCC	849	GGAAACAU CUGAUGAG X CGAA IAGGUUCC	3358
560	TATGTTTC C CTCATGTT	850	AACAUGAG CUGAUGAG X CGAA IAAACAUA	3359
		-		

Table 38

561	ATGTTTCC C TCATGTTG	851	CAACAUGA CUGAUGAG X CGAA IGAAACAU	3360
562	TGTTTCCC T CATGTTGC	852	GCAACAUG CUGAUGAG X CGAA IGGAAACA	3361
564	TTTCCCTC A TGTTGCTG	853	CAGCAACA CUGAUGAG X CGAA IAGGGAAA	
571	CATGTTGC T GTACAAAA	854	UUUUGUAC CUGAUGAG X CGAA ICAACAUG	3363
576	TGCTGTAC A AAACCTAC	855	GUAGGUUU CUGAUGAG X CGAA IUACAGCA	3364
581	TACAAAAC C TACGGACG	856	CGUCCGUA CUGAUGAG X CGAA IUUUUGUA	3365
582	ACAAAACC T ACGGACGG	857	CCGUCCGU CUGAUGAG X CGAA IGUUUUGU	3366
595	ACGGAAAC T GCACCTGT	858	ACAGGUGC CUGAUGAG X CGAA IUUUCCGU	3367
598	GAAACTGC A CCTGTATT	859	AAUACAGG CUGAUGAG X CGAA ICAGUUUC	3368
600	AACTGCAC C TGTATTCC	860	GGAAUACA CUGAUGAG X CGAA IUGCAGUU	3369
601	ACTGCACC T GTATTCCC	861	GGGAAUAC CUGAUGAG X CGAA IGUGCAGU	3370
608	CTGTATTC C CATCCCAT	862	AUGGGAUG CUGAUGAG X CGAA IAAUACAG	3371
609	TGTATTCC C ATCCCATC	863	GAUGGGAU CUGAUGAG X CGAA IGAAUACA	3372
610	GTATTCCC A TCCCATCA	864	UGAUGGGA CUGAUGAG X CGAA IGGAAUAC	3373
613	TTCCCATC C CATCATCT	865	AGAUGAUG CUGAUGAG X CGAA IAUGGGAA	3374
614	TCCCATCC C ATCATCTT	866	AAGAUGAU CUGAUGAG X CGAA IGAUGGGA	3375
615	CCCATCCC A TCATCTTG	867	CAAGAUGA CUGAUGAG X CGAA IGGAUGGG	3376
618	ATCCCATC A TCTTGGGC	868	GCCCAAGA CUGAUGAG X CGAA IAUGGGAU	3377
621	CCATCATC T TGGGCTTT	869	AAAGCCCA CUGAUGAG X CGAA IAUGAUGG	3378
627	TCTTGGGC T TTCGCAAA	870	UUUGCGAA CUGAUGAG X CGAA ICCCAAGA	3379
633	GCTTTCGC A AAATACCT	871	AGGUAUUU CUGAUGAG X CGAA ICGAAAGC	3380
640	CAAAATAC C TATGGGAG	872	CUCCCAUA CUGAUGAG X CGAA IUAUUUUG	3381
641	AAAATACC T ATGGGAGT	873	ACUCCCAU CUGAUGAG X CGAA IGUAUUUU	3382
654	GAGTGGGC C TCAGTCCG	874	CGGACUGA CUGAUGAG X CGAA ICCCACUC	3383
655	AGTGGGCC T CAGTCCGT	875	ACGGACUG CUGAUGAG X CGAA IGCCCACU	3384
657	TGGGCCTC A GTCCGTTT	876	AAACGGAC CUGAUGAG X CGAA IAGGCCCA	3385
661	CCTCAGTC C GTTTCTCT	877	AGAGAAAC CUGAUGAG X CGAA IACUGAGG	3386
667	TCCGTTTC T CTTGGCTC	878	GAGCCAAG CUGAUGAG X CGAA IAAACGGA	3387
669	CGTTTCTC T TGGCTCAG	879	CUGAGCCA CUGAUGAG X CGAA IAGAAACG	3388
674	CTCTTGGC T CAGTTTAC	880	GUAAACUG CUGAUGAG X CGAA ICCAAGAG	3389
676	CTTGGCTC A GTTTACTA	881	UAGUAAAC CUGAUGAG X CGAA IAGCCAAG	3390
683	CAGTTTAC T AGTGCCAT	882	AUGGCACU CUGAUGAG X CGAA IUAAACUG	3391
689	ACTAGTGC C ATTTGTTC	883	GAACAAAU CUGAUGAG X CGAA ICACUAGU	3392
690	CTAGTGCC A TTTGTTCA	884	UGAACAAA CUGAUGAG X CGAA IGCACUAĞ	3393
698	ATTTGTTC A GTGGTTCG	885	CGAACCAC CUGAUGAG X CGAA IAACAAAU	3394
713	CGTAGGGC T TTCCCCCA	886	UGGGGGAA CUGAUGAG X CGAA ICCCUACG	3395
717	GGGCTTTC C CCCACTGT	887	ACAGUGGG CUGAUGAG X CGAA IAAAGCCC	3396
718	GGCTTTCC C CCACTGTC	888	GACAGUGG CUGAUGAG X CGAA IGAAAGCC	3397
719	GCTTTCCC C CACTGTCT	889	AGACAGUG CUGAUGAG X CGAA IGGAAAGC	3398
720	CTTTCCCC C ACTGTCTG	890	CAGACAGU CUGAUGAG X CGAA IGGGAAAG	3399
721	TTTCCCCC A CTGTCTGG	891	CCAGACAG CUGAUGAG X CGAA IGGGGAAA	3400
723	TCCCCCAC T GTCTGGCT	892	AGCCAGAC CUGAUGAG X CGAA IUGGGGGA	3401
727	CCACTGTC T GGCTTTCA	893	UGAAAGCC CUGAUGAG X CGAA IACAGUGG	3402
731	TGTCTGGC T TTCAGTTA	894	UAACUGAA CUGAUGAG X CGAA ICCAGACA	3403
735	TGGCTTTC A GTTATATG	895	CAUAUAAC CUGAUGAG X CGAA IAAAGCCA	3404
764	TTGGGGGC C AAGTCTGT	896	ACAGACUU CUGAUGAG X CGAA ICCCCCAA	3405
765	TGGGGGCC A AGTCTGTA	897	UACAGACU CUGAUGAG X CGAA IGCCCCCA	3406
770	GCCAAGTC T GTACAACA	898	UGUUGUAC CUGAUGAG X CGAA IACUUGGC	3407
775	GTCTGTAC A ACATCTTG	899	CAAGAUGU CUGAUGAG X CGAA IUACAGAC	3408
778	TGTACAAC A TCTTGAGT	900	ACUCAAGA CUGAUGAG X CGAA IUUGUACA	3409
781	ACAACATC T TGAGTCCC	901	GGGACUCA CUGAUGAG X CGAA IAUGUUGU	3410

Table 38

788	CTTGAGTC C CTTTATGC	902	GCAUAAAG CUGAUGAG X CGAA IACUCAAG	3411
789	TTGAGTCC C TTTATGCC	903	GGCAUAAA CUGAUGAG X CGAA IGACUCAA	3412
790	TGAGTCCC T TTATGCCG	904	CGGCAUAA CUGAUGAG X CGAA IGGACUCA	3413
797	CTTTATGC C GCTGTTAC	905	GUAACAGC CUGAUGAG X CGAA ICAUAAAG	3414
800	TATGCCGC T GTTACCAA	906	UUGGUAAC CUGAUGAG X CGAA ICGGCAUA	3415
806	GCTGTTAC C AATTTTCT	907	AGAAAAUU CUGAUGAG X CGAA IUAACAGC	3416
807	CTGTTACC A ATTTTCTT	908	AAGAAAAU CUGAUGAG X CGAA IGUAACAG	3417
814	CAATTITC T TITGTCIT	909	AAGACAAA CUGAUGAG X CGAA IAAAAUUG	3418
821	CTTTTGTC T TTGGGTAT	910	AUACCCAA CUGAUGAG X CGAA IACAAAAG	3419
832	GGGTATAC A TTTAAACC	911	GGUUUAAA CUGAUGAG X CGAA IUAUACCC	3420
840	ATTTABAC C CTCACAAA	912	UUUGUGAG CUGAUGAG X CGAA IUUUAAAU	3421
841	TTTAAACC C TCACAAAA	913	UUUUGUGA CUGAUGAG X CGAA IGUUUAAA	3422
842	TTAAACCC T CACAAAAC	914	GUUUUGUG CUGAUGAG X CGAA IGGUUUAA	3423
844	AAACCCTC A CAAAACAA	915	UUGUUUUG CUGAUGAG X CGAA IAGGGUUU	3424
846	ACCCTCAC A AAACAAAA	916	UUUUGUUU CUGAUGAG X CGAA IUGAGGGU	3425
851	CACAAAAC A AAAAGATG	917	CAUCUUUU CUGAUGAG X CGAA IUUUUGUG	3426
869	GGATATTC C CTTAACTT	918	AAGUUAAG CUGAUGAG X CGAA IAAUAUCC	3427
870	GATATTCC C TTAACTTC	919	GAAGUUAA CUGAUGAG X CGAA IGAAUAUC	3428
871	ATATTCCC T TAACTTCA	920	UGAAGUUA CUGAUGAG X CGAA IGGAAUAU	3429
876	CCCTTAAC T TCATGGGA	921	UCCCAUGA CUGAUGAG X CGAA IUUAAGGG	3430
879	TTAACTTC A TGGGATAT	922	AUAUCCCA CUGAUGAG X CGAA IAAGUUAA	3431
906	GTTGGGGC A CATTGCCA	923	UGGCAAUG CUGAUGAG X CGAA ICCCCAAC	3432
908	TGGGGCAC A TTGCCACA	924	UGUGGCAA CUGAUGAG X CGAA IUGCCCCA	3433
913	CACATTGC C ACAGGAAC	925	GUUCCUGU CUGAUGAG X CGAA ICAAUGUG	3434
	ACATTGCC A CAGGAACA	926	UGUUCCUG CUGAUGAG X CGAA IGCAAUGU	3435
914	ATTGCCAC A GGAACATA	927	UAUGUUCC CUGAUGAG X CGAA IUGGCAAU	3436
916	ACAGGAAC A TATTGTAC	928	GUACAAUA CUGAUGAG X CGAA IUUCCUGU	3437
	TATTGTAC A AAAAATCA	929	UGAUUUUU CUGAUGAG X CGAA IUACAAUA	3438
931	AAAAAATC A AAATGTGT	930	ACACAUUU CUGAUGAG X CGAA IAUUUUUU	3439
958	TAGGAAAC T TCCTGTAA	931	UUACAGGA CUGAUGAG X CGAA IUUUCCUA	3440
961	GAAACTTC C TGTAAACA	932	UGUUUACA CUGAUGAG X CGAA IAAGUUUC	3441
962	AAACTTCC T GTAAACAG	933	CUGUUUAC CUGAUGAG X CGAA IGAAGUUU	3442
962	CTGTAAAC A GGCCTATT	934	AAUAGGCC CUGAUGAG X CGAA IUUUACAG	3443
969	AAACAGGC C TATTGATT	935	AAUCAAUA CUGAUGAG X CGAA ICCUGUUU	3444
974	AACAGGCC T ATTGATTG	936	CAAUCAAU CUGAUGAG X CGAA IGCCUGUU	3445
	AGTATGTC A ACGAATTG	937	CAAUUCGU CUGAUGAG X CGAA IACAUACU	3446
994	TGTGGGTC T TTTGGGGT	938	ACCCCAAA CUGAUGAG X CGAA IACCCACA	3447
1009	GGGTTTGC C GCCCCTTT	939	AAAGGGGC CUGAUGAG X CGAA ICAAACCC	3448
	TTTGCCGC C CCTTTCAC	940	GUGAAAGG CUGAUGAG X CGAA ICGGCAAA	3449
1025	TTGCCGCC C CTTTCACG	941	CGUGAAAG CUGAUGAG X CGAA IGCGGCAA	3450
1026	TGCCGCCC C TTTCACGC	942	GCGUGAAA CUGAUGAG X CGAA IGGCGGCA	3451
1027	GCCGCCCC T TTCACGCA	943	UGCGUGAA CUGAUGAG X CGAA IGGGCGGC	3452
1028	CCCCTTTC A CGCAATGT	944	ACAUUGCG CUGAUGAG X CGAA IAAAGGGG	3453
1032	TTTCACGC A ATGTGGAT	945	AUCCACAU CUGAUGAG X CGAA ICGUGAAA	3454
1036	GGATATTC T GCTTTAAT	945	AUUAAAGC CUGAUGAG X CGAA IAAUAUCC	3455
1049	TATTCTGC T TTAATGCC	947	GGCAUUAA CUGAUGAG X CGAA ICAGAAUA	3456
1052		947	CAUAUAAA CUGAUGAG X CGAA ICAUUAAA	3457
1060	TTTAATGC C TTTATATGC	948	GCAUAUAA CUGAUGAG X CGAA IGCAUUAA	3458
1061	111011000 1 11111111	949	UGUAUGCA CUGAUGAG X CGAA ICAUAUAA	3459
1070	TTATATGC A TGCATACA		UGCUUGUA CUGAUGAG X CGAA ICAUGCAU	3460
1074	ATGCATGC A TACAAGCA	951	GUUUUGCU CUGAUGAG X CGAA TUAUGCAU	3461
1078	ATGCATAC A AGCAAAAC	952	GUUUUGCU CUGAUGAG A CGAA TUAUGCAU	1 -102

Table 38

1082	ATACAAGC A AAACAGGC	953	GCCUGUUU CUGAUGAG X CGAA ICUUGUAU	3462
1087	AGCAAAAC A GGCTTTTA	954	UAAAAGCC CUGAUGAG X CGAA IUUUUGCU	3463
1091	AAACAGGC T TTTACTTT	955	AAAGUAAA CUGAUGAG X CGAA ICCUGUUU	3464
1097	GCTTTTAC T TTCTCGCC	956	GGCGAGAA CUGAUGAG X CGAA IUAAAAGC	3465
1101	TTACTTTC T CGCCAACT	957	AGUUGGCG CUGAUGAG X CGAA IAAAGUAA	3466
1105	TTTCTCGC C AACTTACA	958	UGUAAGUU CUGAUGAG X CGAA ICGAGAAA	3467
1106	TTCTCGCC A ACTTACAA	959	UUGUAAGU CUGAUGAG X CGAA IGCGAGAA	3468
1109	TCGCCAAC T TACAAGGC	960	GCCUUGUA CUGAUGAG X CGAA IUUGGCGA	3469
1113	CAACTTAC A AGGCCTTT	961	AAAGGCCU CUGAUGAG X CGAA IUAAGUUG	3470
1118	TACAAGGC C TTTCTAAG	962	CUUAGAAA CUGAUGAG X CGAA ICCUUGUA	3471
1119	ACAAGGCC T TTCTAAGT	963	ACUUAGAA CUGAUGAG X CGAA IGCCUUGU	3472
1123	GGCCTTTC T AAGTAAAC	964	GUUUACUU CUGAUGAG X CGAA IAAAGGCC	3473
1132	AAGTAAAC A GTATGTGA	965	UCACAUAC CUGAUGAG X CGAA IUUUACUU	3474
1143	ATGTGAAC C TTTACCCC	966	GGGGUAAA CUGAUGAG X CGAA IUUCACAU	3475
1143	TGTGAACC T TTACCCCG	967	CGGGGUAA CUGAUGAG X CGAA IGUUCACA	3476
1149	ACCTTTAC C CCGTTGCT	968	AGCAACGG CUGAUGAG X CGAA IUAAAGGU	3477
	CCTTTACC C CGTTGCTC	969	GAGCAACG CUGAUGAG X CGAA IGUAAAGG	3478
1150	CTTTACCC C GTTGCTCG	970	CGAGCAAC CUGAUGAG X CGAA IGGUAAAG	3479
1151	CCCGTTGC T CGGCAACG	971	CGUUGCCG CUGAUGAG X CGAA ICAACGGG	3480
1162	TGCTCGGC A ACGGCCTG	972	CAGGCCGU CUGAUGAG X CGAA ICCGAGCA	3481
	GCAACGGC C TGGTCTAT	973	AUAGACCA CUGAUGAG X CGAA ICCGUUGC	3482
1168	CAACGGCC T GGTCTATG	974	CAUAGACC CUGAUGAG X CGAA IGCCGUUG	3483
1174	GCCTGGTC T ATGCCAAG	975	CUUGGCAU CUGAUGAG X CGAA IACCAGGC	3484
	GTCTATGC C AAGTGTTT	976	AAACACUU CUGAUGAG X CGAA ICAUAGAC	3485
1179	TCTATGCC A AGTGTTTG	977	CAAACACU CUGAUGAG X CGAA IGCAUAGA	3486
1180	GTGTTTGC T GACGCAAC	978	GUUGCGUC CUGAUGAG X CGAA ICAAACAC	3487
1190	GCTGACGC A ACCCCCAC	979	GUGGGGU CUGAUGAG X CGAA ICGUCAGC	3488
1196	GACGCAAC C CCCACTGG	980	CCAGUGGG CUGAUGAG X CGAA IUUGCGUC	3489
1199	ACGCAACC C CCACTGGT	981	ACCAGUGG CUGAUGAG X CGAA IGUUGCGU	3490
	CGCAACCC C CACTGGTT	982	AACCAGUG CUGAUGAG X CGAA IGGUUGCG	3491
1201	GCAACCCC C ACTGGTTG	983	CAACCAGU CUGAUGAG X CGAA IGGGUUGC	3492
1202	CAACCCC A CTGGTTGG	984	CCAACCAG CUGAUGAG X CGAA IGGGGUUG	3493
	ACCCCCAC T GGTTGGGG	985	CCCCAACC CUGAUGAG X CGAA IUGGGGGU	3494
1205	GTTGGGGC T TGGCCATA	986	UAUGGCCA CUGAUGAG X CGAA ICCCCAAC	3495
1220	GGCTTGGC C ATAGGCCA	987	UGGCCUAU CUGAUGAG X CGAA ICCAAGCC	3496
1221	GCTTGGCC A TAGGCCAT	988	AUGGCCUA CUGAUGAG X CGAA IGCCAAGC	3497
1221	CCATAGGC C ATCAGCGC	989	GCGCUGAU CUGAUGAG X CGAA ICCUAUGG	3498
1227	CATAGGC C ATCAGCGCA	990	UGCGCUGA CUGAUGAG X CGAA IGCCUAUG	3499
	AGGCCATC A GCGCATGC	991	GCAUGCGC CUGAUGAG X CGAA IAUGGCCU	3500
1231	ATCAGCGC A TGCGTGGA	992	UCCACGCA CUGAUGAG X CGAA ICGCUGAU	3501
1236	CGTGGAAC C TTTGTGTC	993	GACACAAA CUGAUGAG X CGAA IUUCCACG	3502
1247	GTGGAACC T TTGTGTCT	994	AGACACAA CUGAUGAG X CGAA IGUUCCAC	3503
1248	TTTGTGTC T CCTCTGCC	995	GGCAGAGG CUGAUGAG X CGAA IACACAAA	3504
1258	TGTGTCTC C TCTGCCGA	996	UCGGCAGA CUGAUGAG X CGAA IAGACACA	3505
1259	GTGTCTCC T CTGCCGAT	997	AUCGGCAG CUGAUGAG X CGAA IGAGACAC	3506
1261	GTCTCCTC T GCCGATCC	998	GGAUCGGC CUGAUGAG X CGAA IAGGAGAC	3507
	TOCTCTGC C GATCCATA	999	UAUGGAUC CUGAUGAG X CGAA ICAGAGGA	3508
1264	TGCCGATC C ATACOGCG	1000	CGCGGUAU CUGAUGAG X CGAA IAUCGGCA	3509
	GCCGATCC A TACCGCGG	1001	CCGCGGUA CUGAUGAG X CGAA IGAUCGGC	3510
1270	ATCCATAC C GCGGAACT	1002	AGUUCCGC CUGAUGAG X CGAA IUAUGGAU	3511
1274	CGCGGAAC T CCTAGCCG	1002	CGGCUAGG CUGAUGAG X CGAA IUUCCGCG	3512
1282	CGCGGAAC T CCTAGCCG	1003		

Table 38

1284	CGGAACTC C TAGCCGCT	1004	AGCGGCUA CUGAUGAG X CGAA IAGUUCCG	3513
1285	GGAACTCC T AGCCGCTT	1005	AAGCGGCU CUGAUGAG X CGAA IGAGUUCC	3514
1289	CTCCTAGC C GCTTGTTT	1006	AAACAAGC CUGAUGAG X CGAA ICUAGGAG	3515
1292	CTAGCCGC T TGTTTTGC	1007	GCAAAACA CUGAUGAG X CGAA ICGGCUAG	3516
1301	TGTTTTGC T CGCAGCAG	1008	CUGCUGCG CUGAUGAG X CGAA ICAAAACA	3517
1305	TTGCTCGC A GCAGGTCT	1009	AGACCUGC CUGAUGAG X CGAA ICGAGCAA	3518
1308	CTCGCAGC A GGTCTGGG	1010	CCCAGACC CUGAUGAG X CGAA ICUGCGAG	3519
1313	AGCAGGTC T GGGGCAAA	1011	UUUGCCCC CUGAUGAG X CGAA IACCUGCU	3520
1319	TCTGGGGC A AAACTCAT	1012	AUGAGUUU CUGAUGAG X CGAA ICCCCAGA	3521
1324	GGCAAAAC T CATCGGGA	1013	UCCCGAUG CUGAUGAG X CGAA IUUUUGCC	3522
1326	CAAAACTC A TCGGGACT	1014	AGUCCCGA CUGAUGAG X CGAA IAGUUUUG	3523
1334	ATCGGGAC T GACAATTC	1015	GAAUUGUC CUGAUGAG X CGAA IUCCCGAU	3524
1338	GGACTGAC A ATTCTGTC	1016	GACAGAAU CUGAUGAG X CGAA IUCAGUCC	3525
1343	GACAATTC T GTCGTGCT	1017	AGCACGAC CUGAUGAG X CGAA IAAUUGUC	3526
1351	TGTCGTGC T CTCCCGCA	1018	UGCGGGAG CUGAUGAG X CGAA ICACGACA	3527
1353	TCGTGCTC T CCCGCAAA	1019	UUUGCGGG CUGAUGAG X CGAA IAGCACGA	3528
1355	GTGCTCTC C CGCAAATA	1020	UAUUUGCG CUGAUGAG X CGAA IAGAGCAC	3529
1356	TGCTCTCC C GCAAATAT	1021	AUAUUUGC CUGAUGAG X CGAA IGAGAGCA	3530
1359	TCTCCCGC A AATATACA	1022	UGUAUAUU CUGAUGAG X CGAA ICGGGAGA	3531
1367	AAATATAC A TCATTTCC	1023	GGAAAUGA CUGAUGAG X CGAA IUAUAUUU	3532
1370	TATACATC A TTTCCATG	1024	CAUGGAAA CUGAUGAG X CGAA IAUGUAUA	3533
1375	ATCATTTC C ATGGCTGC	1025	GCAGCCAU CUGAUGAG X CGAA IAAAUGAU	3534
1376	TCATTTCC A TGGCTGCT	1026	AGCAGCCA CUGAUGAG X CGAA IGAAAUGA	3535
1381	TCCATGGC T GCTAGGCT	1027	AGCCUAGC CUGAUGAG X CGAA ICCAUGGA	3536
1384	ATGGCTGC T AGGCTGTG	1028	CACAGCCU CUGAUGAG X CGAA ICAGCCAU	3537
1389	TGCTAGGC T GTGCTGCC	1029	GGCAGCAC CUGAUGAG X CGAA ICCUAGCA	3538
1394	GGCTGTGC T GCCAACTG	1030	CAGUUGGC CUGAUGAG X CGAA ICACAGCC	3539
1397	TGTGCTGC C AACTGGAT	1031	AUCCAGUU CUGAUGAG X CGAA ICAGCACA	3540
1398	GTGCTGCC A ACTGGATC	1032	GAUCCAGU CUGAUGAG X CGAA IGCAGCAC	3541
1401	CTGCCAAC T GGATCCTA	1033	UAGGAUCC CUGAUGAG X CGAA IUUGGCAG	3542
1407	ACTGGATC C TACGCGGG	1034	CCCGCGUA CUGAUGAG X CGAA IAUCCAGU	3543
1408	CTGGATCC T ACGCGGGA	1035	UCCCGCGU CUGAUGAG X CGAA IGAUCCAG	3544
1421	GGGACGTC C TTTGTTTA	1036	UAAACAAA CUGAUGAG X CGAA IACGUCCC	3545
1422	GGACGTCC T TTGTTTAC	1037	GUAAACAA CUGAUGAG X CGAA IGACGUCC	3546
1434	TTTACGTC C CGTCGGCG	1038	CGCCGACG CUGAUGAG X CGAA IACGUAAA	3547
1435	TTACGTCC C GTCGGCGC	1039	GCGCCGAC CUGAUGAG X CGAA IGACGUAA	3548
1444	GTCGGCGC T GAATCCCG	1040	CGGGAUUC CUGAUGAG X CGAA ICGCCGAC	3549
1450	GCTGAATC C CGCGGACG	1041	CGUCCGCG CUGAUGAG X CGAA IAUUCAGC	3550
1451	CTGAATCC C GCGGACGA	1042	UCGUCCGC CUGAUGAG X CGAA IGAUUCAG	3551
1461	CGGACGAC C CCTCCCGG	1043	CCGGGAGG CUGAUGAG X CGAA IUCGUCCG	3552
1462	GGACGACC C CTCCCGGG	1044	CCCGGGAG CUGAUGAG X CGAA IGUCGUCC	3553
1463	GACGACCC C TCCCGGGG	1045	CCCCGGGA CUGAUGAG X CGAA IGGUCGUC	3554
1464	ACGACCCC T CCCGGGGC	1046	GCCCCGGG CUGAUGAG X CGAA IGGGUCGU	3555
1466	GACCCCTC C CGGGGCCG	1047	CGGCCCCG CUGAUGAG X CGAA IAGGGGUC	3556
1467	ACCCCTCC C GGGGCCGC	1048	GCGGCCCC CUGAUGAG X CGAA IGAGGGGU	3557
1473	CCCGGGGC C GCTTGGGG	1049	CCCCAAGC CUGAUGAG X CGAA ICCCCGGG	3558
1476	GGGGCCGC T TGGGGCTC	1050	GAGCCCCA CUGAUGAG X CGAA ICGGCCCC	3559
1483	CTTGGGGC T CTACCGCC	1051	GGCGGUAG CUGAUGAG X CGAA ICCCCAAG	3560
1485	TGGGGCTC T ACCGCCCG	1052	CGGGCGGU CUGAUGAG X CGAA IAGCCCCA	3561
1488	GGCTCTAC C GCCCGCTT	1053	AAGCGGGC CUGAUGAG X CGAA IUAGAGCC	3562
1491	TCTACCGC C CGCTTCTC	1054	GAGAAGCG CUGAUGAG X CGAA ICGGUAGA	3563
1451	101110000 0 00011010			

Table 38

1492	CTACCGCC C GCTTCTCC	1055	GGAGAAGC CUGAUGAG X CGAA IGCGGUAG	3564
1495	CCGCCCGC T TCTCCGCC	1056	GGCGGAGA CUGAUGAG X CGAA ICGGGCGG	3565
1498	CCCGCTTC T CCGCCTAT	1057	AUAGGCGG CUGAUGAG X CGAA IAAGCGGG	3566
1500	CGCTTCTC C GCCTATTG	1058	CAAUAGGC CUGAUGAG X CGAA IAGAAGCG	3567
1503	TTCTCCGC C TATTGTAC	1059	GUACAAUA CUGAUGAG X CGAA ICGGAGAA	3568
1504	TCTCCGCC T ATTGTACC	1060	GGUACAAU CUGAUGAG X CGAA IGCGGAGA	3569
1512	TATTGTAC C GACCGTCC	1061	GGACGGUC CUGAUGAG X CGAA IUACAAUA	3570
1516	GTACCGAC C GTCCACGG	1062	CCGUGGAC CUGAUGAG X CGAA IUCGGUAC	3571
1520	CGACCGTC C ACGGGGCG	1063	CGCCCCGU CUGAUGAG X CGAA IACGGUCG	3572
1521	GACCGTCC A CGGGGCGC	1064	GCGCCCCG CUGAUGAG X CGAA IGACGGUC	3573
1530	CGGGGCGC A CCTCTCTT	1065	AAGAGAGG CUGAUGAG X CGAA ICGCCCCG	3574
1532	GGGCGCAC C TCTCTTTA	1066	UAAAGAGA CUGAUGAG X CGAA IUGCGCCC	3575
1533	GGCGCACC T CTCTTTAC	1067	GUAAAGAG CUGAUGAG X CGAA IGUGCGCC	3576
1535	CGCACCTC T CTTTACGC	1068	GCGUAAAG CUGAUGAG X CGAA IAGGUGCG	3577
1537	CACCTCTC T TTACGCGG	1069	CCGCGUAA CUGAUGAG X CGAA IAGAGGUG	3578
1548	ACGCGGAC T CCCCGTCT	1070	AGACGGGG CUGAUGAG X CGAA IUCCGCGU	3579
1550	GCGGACTC C CCGTCTGT	1071	ACAGACGG CUGAUGAG X CGAA IAGUCCGC	3580
1551	CGGACTCC C CGTCTGTG	1072	CACAGACG CUGAUGAG X CGAA IGAGUCCG	3581
1552	GGACTCCC C GTCTGTGC	1073	GCACAGAC CUGAUGAG X CGAA IGGAGUCC	3582
1556	TCCCCGTC T GTGCCTTC	1074	GAAGGCAC CUGAUGAG X CGAA IACGGGGA	3583
1561	GTCTGTGC C TTCTCATC	1075	GAUGAGAA CUGAUGAG X CGAA ICACAGAC	3584
1562	TCTGTGCC T TCTCATCT	1076	AGAUGAGA CUGAUGAG X CGAA IGCACAGA	3585
1565	GTGCCTTC T CATCTGCC	1077	GGCAGAUG CUGAUGAG X CGAA IAAGGCAC	3586
1567	GCCTTCTC A TCTGCCGG	1078	CCGGCAGA CUGAUGAG X CGAA IAGAAGGC	3587
1570	TTCTCATC T GCCGGACC	1079	GGUCCGGC CUGAUGAG X CGAA IAUGAGAA	3588
1573	TCATCTGC C GGACCGTG	1080	CACGGUCC CUGAUGAG X CGAA ICAGAUGA	3589
1578	TGCCGGAC C GTGTGCAC	1081	GUGCACAC CUGAUGAG X CGAA IUCCGGCA	3590
1585	CCGTGTGC A CTTCGCTT	1082	AAGCGAAG CUGAUGAG X CGAA ICACACGG	3591
1587	GTGTGCAC T TCGCTTCA	1083	UGAAGCGA CUGAUGAG X CGAA IUGCACAC	3592
1592	CACTTCGC T TCACCTCT	1084	AGAGGUGA CUGAUGAG X CGAA ICGAAGUG	3593
1595	TTCGCTTC A CCTCTGCA	1085	UGCAGAGG CUGAUGAG X CGAA IAAGCGAA	3594
1597	CGCTTCAC C TCTGCACG	1086	CGUGCAGA CUGAUGAG X CGAA IUGAAGCG	3595
1598	GCTTCACC T CTGCACGT	1087	ACGUGCAG CUGAUGAG X CGAA IGUGAAGC	3596
1600	TTCACCTC T GCACGTCG	1088	CGACGUGC CUGAUGAG X CGAA IAGGUGAA	3597
1603	ACCTCTGC A CGTCGCAT	1089	AUGCGACG CUGAUGAG X CGAA ICAGAGGU	3598
1610	CACGTCGC A TGGAGACC	1090	GGUCUCCA CUGAUGAG X CGAA ICGACGUG	3599
1618	ATGGAGAC C ACCGTGAA	1091	UUCACGGU CUGAUGAG X CGAA IUCUCCAU	3600
1619	TGGAGACC A CCGTGAAC	1092	GUUCACGG CUGAUGAG X CGAA IGUCUCCA	3601
1621	GAGACCAC C GTGAACGC	1093	GCGUUCAC CUGAUGAG X CGAA IUGGUCUC	3602
1630	GTGAACGC C CACAGGAA	1094	UUCCUGUG CUGAUGAG X CGAA ICGUUCAC	3604
1631	TGAACGCC C ACAGGAAC	1095	GUUCCUGU CUGAUGAG X CGAA IGCGUUCA	3604
1632	GAACGCCC A CAGGAACC	1096	GGUUCCUG CUGAUGAG X CGAA IGGCGUUC	3606
1634	ACGCCCAC A GGAACCTG	1097	CAGGUUCC CUGAUGAG X CGAA IUGGGCGU	3607
1640	ACAGGAAC C TGCCCAAG	1098	CUUGGGCA CUGAUGAG X CGAA IUUCCUGU CCUUGGGC CUGAUGAG X CGAA IGUUCCUG	3608
1641	CAGGAACC T GCCCAAGG	1099		3609
1644	GAACCTGC C CAAGGTCT	1100	AGACCUUG CUGAUGAG X CGAA ICAGGUUC AAGACCUU CUGAUGAG X CGAA IGCAGGUU	3610
1645	AACCTGCC C AAGGTCTT	1101	CAAGACCUU CUGAUGAG X CGAA IGCAGGUU CAAGACCU CUGAUGAG X CGAA IGGCAGGU	3611
1646	ACCTGCCC A AGGTCTTG	1102	CAAGACCU CUGAUGAG X CGAA IGGCAGGU CUUAUGCA CUGAUGAG X CGAA IACCUUGG	3612
1652	CCAAGGTC T TGCATAAG	1103	UCCUCUUA CUGAUGAG X CGAA IACCUUGG	3613
1656	GGTCTTGC A TAAGAGGA	1104	AGUCCAAG CUGAUGAG X CGAA TCAAGACC	3614
1666	AAGAGGAC T CTTGGACT	1105	AGUCCAAG CUGAUGAG X CGAA TUCCUCUU	3324

Table 38

			AAAGUCCA CUGAUGAG X CGAA IAGUCCUC	3615
1668	GAGGACTC T TGGACTTT	1106		3616
1674	TCTTGGAC T TTCAGCAA	1107	UUGCUGAA CUGAUGAG X CGAA IUCCAAGA GACAUUGC CUGAUGAG X CGAA IAAAGUCC	3617
1678	GGACTTTC A GCAATGTC	1108		3618
1681	CTTTCAGC A ATGTCAAC	1109	GUUGACAU CUGAUGAG X CGAA ICUGAAAG UCGGUCGU CUGAUGAG X CGAA IACAUUGC	3619
1687	GCAATGTC A ACGACCGA	1110		3620
1693	TCAACGAC C GACCTTGA	1111	UCAAGGUC CUGAUGAG X CGAA IUCGUUGA	3621
1697	CGACCGAC C TTGAGGCA	1112	UGCCUCAA CUGAUGAG X CGAA IUCGGUCG	3622
1698	GACCGACC T TGAGGCAT	1113	AUGCCUCA CUGAUGAG X CGAA IGUCGGUC	3623
1705	CTTGAGGC A TACTTCAA	1114	UUGAAGUA CUGAUGAG X CGAA ICCUCAAG	
1709	AGGCATAC T TCAAAGAC	1115	GUCUUUGA CUGAUGAG X CGAA IUAUGCCU	3624
1712	CATACTTC A AAGACTGT	1116	ACAGUCUU CUGAUGAG X CGAA IAAGUAUG	3625
1718	TCAAAGAC T GTGTGTTT	1117	AAACACAC CUGAUGAG X CGAA IUCUUUGA	
1769	TAAAGGTC T TTGTACTA	1118	UAGUACAA CUGAUGAG X CGAA IACCUUUA	3627
1776	CTTTGTAC T AGGAGGCT	1119	AGCCUCCU CUGAUGAG X CGAA IUACAAAG	3628
1784	TAGGAGGC T GTAGGCAT	1120	AUGCCUAC CUGAUGAG X CGAA ICCUCCUA	3629
1791	CTGTAGGC A TAAATTGG	1121	CCAAUUUA CUGAUGAG X CGAA ICCUACAG	3630
1807	GTGTGTTC A CCAGCACC	1122	GGUGCUGG CUGAUGAG X CGAA IAACACAC	3631
1809	GTGTTCAC C AGCACCAT	1123	AUGGUGCU CUGAUGAG X CGAA IUGAACAC	3632
1810	TGTTCACC A GCACCATG	1124	CAUGGUGC CUGAUGAG X CGAA IGUGAACA	3633
1813	TCACCAGC A CCATGCAA	1125	UUGCAUGG CUGAUGAG X CGAA ICUGGUGA	3634
1815	ACCAGCAC C ATGCAACT	1126	AGUUGCAU CUGAUGAG X CGAA IUGCUGGU	3635
1816	CCAGCACC A TGCAACTT	1127	AAGUUGCA CUGAUGAG X CGAA IGUGCUGG	3636
1820	CACCATGC A ACTITITC	1128	GAAAAAGU CUGAUGAG X CGAA ICAUGGUG	3637
1823	CATGCAAC T TTTTCACC	1129	GGUGAAAA CUGAUGAG X CGAA IUUGCAUG	3638
1829	ACTITIC A CCTCTGCC	1130	GGCAGAGG CUGAUGAG X CGAA IAAAAAGU	3639
1831	TTTTTCAC C TCTGCCTA	1131	UAGGCAGA CUGAUGAG X CGAA IUGAAAAA	3640
1832	TTTTCACC T CTGCCTAA	1132	UUAGGCAG CUGAUGAG X CGAA IGUGAAAA	3641
1834	TTCACCTC T GCCTAATC	1133	GAUUAGGC CUGAUGAG X CGAA IAGGUGAA	3642
1837	ACCTCTGC C TAATCATC	1134	GAUGAUUA CUGAUGAG X CGAA ICAGAGGU	3643
1838	CCTCTGCC T AATCATCT	1135	AGAUGAUU CUGAUGAG X CGAA IGCAGAGG	3644
1843	GCCTAATC A TCTCATGT	1136	ACAUGAGA CUGAUGAG X CGAA IAUUAGGC	3645
1846	TAATCATC T CATGTTCA	1137	UGAACAUG CUGAUGAG X CGAA IAUGAUUA	3646
1848	ATCATCTC A TGTTCATG	1138	CAUGAACA CUGAUGAG X CGAA IAGAUGAU	3647
1854	TCATGTTC A TGTCCTAC	1139	GUAGGACA CUGAUGAG X CGAA IAACAUGA	3648
1859	TTCATGTC C TACTGTTC	1140	GAACAGUA CUGAUGAG X CGAA IACAUGAA	3649
1860	TCATGTCC T ACTGTTCA	1141	UGAACAGU CUGAUGAG X CGAA IGACAUGA	3650
1863	TGTCCTAC T GTTCAAGC	1142	GCUUGAAC CUGAUGAG X CGAA IUAGGACA	3651
1868	TACTGTTC A AGCCTCCA	1143	UGGAGGCU CUGAUGAG X CGAA IAACAGUA	3652
1872	GTTCAAGC C TCCAAGCT	1144	AGCUUGGA CUGAUGAG X CGAA ICUUGAAC	3653
1873	TTCAAGCC T CCAAGCTG	1145	CAGCUUGG CUGAUGAG X CGAA IGCUUGAA	3654
1875	CAAGCCTC C AAGCTGTG	1146	CACAGCUU CUGAUGAG X CGAA IAGGCUUG	3655
1876	AAGCCTCC A AGCTGTGC	1147	GCACAGCU CUGAUGAG X CGAA IGAGGCUU	3656
1880	CTCCAAGC T GTGCCTTG	1148	CAAGGCAC CUGAUGAG X CGAA ICUUGGAG	3657
1885	AGCTGTGC C TTGGGTGG	1149	CCACCCAA CUGAUGAG X CGAA ICACAGCU	3658
1886	GCTGTGCC T TGGGTGGC	1150	GCCACCCA CUGAUGAG X CGAA IGCACAGC	3659
1895	TGGGTGGC T TTGGGGCA	1151	UGCCCCAA CUGAUGAG X CGAA ICCACCCA	3660
1903	TTTGGGGC A TGGACATT	1152	AAUGUCCA CUGAUGAG X CGAA ICCCCAAA	3661
1909	GCATGGAC A TTGACCCG	1153	CGGGUCAA CUGAUGAG X CGAA IUCCAUGC	3662
1915	ACATTGAC C CGTATAAA	1154	UUUAUACG CUGAUGAG X CGAA IUCAAUGU	3663
1916	CATTGACC C GTATAAAG	1155	CUUUAUAC CUGAUGAG X CGAA IGUCAAUG	3664
1935	TTTGGAGC T TCTGTGGA	1156	UCCACAGA CUGAUGAG X CGAA ICUCCAAA	3665

Table 38

				3666
1938	GGAGCTTC T GTGGAGTT	1157	AACUCCAC CUGAUGAG X CGAA IAAGCUCC	3667
1949	GGAGTTAC T CTCTTTTT	1158	AAAAAGAG CUGAUGAG X CGAA IUAACUCC	3668
1951	AGTTACTC T CTTTTTTG	1159	CAAAAAG CUGAUGAG X CGAA IAGUAACU	3669
1953	TTACTCTC T TTTTTGCC	1160	GGCAAAAA CUGAUGAG X CGAA IAGAGUAA	3670
1961	TTTTTTGC C TTCTGACT	1161	AGUCAGAA CUGAUGAG X CGAA ICAAAAAA .	
1962	TTTTTGCC T TCTGACTT	1162	AAGUCAGA CUGAUGAG X CGAA IGCAAAAA	3671
1965	TTGCCTTC T GACTTCTT	1163	AAGAAGUC CUGAUGAG X CGAA IAAGGCAA	3672
1969	CTTCTGAC T TCTTTCCT	1164	AGGAAAGA CUGAUGAG X CGAA IUCAGAAG	3673
1972	CTGACTTC T TTCCTTCT	1165	AGAAGGAA CUGAUGAG X CGAA IAAGUCAG	3674
1976	CTTCTTTC C TTCTATTC	1166	GAAUAGAA CUGAUGAG X CGAA IAAAGAAG	3675
1977	TTCTTTCC T TCTATTCG	1167	CGAAUAGA CUGAUGAG X CGAA IGAAAGAA	3676
1980	TTTCCTTC T ATTCGAGA	1168	UCUCGAAU CUGAUGAG X CGAA IAAGGAAA	3677
1991	TCGAGATC T CCTCGACA	1169	UGUCGAGG CUGAUGAG X CGAA IAUCUCGA	3678
1993	GAGATOTO C TOGACACO	1170	GGUGUCGA CUGAUGAG X CGAA IAGAUCUC	3679
1994	AGATCTCC T CGACACCG	1171	CGGUGUCG CUGAUGAG X CGAA IGAGAUCU	3680
1999	TCCTCGAC A CCGCCTCT	1172	AGAGGCGG CUGAUGAG X CGAA IUCGAGGA	3681
2001	CTCGACAC C GCCTCTGC	1173	GCAGAGGC CUGAUGAG X CGAA IUGUCGAG	3682
2004	GACACCGC C TCTGCTCT	1174	AGAGCAGA CUGAUGAG X CGAA ICGGUGUC	3683
2005	ACACCGCC T CTGCTCTG	1175	CAGAGCAG CUGAUGAG X CGAA IGCGGUGU	3684
2007	ACCGCCTC T GCTCTGTA	1176	UACAGAGC CUGAUGAG X CGAA IAGGCGGU	3685
2010	GCCTCTGC T CTGTATCG	1177	CGAUACAG CUGAUGAG X CGAA ICAGAGGC	3686
2012	CTCTGCTC T GTATCGGG	1178	CCCGAUAC CUGAUGAG X CGAA IAGCAGAG	3687
2025	CGGGGGC C TTAGAGTC	1179	GACUCUAA CUGAUGAG X CGAA ICCCCCCG	3688
2026	GGGGGGCC T TAGAGTCT	1180	AGACUCUA CUGAUGAG X CGAA IGCCCCCC	3689
2034	TTAGAGTC T CCGGAACA	1181	UGUUCCGG CUGAUGAG X CGAA IACUCUAA	3690
2036	AGAGTCTC C GGAACATT	1182	AAUGUUCC CUGAUGAG X CGAA IAGACUCU	3691
2042	TCCGGAAC A TTGTTCAC	1183	GUGAACAA CUGAUGAG X CGAA IUUCCGGA	3692
2049	CATTGTTC A CCTCACCA	1184	UGGUGAGG CUGAUGAG X CGAA IAACAAUG	3693
2051	TTGTTCAC C TCACCATA	1185	UAUGGUGA CUGAUGAG X CGAA IUGAACAA	3694
2052	TGTTCACC T CACCATAC	1186	GUAUGGUG CUGAUGAG X CGAA IGUGAACA	3695
2054	TTCACCTC A CCATACGG	1187	CCGUAUGG CUGAUGAG X CGAA IAGGUGAA	3696
2056	CACCTCAC C ATACGGCA	1188	UGCCGUAU CUGAUGAG X CGAA IUGAGGUG	3697
2057	ACCTCACC A TACGGCAC	1189	GUGCCGUA CUGAUGAG X CGAA IGUGAGGU	3698
2064	CATACGGC A CTCAGGCA	1190	UGCCUGAG CUGAUGAG X CGAA ICCGUAUG	3699
2066	TACGGCAC T CAGGCAAG	1191	CUUGCCUG CUGAUGAG X CGAA IUGCCGUA	3700
2068	CGGCACTC A GGCAAGCT	1192	AGCUUGCC CUGAUGAG X CGAA IAGUGCCG	3701
2072	ACTCAGGC A AGCTATTC	1193	GAAUAGCU CUGAUGAG X CGAA ICCUGAGU	3702
2076	AGGCAAGC T ATTCTGTG	1194	CACAGAAU CUGAUGAG X CGAA ICUUGCCU	3703
2081	AGCTATTC T GTGTTGGG	1195	CCCAACAC CUGAUGAG X CGAA IAAUAGCU	3704
2105	GATGAATC T AGCCACCT	1196	AGGUGGCU CUGAUGAG X CGAA IAUUCAUC	3705
2109	AATCTAGC C ACCTGGGT	1197	ACCCAGGU CUGAUGAG X CGAA ICUAGAUU	3706
2110	ATCTAGCC A CCTGGGTG	1198	CACCCAGG CUGAUGAG X CGAA IGCUAGAU	3707
2112	CTAGCCAC C TGGGTGGG	1199	CCCACCCA CUGAUGAG X CGAA IUGGCUAG	3708
2113	TAGCCACC T GGGTGGGA	1200	UCCCACCC CUGAUGAG X CGAA IGUGGCUA	3709
2138	GGAAGATC C AGCATCCA	1201	UGGAUGCU CUGAUGAG X CGAA IAUCUUCC	3710
2139	GAAGATCC A GCATCCAG	1202	CUGGAUGC CUGAUGAG X CGAA IGAUCUUC	3711
2142	GATCCAGC A TCCAGGGA	1203	UCCCUGGA CUGAUGAG X CGAA ICUGGAUC	3712
2145	CCAGCATC C AGGGAATT	1204	AAUUCCCU CUGAUGAG X CGAA IAUGCUGG	3713
2146	CAGCATCC A GGGAATTA	1205	UAAUUCCC CUGAUGAG X CGAA IGAUGCUG	3714
2161	TAGTAGTC A GCTATGTC	1206	GACAUAGC CUGAUGAG X CGAA IACUACUA	3715
2164	TAGTCAGC T ATGTCAAC	1207	GUUGACAU CUGAUGAG X CGAA ICUGACUA	3716

Table 38

				2717
2170	GCTATGTC A ACGTTAAT	1208	AUUAACGU CUGAUGAG X CGAA IACAUAGC	3717
2185	ATATGGGC C TAAAAATC	1209	GAUUUUUA CUGAUGAG X CGAA ICCCAUAU	3718
2186	TATGGGCC T AAAAATCA	1210	UGAUUUUU CUGAUGAG X CGAA IGCCCAUA	3719
2194	TAAAAATC A GACAACTA	1211	UAGUUGUC CUGAUGAG X CGAA IAUUUUUA	3720
2198	AATCAGAC A ACTATTGT	1212	ACAAUAGU CUGAUGAG X CGAA IUCUGAUU	3721
2201	CAGACAAC T ATTGTGGT	1213	ACCACAAU CUGAUGAG X CGAA IUUGUCUG	3722
2213	GTGGTTTC A CATTTCCT	1214	AGGAAAUG CUGAUGAG X CGAA IAAACCAC	3723
2215	GGTTTCAC A TITCCTGT	1215	ACAGGAAA CUGAUGAG X CGAA IUGAAACC	3724
2220	CACATTTC C TGTCTTAC	1216	GUAAGACA CUGAUGAG X CGAA IAAAUGUG	3725
2221	ACATTTCC T GTCTTACT	1217	AGUAAGAC CUGAUGAG X CGAA IGAAAUGU	3726
2225	TTCCTGTC T TACTTTTG	1218	CAAAAGUA CUGAUGAG X CGAA IACAGGAA	3727
2229	TGTCTTAC T TTTGGGCG	1219	CGCCCAAA CUGAUGAG X CGAA IUAAGACA	3728
2244	CGAGAAAC T GTTCTTGA	1220	UCAAGAAC CUGAUGAG X CGAA IUUUCUCG	3729
2249	AACTGTTC T TGAATATT	1221	AAUAUUCA CUGAUGAG X CGAA IAACAGUU	3730
2265	TTGGTGTC T TTTGGAGT	1222	ACUCCAAA CUGAUGAG X CGAA IACACCAA	3731
2284	GGATTCGC A CTCCTCCT	1223	AGGAGGAG CUGAUGAG X CGAA ICGAAUCC	3732
2286	ATTCGCAC T CCTCCTGC	1224	GCAGGAGG CUGAUGAG X CGAA IUGCGAAU	3733
2288	TOGCACTO C TOCTGOAT	1225	AUGCAGGA CUGAUGAG X CGAA IAGUGCGA	3734
2289	CGCACTCC T CCTGCATA	1226	UAUGCAGG CUGAUGAG X CGAA IGAGUGCG	3735
2291	CACTCCTC C TGCATATA	1227	UAUAUGCA CUGAUGAG X CGAA IAGGAGUG	3736
2291	ACTCCTCC T GCATATAG	1228	CUAUAUGC CUGAUGAG X CGAA IGAGGAGU	3737
2292	CCTCCTGC A TATAGACC	1229	GGUCUAUA CUGAUGAG X CGAA ICAGGAGG	3738
2303	ATATAGAC C ACCAAATG	1230	CAUUUGGU CUGAUGAG X CGAA IUCUAUAU	3739
2303	TATAGACC A CCAAATGC	1231	GCAUUUGG CUGAUGAG X CGAA IGUCUAUA	3740
2304	TAGACCAC C AAATGCCC	1232	GGGCAUUU CUGAUGAG X CGAA IUGGUCUA	3741
2306	AGACCACC A AATGCCCC	1233	GGGGCAUU CUGAUGAG X CGAA IGUGGUCU	3742
2313	CCAAATGC C CCTATCTT	1234	AAGAUAGG CUGAUGAG X CGAA ICAUUUGG	3743
	CAAATGCC C CTATCTTA	1235	UAAGAUAG CUGAUGAG X CGAA IGCAUUUG	3744
2314	AAATGCCC C TATCTTAT	1236	AUAAGAUA CUGAUGAG X CGAA IGGCAUUU	3745
2315	AATGCCCC T ATCTTATC	1237	GAUAAGAU CUGAUGAG X CGAA IGGGCAUU	3746
2316	CCCCTATC T TATCAACA	1238	UGUUGAUA CUGAUGAG X CGAA IAUAGGGG	3747
	ATCTTATC A ACACTTCC	1239	GGAAGUGU CUGAUGAG X CGAA IAUAAGAU	3748
2325	TTATCAAC A CTTCCGGA	1240	UCCGGAAG CUGAUGAG X CGAA IUUGAUAA	3749
2328	ATCAACAC T TCCGGAAA	1241	UUUCCGGA CUGAUGAG X CGAA IUGUUGAU	3750
	AACACTTC C GGAAACTA	1242	UAGUUUCC CUGAUGAG X CGAA IAAGUGUU	3751
2333	CCGGAAAC T ACTGTTGT	1243	ACAACAGU CUGAUGAG X CGAA IUUUCCGG	3752
2340	GAAACTAC T GTTGTTAG	1244	CUAACAAC CUGAUGAG X CGAA IUAGUUUC	3753
2343	GAAGAGGC A GGTCCCCT	1245	AGGGGACC CUGAUGAG X CGAA ICCUCUUC	3754
2362	GGCAGGTC C CCTAGAAG	1246	CUUCUAGG CUGAUGAG X CGAA IACCUGCC	3755
2367	GCAGGTCC C CTAGAAGA	1247	UCUUCUAG CUGAUGAG X CGAA IGACCUGC	3756
2368	CAGGTCCC C TAGAAGAA	1248	UUCUUCUA CUGAUGAG X CGAA IGGACCUG	3757
2369	AGGTCCCC T AGAAGAAG	1249	CUUCUUCU CUGAUGAG X CGAA IGGGACCU	3758
	AGAAGAAC T CCCTCGCC	1250	GGCGAGGG CUGAUGAG X CGAA IUUCUUCU	3759
2382	AGAAGACTC C CTCGCCTC	1251	GAGGCGAG CUGAUGAG X CGAA IAGUUCUU	3760
2384	AGAACTCC C TCGCCTCG	1252	CGAGGCGA CUGAUGAG X CGAA IGAGUUCU	3761
2385	GAACTCCC T CGCCTCGC	1253	GCGAGGCG CUGAUGAG X CGAA IGGAGUUC	3762
2386	TCCCTCGC C TCGCAGAC	1254	GUCUGCGA CUGAUGAG X CGAA ICGAGGGA	3763
2390	CCCTCGCC T CGCAGACG	1255	CGUCUGCG CUGAUGAG X CGAA IGCGAGGG	3764
2391	CCCTCGCC T CGCAGACG	1256	CCUUCGUC CUGAUGAG X CGAA ICGAGGCG	3765
2395	CGCCTCGC A GACGAAGG	1257	GGCGAUUG CUGAUGAG X CGAA IACCUUCG	3766
2406		1258	GCGGCGAU CUGAUGAG X CGAA IAGACCUU	3767
2408	AAGGTCTC A ATCGCCGC	1258	GCGCGATO GT	

Table 38

		1259	UGCGACGC CUGAUGAG X CGAA ICGAUUGA	3768
2414	TCAATCGC C GCGTCGCA	1260	AGAUCUUC CUGAUGAG X CGAA ICGACGCG	3769
2422	CGCGTCGC A GAAGATCT	1261	CGAGAUUG CUGAUGAG X CGAA IAUCUUCU	3770
2430	AGAAGATC T CAATCTCG	1262	CCCGAGAU CUGAUGAG X CGAA IAGAUCUU	3771
2432	AAGATCTC A ATCTCGGG	1263	GAUUCCCG CUGAUGAG X CGAA IAUUGAGA	3772
2436	TCTCAATC T CGGGAATC		UAACAUUG CUGAUGAG X CGAA IAUUCCCG	3773
2445	CGGGAATC T CAATGTTA	1264	ACUAACAU CUGAUGAG X CGAA IAGAUUCC	3774
2447	GGAATCTC A ATGTTAGT	1265	GUGUCCAA CUGAUGAG X CGAA IAAUACUA	3775
2460	TAGTATTC C TTGGACAC	1266	UGUGUCCA CUGAUGAG X CGAA IGAAUACU	3776
2461	AGTATTCC T TGGACACA	1267	ACCUUAUG CUGAUGAG X CGAA IUCCAAGG	3777
2467	CCTTGGAC A CATAAGGT	1268	CCACCUUA CUGAUGAG X CGAA IUGUCCAA	3778
2469	TTGGACAC A TAAGGTGG	1269	CCCCGUAA CUGAUGAG X CGAA IUUUCCCA	3779
2483	TGGGAAAC T TTACGGGG	1270	AAGAAUAA CUGAUGAG X CGAA ICCCCGUA	3780
2493	TACGGGGC T TTATTCTT	1271	ACCGUAGA CUGAUGAG X CGAA IAAUAAAG	3781
2500	CTTTATTC T TCTACGGT	1272	GGUACCGU CUGAUGAG X CGAA TAAGAAUA	3782
2503	TATTCTTC T ACGGTACC	1273	UAAAGCAA CUGAUGAG X CGAA TAAGAAUA UAAAGCAA CUGAUGAG X CGAA TUACCGUA	3783
2511	TACGGTAC C TTGCTTTA	1274	UNAAGCAA CUGAUGAG X CGAA IUACCGUA UUAAAGCA CUGAUGAG X CGAA IGUACCGU	3784
2512	ACGGTACC T TGCTTTAA	1275		3785
2516	TACCTTGC T TTAATCCT	1276	AGGAUUAA CUGAUGAG X CGAA ICAAGGUA GCCAUUUA CUGAUGAG X CGAA IAUUAAAG	3786
2523	CTTTAATC C TAAATGGC	1277		3787
2524	TTTAATCC T AAATGGCA	1278	UGCCAUUU CUGAUGAG X CGAA IGAUUAAA	3788
2532	TAAATGGC A AACTCCTT	1279	AAGGAGUU CUGAUGAG X CGAA ICCAUUUA	3789
2536	TGGCAAAC T CCTTCTTT	1280	AAAGAAGG CUGAUGAG X CGAA IUUUGCCA	3790
2538	GCAAACTC C TTCTTTTC	1281	GAAAAGAA CUGAUGAG X CGAA IAGUUUGC	3790
2539	CAAACTCC T TCTTTTCC	1282	GGAAAGA CUGAUGAG X CGAA IGAGUUUG	3792
2542	ACTCCTTC T TTTCCTGA	1283	UCAGGAAA CUGAUGAG X CGAA TAAGGAGU	3793
2547	TTCTTTTC C TGACATTC	1284	GAAUGUCA CUGAUGAG X CGAA IAAAAGAA	3794
2548	TCTTTTCC T GACATTCA	1285	UGAAUGUC CUGAUGAG X CGAA IGAAAAGA	3795
2552	TTCCTGAC A TTCATTTG	1286	CAAAUGAA CUGAUGAG X CGAA IUCAGGAA	3796
2556	TGACATTC A TTTGCAGG	1287	CCUGCAAA CUGAUGAG X CGAA IAAUGUCA	3797
2562	TCATTTGC A GGAGGACA	1288	UGUCCUCC CUGAUGAG X CGAA ICAAAUGA	3798
2570	AGGAGGAC A TTGTTGAT	1289	AUCAACAA CUGAUGAG X CGAA IUCCUCCU	3799
2589	ATGTAAGC A ATTTGTGG	1290	CCACAAAU CUGAUGAG X CGAA ICUUACAU CUGUAAGG CUGAUGAG X CGAA ICCCCACA	3800
2601	TGTGGGGC C CCTTACAG	1291		3801
2602	GTGGGGCC C CTTACAGT	1292	ACUGUAAG CUGAUGAG X CGAA IGCCCCAC	3802
2603	TGGGGCCC C TTACAGTA	1293	UACUGUAA CUGAUGAG X CGAA IGGCCCCA	3803
2604	GGGGCCCC T TACAGTAA	1294	UUACUGUA CUGAUGAG X CGAA IGGGCCCC	3804
2608	CCCCTTAC A GTAAATGA	1295	UCAUUUAC CUGAUGAG X CGAA IUAAGGGG	3805
2621	ATGAAAAC A GGAGACTT	1296	AAGUCUCC CUGAUGAG X CGAA IUUUUCAU	3806
2628	CAGGAGAC T TAAATTAA	1297	UUAAUUUA CUGAUGAG X CGAA IUCUCCUG GCAGGCAU CUGAUGAG X CGAA IUUAAUUU	3807
2638	AAATTAAC T ATGCCTGC	1298		3808
2643	AACTATGC C TGCTAGGT	1299	ACCUAGCA CUGAUGAG X CGAA ICAUAGUU AACCUAGC CUGAUGAG X CGAA IGCAUAGU	3809
2644	ACTATGCC T GCTAGGTT	1300		3810
2647	ATGCCTGC T AGGTTTTA	1301	UAAAACCU CUGAUGAG X CGAA ICAGGCAU	3811
2658	GTTTTATC C CAATGTTA	1302	UAACAUUG CUGAUGAG X CGAA IAUAAAAC	3812
2659	TTTTATCC C AATGTTAC	1303	GUAACAUU CUGAUGAG X CGAA IGAUAAAA	3812
2660	TTTATCCC A ATGTTACT	1304	AGUAACAU CUGAUGAG X CGAA IGGAUAAA	3814
2668	AATGTTAC T AAATATTT	1305	AAAUAUUU CUGAUGAG X CGAA IUAACAUU	3814
2679	ATATTTGC C CTTAGATA	1306	UAUCUAAG CUGAUGAG X CGAA ICAAAUAU	3816
2680	TATTTGCC C TTAGATAA	1307	UUAUCUAA CUGAUGAG X CGAA IGCAAAUA	3817
2681	ATTTGCCC T TAGATAAA	1308	UUUAUCUA CUGAUGAG X CGAA IGGCAAAU	3817
2696	AAGGGATC A AACCGTAT	1309	AUACGGUU CUGAUGAG X CGAA IAUCCCUU	7010

Table 38

				3819
2700	GATCAAAC C GTATTATC	1310	GAUAAUAC CUGAUGAG X CGAA IUUUGAUC	3820
2709	GTATTATC C AGAGTATG	1311	CAUACUCU CUGAUGAG X CGAA IAUAAUAC	
2710	TATTATCC A GAGTATGT	1312	ACAUACUC CUGAUGAG X CGAA IGAUAAUA	3821
2727	AGITAATC A TTACTTCC	1313	GGAAGUAA CUGAUGAG X CGAA IAUUAACU	3822
2732	ATCATTAC T TCCAGACG	1314	CGUCUGGA CUGAUGAG X CGAA IUAAUGAU	3823
2735	ATTACTTC C AGACGCGA	1315	UCGCGUCU CUGAUGAG X CGAA IAAGUAAU	3824
2736	TTACTTCC A GACGCGAC	1316	GUCGCGUC CUGAUGAG X CGAA IGAAGUAA	3825
2745	GACGCGAC A TTATTTAC	1317	GUAAAUAA CUGAUGAG X CGAA IUCGCGUC	3826
2754	TTATTTAC A CACTCTTT	1318	AAAGAGUG CUGAUGAG X CGAA IUAAAUAA	3827
2756	ATTTACAC A CTCTTTGG	1319	CCAAAGAG CUGAUGAG X CGAA IUGUAAAU	3828
2758	TTACACAC T CTTTGGAA	1320	UUCCAAAG CUGAUGAG X CGAA IUGUGUAA	3829
2760	ACACACTC T TTGGAAGG	1321	CCUUCCAA CUGAUGAG X CGAA IAGUGUGU	3830
2777	CGGGGATC T TATATAAA	1322	UUUAUAUA CUGAUGAG X CGAA IAUCCCCG	3831
2794	AGAGAGTC C ACACGTAG	1323	CUACGUGU CUGAUGAG X CGAA IACUCUCU	3832
2795	GAGAGTCC A CACGTAGC	1324	GCUACGUG CUGAUGAG X CGAA IGACUCUC	3833
2797	GAGTCCAC A CGTAGCGC	1325	GCGCUACG CUGAUGAG X CGAA IUGGACUC	3834
2806	CGTAGCGC C TCATTTTG	1326	CAAAAUGA CUGAUGAG X CGAA ICGCUACG	3835
2807	GTAGCGCC T CATTITGC	1327	GCAAAAUG CUGAUGAG X CGAA IGCGCUAC	3836
2809	AGCGCCTC A TTTTGCGG	1328	CCGCAAAA CUGAUGAG X CGAA IAGGCGCU	3837
2821	TGCGGGTC A CCATATTC	1329	GAAUAUGG CUGAUGAG X CGAA IACCCGCA	3838
2823	CGGGTCAC C ATATTCTT	1330	AAGAAUAU CUGAUGAG X CGAA IUGACCCG	3839
2824	GGGTCACC A TATTCTTG	1331	CAAGAAUA CUGAUGAG X CGAA IGUGACCC	3840
2830	CCATATTC T TGGGAACA	1332	UGUUCCCA CUGAUGAG X CGAA IAAUAUGG	3841
2838	TTGGGAAC A AGATCTAC	1333	GUAGAUCU CUGAUGAG X CGAA IUUCCCAA	3842
2844	ACAGGATC T ACAGCATG	1334	CAUGCUGU CUGAUGAG X CGAA IAUCUUGU	3843
2847	AGATCTAC A GCATGGGA	1335	UCCCAUGC CUGAUGAG X CGAA IUAGAUCU	3844
2850	TCTACAGC, A TGGGAGGT	1336	ACCUCCCA CUGAUGAG X CGAA ICUGUAGA	3845
2864	GGTTGGTC T TCCAAACC	1337	GGUUUGGA CUGAUGAG X CGAA IACCAACC	3846
2867	TGGTCTTC C AAACCTCG	1338	CGAGGUUU CUGAUGAG X CGAA IAAGACCA	3847
2868	GGTCTTCC A AACCTCGA	1339	UCGAGGUU CUGAUGAG X CGAA IGAAGACC	3848
2872	TTCCAAAC C TCGAAAAG	1340	CUUUUCGA CUGAUGAG X CGAA IUUUGGAA	3849
2873	TCCAAACC T CGAAAAGG	1341	CCUUUUCG CUGAUGAG X CGAA IGUUUGGA	3850
2883	GAAAAGGC A TGGGGACA	1342	UGUCCCCA CUGAUGAG X CGAA ICCUUUUC	3851
2891	ATGGGGAC A AATCTTTC	1343	GAAAGAUU CUGAUGAG X CGAA IUCCCCAU	3852
2896	GACAAATC T TTCTGTCC	1344	GGACAGAA CUGAUGAG X CGAA IAUUUGUC	3853
2900	AATCTTTC T GTCCCCAA	1345	UUGGGGAC CUGAUGAG X CGAA IAAAGAUU	3854
2904	TTTCTGTC C CCAATCCC	1346	GGGAUUGG CUGAUGAG X CGAA IACAGAAA	3855
2905	TTCTGTCC C CAATCCCC	1347	GGGGAUUG CUGAUGAG X CGAA IGACAGAA	3856
2906	TCTGTCCC C AATCCCCT	1348	AGGGGAUU CUGAUGAG X CGAA IGGACAGA	3857
2907	CTGTCCCC A ATCCCCTG	1349	CAGGGGAU CUGAUGAG X CGAA IGGGACAG	3858
2911	CCCCAATC C CCTGGGAT	1350	AUCCCAGG CUGAUGAG X CGAA IAUUGGGG	3859
2912	CCCAATCC C CTGGGATT	1351	AAUCCCAG CUGAUGAG X CGAA IGAUUGGG	3860
2913	CCAATCCC C TGGGATTC	1352	GAAUCCCA CUGAUGAG X CGAA IGGAUUGG	3861
2914	CAATCCCC T GGGATTCT	1353	AGAAUCCC CUGAUGAG X CGAA IGGGAUUG	3862
2922	TGGGATTC T TCCCCGAT	1354	AUCGGGGA CUGAUGAG X CGAA IAAUCCCA	3863
2925	GATTCTTC C CCGATCAT	1355	AUGAUCGG CUGAUGAG X CGAA IAAGAAUC	3864
2925	ATTOTTOC C CGATCATC	1356	GAUGAUCG CUGAUGAG X CGAA IGAAGAAU	3865
2926	TTCTTCCC C GATCATCA	1357	UGAUGAUC CUGAUGAG X CGAA IGGAAGAA	3866
2927	CCCCGATC A TCAGTTGG	1358	CCAACUGA CUGAUGAG X CGAA IAUCGGGG	3867
2932	CGATCATC A GTTGGACC	1359	GGUCCAAC CUGAUGAG X CGAA IAUGAUCG	3868
2935	AGTTGGAC C CTGCATTC	1360	GAAUGCAG CUGAUGAG X CGAA IUCCAACU	3869
2943	AGITGGAC C CIGCATIC	1300		

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Table 38

2944	GTTGGACC C TGCATTCA	1361	UGAAUGCA CUGAUGAG X CGAA IGUCCAAC	3870
2945	TTGGACCC T GCATTCAA	1362	UUGAAUGC CUGAUGAG X CGAA IGGUCCAA	3871
2948	GACCCTGC A TTCAAAGC	1363	GCUUUGAA CUGAUGAG X CGAA ICAGGGUC	3872
2952	CTGCATTC A AAGCCAAC	1364	GUUGGCUU CUGAUGAG X CGAA IAAUGCAG	3873
2957	TTCAAAGC C AACTCAGT	1365	ACUGAGUU CUGAUGAG X CGAA ICUUUGAA	3874
2958	TCAAAGCC A ACTCAGTA	1366	UACUGAGU CUGAUGAG X CGAA IGCUUUGA	3875
2961	AAGCCAAC T CAGTAAAT	1367	AUUUACUG CUGAUGAG X CGAA 1UUGGCUU	3876
2963	GCCAACTC A GTAAATCC	1368	GGAUUUAC CUGAUGAG X CGAA IAGUUGGC	3877
2971	AGTAAATC C AGATTGGG	1369	CCCAAUCU CUGAUGAG X CGAA IAUUUACU	3878
2972	GTAAATCC A GATTGGGA	1370	UCCCAAUC CUGAUGAG X CGAA IGAUUUAC	3879
2982	ATTGGGAC C TCAACCCG	1371	CGGGUUGA CUGAUGAG X CGAA IUCCCAAU	3880
2983	TTGGGACC T CAACCCGC	1372	GCGGGUUG CUGAUGAG X CGAA IGUCCCAA	3881
2985	GGGACCTC A ACCCGCAC	1373	GUGCGGGU CUGAUGAG X CGAA IAGGUCCC	3882
2988	ACCTCAAC C CGCACAAG	1374	CUUGUGCG CUGAUGAG X CGAA IUUGAGGU	3883
2989	CCTCAACC C GCACAAGG	1375	CCUUGUGC CUGAUGAG X CGAA IGUUGAGG	3884
2992	CAACCCGC A CAAGGACA	1376	UGUCCUUG CUGAUGAG X CGAA ICGGGUUG	3885
2992	ACCCGCAC A AGGACAAC	1377	GUUGUCCU CUGAUGAG X CGAA IUGCGGGU	3886
3000	ACAAGGAC A ACTGGCCG	1378	CGGCCAGU CUGAUGAG X CGAA IUCCUUGU	3887
3000	AGGACAAC T GGCCGGAC	1379	GUCCGGCC CUGAUGAG X CGAA IUUGUCCU	3888
3003	CAACTGGC C GGACGCCA	1380	UGGCGUCC CUGAUGAG X CGAA ICCAGUUG	3889
	CCGGACGC C AACAAGGT	1381	ACCUUGUU CUGAUGAG X CGAA ICGUCCGG	3890
3014	CGGACGCC A ACAAGGTG	1382	CACCUUGU CUGAUGAG X CGAA IGCGUCCG	3891
3015	ACGCCAAC A AGGTGGGA	1383	UCCCACCU CUGAUGAG X CGAA IUUGGCGU	3892
3035	GTGGGAGC A TTCGGGCC	1384	GGCCCGAA CUGAUGAG X CGAA ICUCCCAC	3893
	ATTCGGGC C AGGGTTCA	1385	UGAACCCU CUGAUGAG X CGAA ICCCGAAU	3894
3043	TTCGGGCC A GGGTTCAC	1386	GUGAACCC CUGAUGAG X CGAA IGCCCGAA	3895
3044	CAGGGTTC A CCCCTCCC	1387	GGGAGGGG CUGAUGAG X CGAA IAACCCUG	3896
3051	GGGTTCAC C CCTCCCCA	1388	UGGGGAGG CUGAUGAG X CGAA IUGAACCC	3897
3053	GGTTCACC C CTCCCCAT	1389	AUGGGGAG CUGAUGAG X CGAA IGUGAACC	3898
3054	GTTCACCC C TCCCCATG	1390	CAUGGGGA CUGAUGAG X CGAA IGGUGAAC	3899
3055	TTCACCCC T CCCCATGG	1391	CCAUGGGG CUGAUGAG X CGAA IGGGUGAA	3900
3056	CACCCCTC C CCATGGGG	1392	CCCCAUGG CUGAUGAG X CGAA IAGGGGUG	3901
3058	ACCCCTCC C CATGGGG	1393	CCCCCAUG CUGAUGAG X CGAA IGAGGGGU	3902
3059	CCCCTCCC C ATGGGGGA	1394	UCCCCCAU CUGAUGAG X CGAA IGGAGGGG	3903
3060		1395	GUCCCCCA CUGAUGAG X CGAA IGGGAGGG	3904
3061	CCCTCCCC A TGGGGGAC	1396	ACCCCAAC CUGAUGAG X CGAA IUCCCCCA	3905
3070	TGGGGGAC T GTTGGGGT GGTGGAGC C CTCACGCT	1396	AGCGUGAG CUGAUGAG X CGAA ICUCCACC	3906
3084		1397	GAGCGUGA CUGAUGAG X CGAA IGCUCCAC	3907
3085	GTGGAGCC C TCACGCTC	1398	UGAGCGUG CUGAUGAG X CGAA IGGCUCCA	3908
3086	TGGAGCCC T CACGCTCA	1400	CCUGAGCG CUGAUGAG X CGAA IAGGGCUC	3909
3088	GAGCCCTC A CGCTCAGG	1400	AGGCCCUG CUGAUGAG X CGAA ICGUGAGG	3910
3092	CCTCACGC T CAGGGCCT	1401	GUAGGCCC CUGAUGAG X CGAA IAGCGUGA	3911
3094	TCACGCTC A GGGCCTAC	1402	UGUGAGUA CUGAUGAG X CGAA ICCCUGAG	3912
3099	CTCAGGGC C TACTCACA	1403	UUGUGAGU CUGAUGAG X CGAA IGCCCUGA	3913
3100	TCAGGGCC T ACTCACAA	1404	CAGUUGUG CUGAUGAG X CGAA IUAGGCCC	3914
3103	GGGCCTAC T CACAACTG		CACAGUUG CUGAUGAG X CGAA TOAGGCCC	3915
3105	GCCTACTC A CAACTGTG	1406	GGCACAGU CUGAUGAG X CGAA IUGAGUAG	3916
3107	CTACTCAC A ACTGTGCC	1407	GCUGGCAC CUGAUGAG X CGAA TUGAGUAG	3917
3110	CTCACAAC T GTGCCAGC	1408	GAGCUGCU CUGAUGAG X CGAA TOUGUGAG GAGCUGCU CUGAUGAG X CGAA ICACAGUU	3918
3115	AACTGTGC C AGCAGCTC	1409	GAGCUGCU CUGAUGAG X CGAA ICACAGU	3919
3116	ACTGTGCC A GCAGCTCC	1410		3920
3119	GTGCCAGC A GCTCCTCC	1411	GGAGGAGC CUGAUGAG X CGAA ICUGGCAC	3720

Table 38

3122	CCAGCAGC T CCTCCTCC	1412	GGAGGAGG CUGAUGAG X CGAA ICUGCUGG	3921
3124	AGCAGCTC C TCCTCCTG	1413	CAGGAGGA CUGAUGAG X CGAA IAGCUGCU	3922
3125	GCAGCTCC T CCTCCTGC	1414	GCAGGAGG CUGAUGAG X CGAA IGAGCUGC	3923
3127	AGCTCCTC C TCCTGCCT	1415	AGGCAGGA CUGAUGAG X CGAA IAGGAGCU	3924
3128	GCTCCTCC T CCTGCCTC	1416	GAGGCAGG CUGAUGAG X CGAA IGAGGAGC	3925
3130	TCCTCCTC C TGCCTCCA	1417	UGGAGGCA CUGAUGAG X CGAA IAGGAGGA	3926
3131	CCTCCTCC T GCCTCCAC	1418	GUGGAGGC CUGAUGAG X CGAA IGAGGAGG	3927
3134	CCTCCTGC C TCCACCAA	1419	UUGGUGGA CUGAUGAG X CGAA ICAGGAGG	3928
3135	CTCCTGCC T CCACCAAT	1420	AUUGGUGG CUGAUGAG X CGAA IGCAGGAG	3929
3137	CCTGCCTC C ACCAATCG	1421	CGAUUGGU CUGAUGAG X CGAA IAGGCAGG	3930
3138	CTGCCTCC A CCAATCGG	1422	CCGAUUGG CUGAUGAG X CGAA IGAGGCAG	3931
3140	GCCTCCAC C AATCGGCA	1423	UGCCGAUU CUGAUGAG X CGAA IUGGAGGC	3932
3141	CCTCCACC A ATCGGCAG	1424	CUGCCGAU CUGAUGAG X CGAA IGUGGAGG	3933
3148	CAATCGGC A GTCAGGAA	1425	UUCCUGAC CUGAUGAG X CGAA ICCGAUUG	3934
3152	CGGCAGTC A GGAAGGCA	1426	UGCCUUCC CUGAUGAG X CGAA IACUGCCG	3935
3160	AGGAAGGC A GCCTACTC	1427	GAGUAGGC CUGAUGAG X CGAA ICCUUCCU	3936
3163	AAGGCAGC C TACTCCCT	1428	AGGGAGUA CUGAUGAG X CGAA ICUGCCUU	3937
3164	AGGCAGCC T ACTCCCTT	1429	AAGGGAGU CUGAUGAG X CGAA IGCUGCCU	3938
3167	CAGCCTAC T CCCTTATC	1430	GAUAAGGG CUGAUGAG X CGAA IUAGGCUG	3939
3169	GCCTACTC C CTTATCTC	1431	GAGAUAAG CUGAUGAG X CGAA IAGUAGGC	3940
3170	CCTACTCC C TTATCTCC	1432	GGAGAUAA CUGAUGAG X CGAA IGAGUAGG	3941
3171	CTACTCCC T TATCTCCA	1433	UGGAGAUA CUGAUGAG X CGAA IGGAGUAG	3942
3176	CCCTTATC T CCACCTCT	1434	AGAGGUGG CUGAUGAG X CGAA IAUAAGGG	3943
3178	CTTATCTC C ACCTCTAA	1435	UUAGAGGU CUGAUGAG X CGAA IAGAUAAG	3944
3179	TTATCTCC A CCTCTAAG	1436	CUUAGAGG CUGAUGAG X CGAA IGAGAUAA	3945
3181	ATCTCCAC C TCTAAGGG	1437	CCCUUAGA CUGAUGAG X CGAA IUGGAGAU	3946
3182	TCTCCACC T CTAAGGGA	1438	UCCCUUAG CUGAUGAG X CGAA IGUGGAGA	3947
3184	TCCACCTC T AAGGGACA	1439	UGUCCCUU CUGAUGAG X CGAA IAGGUGGA	3948
3192	TAAGGGAC A CTCATCCT	1440	AGGAUGAG CUGAUGAG X CGAA IUCCCUUA	3949
3194	AGGGACAC T CATCCTCA	1441	UGAGGAUG CUGAUGAG X CGAA IUGUCCCU	3950
3196	GGACACTC A TCCTCAGG	1442	CCUGAGGA CUGAUGAG X CGAA IAGUGUCC	3951
3199	CACTCATC C TCAGGCCA	1443	UGGCCUGA CUGAUGAG X CGAA IAUGAGUG	3952
3200	ACTCATCC T CAGGCCAT	1444	AUGGCCUG CUGAUGAG X CGAA IGAUGAGU	3953
3202	TCATCCTC A GGCCATGC	1445	GCAUGGCC CUGAUGAG X CGAA IAGGAUGA	3954
3206	CCTCAGGC C ATGCAGTG	1446	CACUGCAU CUGAUGAG X CGAA ICCUGAGG	3955
3207	CTCAGGCC A TGCAGTGG	1447	CCACUGCA CUGAUGAG X CGAA IGCCUGAG	3956

Input Sequence = AF100308. Cut Site = CH/.
Stem Length = 8 Core Sequence = CUGAUGAG x CGAA (X = GCCGUUAGGC or other stem II)
AF100308 (Hepatitis B virus strain 2-18, 3215 bp)

lable 39

Table 39: Human HBV G-cleaver Ribozyme and Substrate Sequence

Substrate	o	Ribozyme	Rz Seq ID
ACUUUCCU G CUGGUGGC 1448		GCCACCAG UGAUG GCAUGCACUAUGC GCG AGGAAAGU	3957
GGRACAGU G AGCCCUGC 1449		GCAGGGCU UGAUG GCAUGCACUAUGC GCG ACUGUUCC	3958
UGAGCCCU G CUCAGAAU 1450		AUTOUGAG UGAUG GCAUGCACUAUGC GCG AGGGCUCA	3959
CUGUCUCU G CCAUAUCG 1451	ì	CGAUAUGG UGAUG GCAUGCACUAUGC GCG AGAGACAG	3960
AUCUUAUC G AAGACUGG 1452	ı	CCAGUCUU UGAUG GCAUGCACUAUGC GCG GAUAAGAU	3961
CCUGUACC G AACAUGGA 1453		UCCAUGUU UGAUG GCAUGCACUADGC GCG GGUACAGG	3962
AGRACAUC G CAUCAGGA 1454	L	UCCUGAUG UGAUG GCAUGCACUAUGC GCG GAUGUUCU	3963
GGACCCCU G CUCGUGUU 1455	L	AACACGAG UGAUG GCAUGCACUAUGC GCG AGGGUCC	3964
UUCUUGUU G ACAAAAU 1456	L	AUJUJUGU UGAJUG GCAUGCACUAUGC GCG AACAAGAA	3962
CAAAAUUC G CAGUCCCA 1457	L	UGGGACUG UGAUG GCAUGCACUAUGC GCG GAAUUUUG	3966
UGGUUAUC G CUGGAUGU 1458	L	ACAUCCAG UGAUG GCAUGCACUAUGC GCG GAUAACCA	3967
AUGUGUCU G CGCCGUUU 1459	L	AAACGCCG UGAUG GCAUGCACUAUGC GCG AGACACAU	3968
CUUCCUCU G CAUCCUGC 1460	L	GCAGGAUG UGAUG GCAUGCACUAUGC GCG AGAGGAAG	3969
UGCAUCCU G CUGCUAUG 1461	L	CAUAGCAG UGAUG GCAUGCACUAUGC GCG AGGAUGCA	3970
AUCCUGCU G CUAUGCCU 1462	L	AGGCAUAG UGAUG GCAUGCACUAUGC GCG AGCAGGAU	3971
GCUGCUAU G CCUCAUCU 1463		AGAUGAGG UGAUG GCAUGCACUAUGC GCG AUAGCAGC	3972
GOUAUGUU G CCCGUUUG 1464		CAAACGGG UGAUG GCAUGCACUAUGC GCG AACAUACC	3973
CGGACCAU G CAAAACCU 1465	L	AGGUUTUG UGAUG GCAUGCACUAUGC GCG AUGGUCCG	3974
Н	L	GAGUUGUG UGAUG GCAUGCACUAUGC GCG AGGUUUUS	3975
CAACUCCU G CUCAAGGA 1467	L	UCCUUGAG UGAUG GCAUGCACUAUGC GCG AGGAGUUG	3976
CUCAUGUU G CUGUACAA 1468		UNGUACAG UGAUG GCAUGCACUAUGC GCG AACAUGAG	3977
CCGNAACU G CACCUGUA 1469		UACAGGUG UGAUG GCAUGCACUAUGC GCG AGUUUCCG	3978
OGGCUUUC G CAAAUAC 1470	L	GUAUUTUG UGAUG GCAUGCACUAUGC GCG GAAAGCCC	3979
UNACUAGU G CCAUUUGU 1471	L	ACAMAUGG UGAUG GCAUGCACUAUGC GCG ACUAGUAA	3980
AUAUGGAU G AUGUGGUU 1472	L	AACCACAU UGAUG GCAUGCACUAUGC GCG AUCCAUAU	3981
AACAUCUU G AGUCCCUU 1473	L	AAGGACU UGAUG GCAUGCACUAUGC GCG AAGAUGUU	3982
CCCUTUAL G CCGCUGUU 1474	L	AACAGCGG UGAUG GCAUGCACUAUGC GCG AUAAAGGG	3983
UNDADGCC G CUGUDACC 1475		GGUAACAG UGAUG GCAUGCACUAUGC GCG GGCAUAAA	3984
GGCACAUU G CCACAGGA 1476		UCCUBUGG UGAUG GCAUGCACUAUGC GCG AAUGUGCC	3985
GGCCUAUU G AUUGGAAA 1477	L	THE CONTROL OF THE GOALD CONTROL OF STANDERS	3986

3987	3988	3989	3990	3991	3992	3993	3994	3995	3996	3997	3998	3999	4000	4001	4002	4003	4004	4005	4006	4007	4008	4009	4010	4011	4012	4013	4014	4015	4016	4017	4018	4019	4020
CCACAAUU UGAUG GCAUGCACUAUGC GCG GUUGACAU	AGGGGCGG UGAUG GCAUGCACUAUGC GCG AAACCCCA	GAAAGGGG UGAUG GCAUGCACUAUGC GCG GGCAAACC	CCACAUUG UGAUG GCAUGCACUAUGC GCG GUGAAAGG	CAUUAAAG UGAUG GCAUGCACUAUGC GCG AGAAUAUC	UAUAAAGG UGAUG GCAUGCACUAUGC GCG AUUAAAGC	UAUGCAUG UGAUG GCAUGCACUAUGC GCG AUAUAAAG	CUUGUAUG UGAUG GCAUGCACUAUGC GCG AUGCAUAU	UAAGUUGG UGAUG GCAUGCACUAUGC GCG GAGAAAGU	UAAAGGUU UGAUG GCAUGCACUAUGC GCG ACAUACUG	UUGCCGAG UGAUG GCAUGCACUAUGC GCG AACGGGGU	ACACUUGG UGAUG GCAUGCACUAUGC GCG AUAGACCA	UGCGUCAG UGAUG GCAUGCACUAUGC GCG AAACACUU	SGUUGCGU UGAUG GCAUGCACUAUGC GCG AGCAAACA	GGGGGUUG UGAUG GCAUGCACUAUGC GCG GUCAGCAA	CACGCAUG UGAUG GCAUGCACUAUGC GCG GCUGAUGG	GUUCCACG UGAUG GCAUGCACUAUGC GCG AUGCGCUG	UGGAUCGG UGAUG GCAUGCACUAUGC GCG AGAGGAGA	GUAUGGAU UGAUG GCAUGCACUAUGC GCG GGCAGAGG	SAGUUCCG UGAUG GCAUGCACUAUGC GCG GGUAUGGA	AAAACAAG UGAUG GCAUGCACUAUGC GCG GGCUAGGA	GCUGCGAG UGAUG GCAUGCACUAUGC GCG AAAACAAG	ACCUGCUG UGAUG GCAUGCACUAUGC GCG GAGCAAAA	AGAAUUGU UGAUG GCAUGCACUAUGC GCG AGUCCCGA	COGGAGAG UGAUG GCAUGCACUAUGC GCG ACGACAGA	JADAUTUG UGADG GCAUGCACDADGC GCG GGGAGAGC	CAGCCUAG UGAUG GCAUGCACUAUGC GCG AGCCAUGG	GUUGGCAG UGAUG GCAUGCACUAUGC GCG ACAGCCUA	CCAGUUGG UGAUG GCAUGCACUAUGC GCG AGCACAGC	ACGUCCCG UGAUG GCAUGCACUAUGC GCG GUAGGAUC	GGAUUCAG UGAUG GCAUGCACUAUGC GCG GCCGACGG	GCGGGAUU UGAUG GCAUGCACUAUGC GCG AGCGCCGA	GUCGUCCG UGAUG GCAUGCACUAUGC GCG GGGAUUCA	GGAGGGGU UGAUG GCAUGCACUAUGC GCG GUCCGCGG
1478 C	1479 A	1480 G	1481 C	1482 C	1483 U	1484 U	1485 C	1486 U	1487 U	1488 U	1489 A	1490 U	1491 G	1492 G	1493 C	1494 G	1495 U	1496 G	1497 G	1498 A	1499 G	1500 A	1501 A	1502 C	1503 0	1504 C	1505 G	1506	1507	1508 G	1509 G	1510 G	1511 G
AUGUCAAC G AAUUGUGG	nagagnin a coaccccu	Gennuece a cocomino	CCUUUCAC G CAAUGUGG	GAUAUUCU G CUUUAAUG	GCUUUNAU G CCUUUNUN	CUUUAUAU G CAUGCAUA	AUAUGCAU G CAUACAAG	ACUIDICUE G CCAACUUA	CAGUAUGU G AACCUUUA	ACCCCGUU G CUCGGCAA	UGGUCUAU G CCAAGUGU	AAGUGUUU G CUGACGCA	ueunuecu e acecaace	UUGCUGAC G CAACCCCC	CCAUCAGC G CAUGCGUG	CAGCGCAU G CGUGGAAC	ucuccucu g cogaucca	CCUCUGCC G AUCCAUAC	UCCAUACC G CGGAACUC	uccuages a conguun	CUUGUUU G CUCGCAGC	UUUUGCUC G CAGCAGGU	UCGGGACU G ACAAUUCU	ncnencen e cococces	ø	CCAUGGCU G CUAGGCUG	UAGGCUGU G CUGCCAAC	gengugen g ccaacugg	GAUCCUAC G CGGGACGU	CCGUCGGC G CUGAAUCC	UCGGCGCU G AAUCCCGC	UGAAUCCC G CGGACGAC	CCGCGGAC G ACCCCUCC
166	1020	1023	1034	1050	1058	1068	1072	1103	1139	1155	1177	1188	1191	1194	1234	1238	1262	1265	1275	1290	1299	1303	1335	1349	1357	1382	1392	1395	1411	1442	1445	1452	1458

4021	4022	4023	4024	4025	4026	4027	4028	4029	4030	4031	4032	4033	4034	4035	4036	4037	4038	4039	4040	4041	4042	4043	4044	4045	4046	4047	4048	4049	4050	4051	4052	4053	4054
GCCCCAAG UGAUG GCAUGCACUAUGC GCG GGCCCCGG	GAAGCGGG UGAUG GCAUGCACUAUGC GCG GGUAGAGC	CGGAGAAG UGAUG GCAUGCACUAUGC GCG GGGCGGUA	ACAAUAGG UGAUG GCAUGCACUAUGC GCG GGAGAAGC	UGGACGGU UGAUG GCAUGCACUAUGC GCG GGUACAAU	GAGAGGUG UGAUG GCAUGCACUAUGC GCG GCCCCGUG	GGAGUCCG UGAUG GCAUGCACUAUGC GCG GUAAAGAG	UGAGAAGG UGAUG GCAUGCACUAUGC GCG ACAGACGG	CGGUCCGG UGAUG GCAUGCACUAUGC GCG AGAUGAGA	GOGRAGUG UGAUG GCAUGCACUAUGC GCG ACACGGUC	AGGUGAAG UGAUG GCAUGCACUAUGC GCG GAAGUGCA	GOGACGUG UGAUG GCAUGCACUAUGC GCG AGAGGUGA	UCUCCAUG UGAUG GCAUGCACUAUGC GCG GACGUGCA	UGGCCGUU UGAUG GCAUGCACUAUGC GCG ACGGUGGU	CCUGUGGG UGAUG GCAUGCACUAUGC GCG GUUCACGG	ACCUUGGG UGAUG GCAUGCACUAUGC GCG AGGUUCCU	CUCUUAUG UGAUG GCAUGCACUAUGC GCG AAGACCUU	AGGUCGGU UGAUG GCAUGCACUAUGC GCG GUUGACAU	CUCAAGGU UGAUG GCAUGCACUAUGC GCG GGUCGUUG	GUAUGCCU UGAUG GCAUGCACUAUGC GCG AAGGUCGG	CUCCCACU UGAUG GCAUGCACUAUGC GCG AUUAAACA	AAAAGUUG UGAUG GCAUGCACUAUGC GCG AUGGUGCU	UGAUUAGG UGAUG GCAUGCACUAUGC GCG AGAGGUGA	ACCCAAGG UGAUG GCAUGCACUAUGC GCG ACAGCUUG	AUACGGGU UGAUG GCAUGCACUAUGC GCG AAUGUCCA	UCAGAAGG UGAUG GCAUGCACUAUGC GCG AAAAAAGA	AAAGAAGU UGAUG GCAUGCACUAUGC GCG AGAAGGCA	GGAGAUCU UGAUG GCAUGCACUAUGC GCG GAAUAGAA	GGCGGUGU UGAUG GCAUGCACUAUGC GCG GAGGAGAU	AGCAGAGG UGAUG GCAUGCACUAUGC GCG GGUGUCGA	AUACAGAG UGAUG GCAUGCACUAUGC GCG AGAGGCGG	CAUCAACU UGAUG GCAUGCACUAUGC GCG ACCCCAAC	AGAUNCAU UGAUG GCAUGCACUAUGC GCG AACUCACC	GCUAGAUU UGAUG GCAUGCACUAUGC GCG AUCAACUC
1512	1513	1514	1515	1516	1517	1518	1519	1520	1521	1522	1523	1524	1525	1526	1527	1528	1529	1530	1531	1532	1533	1534	1535	1536	1537	1538	1539	1540	1541	1542	1543	1544	1545
ccasacc a cunasasc	acucuace a eccaeuue	UACCGCCC G CUUCUCCG	acuncuca a convinai	AUDGUACC G ACCGUCCA	CACGGGG G CACCUCUC	CUCUUUAC G CGGACUCC	ccaucuau a ccuucuca	ucucaucu e ccesacce	GACCGUGU G CACUUCGC	UGCACUUC G CUUCACCU	ucaccucu a cacquege	UGCACGUC G CAUGGAGA	ACCACCGU G AACGCCCA	CCGUGAAC G CCCACAGG	AGGAACCU G CCCAAGGU	AAGGUCUU G CAUAAGAG	AUGUCAAC G ACCGACCU	CAACGACC G ACCUUGAG	CCGACCUU G AGGCAUAC	UGUTUDAN G AGUGGGAG	AGCACCAU G CAACUUUU	UCACCUCU G CCUAAUCA	съявсиви в ссиивави	UGGACAUU G ACCCGUAU	ucuuuuu a ccuucuaa	ueccanca e vanacana	UUCUAUUC G AGAUCUCC	AUCUCCUC G ACACCGCC	UCGACACC G CCUCUGCU	ccaccaca a cacadam	GUUGGGGU G AGUUGAUG	GGUGAGUU G AUGAAUCU	GAGUUGAU G AAUCUAGC
1474	1489	1493	1201	1513	1528	1542	1559	1571	1583	1590	1601	1608	1624	1628	1642	1654	1690	1694	1700	1730	1818	1835	1883	1912	1959	1966	1985	1996	2002	2008	2002	2097	2100

2237	UUUUGGGC G AGAAACUG	1546	CAGUUCU UGAUG GCAUGCACUAUGC GCG GCCCAAAA	4055
2251	CUGUUCUU G AAUAUUUG	1547	CAMAUNUU UGAUG GCAUGCACUAUGC GCG AAGAACAG	4056
2282	GUGGAUUC G CACUCCUC	1548	GAGGAGUG UGAUG GCAUGCACUAUGC GCG GAAUCCAC	4057
2293	CUCCUCCU G CAUAUAGA	1549	UCUAUAUG UGAUG GCAUGCACUAUGC GCG AGGAGGAG	4058
2311	CACCAAAU G CCCCUAUC	1550	GAUAGGGG UGAUG GCAUGCACUAUGC GCG AUTUGGUG	4059
2354	UGUUAGAC G AAGAGGCA	1551	UGCCUCUU UGAUG GCAUGCACUAUGC GCG GUCUAACA	4060
2388	ACUCCCUC G CCUCGCAG	1552	CUGCGAGG UGAUG GCAUGCACUAUGC GCG GAGGGAGU	4061
2393	CUCGCCUC G CAGACGAA	1553	UNCGUCUG UGAUG GCAUGCACUAUGC GCG GAGGCGAG	4062
2399	UCGCAGAC G AAGGUCUC	1554	GAGACCUU UGAUG GCAUGCACUAUGC GCG GUCUGCGA	4063
2412	UCUCAAUC G CCGCGUCG	1555	CGACGCGG UGAUG GCAUGCACUAUGC GCG GAUUGAGA	4064
2415	CAAUCGCC G CGUCGCAG	1556	CUGCGACG UGAUG GCAUGCACUAUGC GCG GGCGAUUG	4065
2420	GCCGCGUC G CAGAAGAU	1557	AUCUUCUG UGAUG GCAUGCACUAUGC GCG GACGCGGC	4066
2514	GGUACCUU G CUUUNAUC	1558	GAUUAAAG UGAUG GCAUGCACUAUGC GCG AAGGUACC	4067
2549	CUUUUCCU G ACAUUCAU	1559	AUGRAUGU UGAUG GCAUGCACUAUGC GCG AGGAAAAG	4068
2560	AUUCAUUU G CAGGAGGA	1560	UCCUCCUG UGAUG GCAUGCACUAUGC GCG AAAUGAAU	4069
2576	ACAUUGUU G AUAGAUGU	1561	ACAUCUAU UGAUG GCAUGCACUAUGC GCG AACAAUGU	4070
2615	CAGUAAAU G AAAACAGG	1562	CCUGUIUU UGAUG GCAUGCACUAUGC GCG AUUUACUG	4071
2641	UNAACUAU G CCUGCUAG	1563	CUAGCAGG UGAUG GCAUGCACUAUGC GCG AUAGUUAA	4072
2645	cuangeen e cuaggnun	1564	AAACCUAG UGAUG GCAUGCACUAUGC GCG AGGCAUAG	4073
2677	AAAUAUUU G CCCUUAGA	1565	UCUAAGGG UGAUG GCAUGCACUAUGC GCG AAAUAUUU	4074
2740	UUCCAGAC G CGACAUUA	1566	UAAUGUCG UGAUG GCAUGCACUAUGC GCG GUCUGGAA	4075
2742	CCAGACGC G ACAUDAUD	1567	ANUAAUGU UGAUG GCAUGCACUAUGC GCG GCGUCUGG	4076
2804	CACGUAGE G CCUCAUUU	1568	AAAUGAGG UGAUG GCAUGCACUAUGC GCG GCUACGUG	4077
2814	CUCAUUUU G CGGGUCAC	1569	GUGACCCG UGAUG GCAUGCACUAUGC GCG AAAAUGAG	4078
2875	CAAACCUC G AAAAGGCA	1570	UGCCUUUU UGAUG GCAUGCACUAUGC GCG GAGGUUUG	4079
2928	nonnocco e vnovnove	1571	CUGAUGAU UGAUG GCAUGCACUAUGC GCG GGGGAAGA	4080
2946	UGGACCCU G CAUUCAAA	1572	UUUGAAUG UGAUG GCAUGCACUAUGC GCG AGGGUCCA	4081
2990	CUCAACCC G CACAAGGA	1573	UCCUUGUG UGAUG GCAUGCACUAUGC GCG GGGUUGAG	4082
3012	GGCCGGAC G CCAACAAG	1574	CUUGUUGG UGAUG GCAUGCACUAUGC GCG GUCCGGCC	4083
3090	GCCCUCAC G CUCAGGGC	1575	GCCCUGAG UGAUG GCAUGCACUAUGC GCG GUGAGGGC	4084
3113	ACAACUGU G CCAGCAGC	1576	GCUGCUGG UGAUG GCAUGCACUAUGC GCG ACAGUUGU	4085
3132	COCCOCCO e CCOCCACC	22ST	GGUGGAGG UGAUG GCAUGCACUAUGC GCG AGGAGGAG	4086
51	AGGCCCU G UACUUUCC	1578	GGAAAGUA UGAUG GCAUGCACUAUGC GCG AGGGCCCU	4087
106	AGAAUACU G UCUCUGCC	1579	GGCAGAGA UGAUG GCAUGCACUAUGC GCG AGUAUUCU	4088

148	GGGACCCU G UACCGAAC	1580	GUUCGGUA UGAUG GCAUGCACUAUGC GCG AGGGUCCC	4089
198	coecacea e navereec	1581	GCCUGUAA UGAUG GCAUGCACUAUGC GCG ACGAGCAG	4090
219	UUUUUCUU G UUGACAAA	1582	UUUGUCAA UGAUG GCAUGCACUAUGC GCG AAGAAAAA	4091
297	ACACCCGU G UGUCUUGG	1583	CCAAGACA UGAUG GCAUGCACUAUGC GCG ACGGGUGU	4092
588	Acceden e ucuneece	1584	GGCCAAGA UGAUG GCAUGCACUAUGC GCG ACACGGGU	4093
347	ACCAACCU G UUGUCCUC	1585	GAGGACAA UGAUG GCAUGCACUAUGC GCG AGGUUGGU	4094
350	AACCUGUU G UCCUCCAA	1586	UUGGAGGA UGAUG GCAUGCACUAUGC GCG AACAGGUU	4095
362	UCCAAUUU G UCCUGGUU	1587	AACCAGGA UGAUG GCAUGCACUAUGC GCG AAAUUGGA	4096
381	CGCUGGAU G UGUCUGCG	1588	CGCAGACA UGAUG GCAUGCACUAUGC GCG AUCCAGCG	4097
383	CUGGAUGU G UCUGCGGC	1589	GCCGCAGA UGAUG GCAUGCACUAUGC GCG ACAUCCAG	4098
438	AUCUUCUU G UUGGUUCU	1590	AGAACCAA UGAUG GCAUGCACUAUGC GCG AAGAAGAU	4099
465	CAAGGUAU G UUGCCCGU	1591	ACGGGCAA UGAUG GCAUGCACUAUGC GCG AUACCUUG	4100
476	accedunt a uccucusa	1592	UUNGAGGA UGAUG GCAUGCACUAUGC GCG AAACGGGC	4101
555	ACCUCUAU G UUUCCCUC	1593	GAGGGAAA UGAUG GCAUGCACUAUGC GCG AUAGAGGU	4102
995	UCCCUCAU G UUGCUGUA	1594	UACAGCAA UGAUG GCAUGCACUAUGC GCG AUGAGGGA	4103
572	AUGUUGCU G UACAAAAC	1595	GUUUUGUA UGAUG GCAUGCACUAUGC GCG AGCAACAU	4104
602	CUGCACCU G UNUUCCCA	1596	UGGGAAUA UGAUG GCAUGCACUAUGC GCG AGGUGCAG	4105
694	UGCCAUUU G UUCAGUGG	1597	CCACUGAA UGAUG GCAUGCACUAUGC GCG AAAUGGCA	4106
724	ccccacu e ucusecuu	1598	AAGCCAGA UGAUG GCAUGCACUAUGC GCG AGUGGGGG	4107
750	UGGAUGAU G UGGUUUUG	1599	CANANCCA UGAUG GCAUGCACUAUGC GCG AUCAUCCA	4108
771	ccaagucu g uacaacau	1600	AUGUUGUA UGAUG GCAUGCACUAUGC GCG AGACUUGG	4109
801	AUGCCGCU G UUACCAAU	1091	AUUGGUAA UGAUG GCAUGCACUAUGC GCG AGCGGCAU	4110
818	uncum e acameee	1602	CCCAAAGA UGAUG GCAUGCACUAUGC GCG AAAAGAAA	4111
888	UGGGAUAU G UAAUUGGG	1603	CCCAAUUA UGAUG GCAUGCACUAUGC GCG AUAUCCCA	4112
927	AACAUAUU G UACAAAA	1604	UNDURUM DEAUG GCAUGCACUAUGC GCG AAUAUGUU	4113
944	AUCARARU G UGUUUNG	1605	CUNNANCA UGAUG GCAUGCACUAUGC GCG AUUUUGAU	4114
946	CAAAAUGU G UUUUAGGA	1606	UCCUARAR UGAUG GCAUGCACUAUGC GCG ACAUUUUG	4115
963	AACUUCCU G URAACAGG	1607	CCUGUUNA UGAUG GCAUGCACUAUGC GCG AGGAAGUU	4116
166	GAAAGUAU G UCAACGAA	1608	UNCGUUGA UGAUG GCAUGCACUAUGC GCG AUACUUUC	4117
1002	AACGAAUU G UGGGUCUU	1609	NAGACCCA UGAUG GCAUGCACUAUGC GCG AAUUCGUU	4118
1039	CACGCAAU G UGGAUAUU	1610	AAUAUCCA UGAUG GCAUGCACUAUGC GCG AUUGCGUG	4119
1137	AACAGUAU G UGAACCUU	1611	AAGGUUCA UGAUG GCAUGCACUAUGC GCG AUACUGUU	4120
1184	ueccaagu e uuuscuga	1612	ncadcada ugaug gcaugcacuaugc gcg acuuggca	4121
1251	GAACCUUU G UGUCUCCU	1613	SEGRENCE DEVIDE GENUGE GEG SARGEUDE	4122

4123	4124	4125	4126	4127	4128	4129	4130	4131	4132	4133	4134	4135	4136	4137	4138	4139	4140	4141	4142	4143	4144	4145	4146	4147	4148	4149	4150	4151	4152	4153	4154	4155	4156
AGAGGAGA UGAUG GCAUGCACUAUGC GCG ACAAAGGU	GAGCAAAA UGAUG GCAUGCACUAUGC GCG AAGCGGCU	GAGCACGA UGAUG GCAUGCACUAUGC GCG AGAAUUGU	UGGCAGCA UGADG GCAUGCACUAUGC GCG AGCCUAGC	GACGUADA UGAUG GCAUGCACUAUGC GCG ADAGGACG	GGUCGGUA UGAUG GCAUGCACUAUGC GCG AAUAGGCG	AGAAGGCA UGAUG GCAUGCACUAUGC GCG AGACGGGG	GAAGUGCA UGAUG GCAUGCACUAUGC GCG ACGGUCCG	GUCGUUGA UGAUG GCAUGCACUAUGC GCG AUUGCUGA	UAAACACA UGAUG GCAUGCACUAUGC GCG AGUCUTUG	AUUAAACA UGAUG GCAUGCACUAUGC GCG ACAGUCUU	UCAUDAAA UGAUG GCAUGCACDAUGC GCG ACACAGUC	UCCUAGUA UGAUG GCAUGCACUAUGC GCG AAAGACCU	UAUGCCUA UGAUG GCAUGCACUAUGC GCG AGCCUCCU	GGUGAACA UGAUG GCAUGCACUAUGC GCG ACCAAUUU	CUGGUGAA UGAUG GCAUGCACUAUGC GCG ACACCAAU	GACAUGAA UGAUG GCAUGCACUAUGC GCG AUGAGAUG	CAGUAGGA UGAUG GCAUGCACUAUGC GCG AUGAACAU	GOCUUGAA UGAUG GCAUGCACUAUGC GCG AGUAGGAC	CCAAGGCA UGAUG GCAUGCACUAUGC GCG AGCUUGGA	UAACUCCA UGAUG GCAUGCACUAUGC GCG AGAAGCUC	CCCCGAUA UGAUG GCAUGCACUAUGC GCG AGAGCAGA	GAGGUGAA UGAUG GCAUGCACUAUGC GCG AAUGUUCC	CCCCAACA UGAUG GCAUGCACUAUGC GCG AGAAUAGC	CACCCCAA UGAUG GCAUGCACUAUGC GCG ACAGAAUA	AACGUUGA UGAUG GCAUGCACUAUGC GCG AUAGCUGA	UGAAACCA UGAUG GCAUGCACUAUGC GCG AAUAGUUG	AAGUAAGA UGAUG GCAUGCACUAUGC GCG AGGAAAUG	UUCAAGAA UGAUG GCAUGCACUAUGC GCG AGUUUCUC	CCAAAAGA UGAUG GCAUGCACUAUGC GCG ACCAAAUA	CGAAUCCA UGAUG GCAUGCACUAUGC GCG ACUCCAAA	UCUAACAA UGAUG GCAUGCACUAUGC GCG AGUAGUUU		AAUACUAA UGAUG GCAUGCACUAUGC GCG AUUGAGAU
1614	1615	1616	1617	1618	1619	1620	1621	1622	1623	1624	1625	1626	1627	1628	1629	1630	1631	1632	1633	1634	1635	1636	1637	1638	1639	1640	1641	1642	1643	1644	1645	1646	1647
Accuundu a ucuccucu	AGCCGCUU G UUUUGCUC	ACAMUUCU G UCGUGCUC	GCUAGGCU G UGCUGCCA	cencenna e nunycene	CGCCUAUU G UACCGACC	coccence e necennen	CGGACCGU G UGCACUUC	UCAGCAAU G UCAACGAC	CAAAGACU G UGUGUUUA	AAGACUGU G UGUUUAAU	GACUGUGU G UUUAAUGA	AGGUCUUU G UACUAGGA	AGGAGGCU G UAGGCAUA	AAAUUGGU G UGUUCACC	AUUGGUGU G UUCACCAG	CAUCUCAU G UUCAUGUC	AUGUUCAU G UCCUACUG	GUCCUACU G UUCAAGCC	uccaageu e ugceuuge	GAGCUUCU G UGGAGUUA	ucuecucu e uAuceeee	GGAACAUU G UUCACCUC	GCUAUUCU G UGUUGGGG	UNUCCUGU G UUGGGGUG	UCAGCUAU G UCAACGUU	CAACUAUU G UGGUUUCA	caunuccu e ucunacuu	GAGAAACU G UUCUUGAA	DAUJUGGU G UCUUJUGG	UUUGGAGU G UGGAUUCG	AAACUACU G UUGUUAGA	O	AUCUCAAU G UUAGUAUU
1253	1294	1344	1390	1425	1508	1557	1581	1684	1719	1721	1723	1772	1785	1801	1803	1850	1856	1864	1881	1939	2013	2045	2082	2084	2167	2205	2222	2245	2362	2274	2344	2347	2450

Table 39

2573	AGGACAUU G UUGAUAGA	1648	UCUAUCAA UGAUG GCAUGCACUAUGC GCG AAUGUCCU	4157
2583	UGAUAGAU G UAAGCAAU	1649	AUDGCUUN UGNUG GCAUGCACUAUGC GCG AUCUAUCA	4158
2594	AGCAAUUU G UGGGGCCC	1650	GGGCCCCA UGAUG GCAUGCACUAUGC GCG AAAUUGCU	4159
2663	AUCCCAAU G UUACUAAA	1651	UUUAGUAA UGAUG GCAUGCACUAUGC GCG AUUGGGAU	4160
2717	CAGAGUAU G UAGUUAAU	1652	AUUAACUA UGAUG GCAUGCACUAUGC GCG AUACUCUG	4161
2901	AUCUUUCU G UCCCCAAU	1653	AUUGGGGA UGAUG GCAUGCACUAUGC GCG AGAAAGAU	4162
3071	GGGGGACU G UUGGGGGUG	1654	CACCCCAA UGAUG GCAUGCACUAUGC GCG AGUCCCCC	4163
3111	UCACAACU G UGCCAGCA	1655	UGCUGGCA UGAUG GCAUGCACUAUGC GCG AGUUGUGA	4164

Input Sequence = AF100308. Cut Site = YG/M cr UG/U. Stem Length = 8. Core Sequence = UGAUG GCAUGCACUAUGC GCG AF100308 (Hepatitis B virus strain 2-18, 3215 bp)

Fable 40: Human HBV Zinzyme Ribozyme and Substrate Sequence

Table 40

4167 4169 4171 4172 4173 4174 4175 4176 4177 4179 4180 4181 4182 4184 4185 4190 4192 4165 4168 4183 4187 4191 CGAUAUGG GCcgagagGCGaGuCagGuCu AGAGACAG AACACGAG GCcgaaagGCGaGuCaaGGuCu AGGGGUCC UGGGACUG GCcgaaagGCGaGuCaaGGuCu GAAUUUUG ACAUCCAG GCcgaaagGCGaGuCaaGGuCu GAUAACCA AAACGCCG GCcgaaagGCGaGuCaaGGuCu AGACACAU GCAGGAUG GCcgaaagGCGaGuCaaGGuCu AGAGGAAG CAUAGCAG GCcgaaagGCGaGuCaaGGuCu AGGAUGCA AGGCAUAG GCcgaaagGCGaGuCaaGGuCu AGCAGGAU AGAUGAGG GCcgaaagGCGaGuCaaGGuCu AUAGCAGC CAAACGGG GCcgaaagGCGaGuCaaGGuCu AACAUACC AGGUUUUG GCcgaaagGCGaGuCaaGGuCu AUGGUCCG GAGUUGUG GCccaaaaGCGaGuCaaGGuCu AGGUUUUG JCCUUGAG GCcgaaagGCGaGuCaaGGuCu AGGAGUUG UUGUACAG GCcgaaagGCGaGuCaaGGuCu AACAUGAG UACAGGUG GCcgaaagGCGaGuCaaGGuCu AGUUUCCG GUAUUUUG GCcgaaagGCGaGuCaaGGuCu GAAAGCCC ACAAAUGG GCcgaaagGCGaGuCaaGGuCu ACUAGUAA AACAGOGG GCcgaaagGCGaGuCaaGGuCu AUAAAGGG GGUAACAG GCcgaaagGCGaGuCaaGGuCu GGCAUAAA UCCUGUGG GCcgaaagGCGaGuCaaGGuCu AAUGUGCC AGGGGGG GCcgaaagGCGaGuCaaGGuCu AAACCCCA SAAAGGGG GCcgaaagGCGaGuCaaGGuCu GGCAAACC SCACAUUG GCcgaaagGCGaGuCaaGGuCu GUGAAAGG CAUDAAAG GCcqaaaqGCGaGuCaaGGuCu AGAAUAUC JAUAAAGG GCcgaaagGCGaGuCaaGGuCu AUUAAAGC JAUGCAUG GCcgaaagGCGaGuCaaGGuCu AUAUAAAG TUTGUAUG GCcqaaaqGCGaGuCaaGGuCu AUGCAUAU GCCACCAG GCcgaaagGCGaGuCaaGGuCu AGGAAAGU AUUCUGAG GCcqaaagGCGaGuCaaGGuCu AGGGCUCA UCCUGAUG GCcqaaagCGaGuCaagGuCu GAUGUUCU Ribozyme Seg ID 1455 1451 1454 1459 1460 1462 1464 1465 1466 1469 1470 1471 1474 1475 1476 1479 1481 1457 1458 1461 1463 1467 1468 1480 1482 1483 1484 1485 1450 ACUUUCCU G CUGGUGGC DGAGCCCU G CUCAGAAU CUGUCUCU G CCAUAUCG AGAACAUC G CAUCAGGA GGACCCCU G CUCGUGUU CAAAAUUC G CAGUCCCA UGGUUAUC G CUGGAUGU AUGUGUCU G CGGCGUUU curccucu a cauccuac UGCAUCCU G CUGCUAUG AUCCUGCU G CUAUGCCU GCUGCUAU G CCUCAUCU GGUAUGUU G CCCGUUUG CGGACCAU G CAAAACCU CAAAACCU G CACAACUC CAACUCCU G CUCAAGGA CUCAUGUU G CUGUACAA CGGAAACU G CACCUGUA GGGCUUUC G CAAAAUAC UNACUAGO G CCAUTUGO cccuunau a ccacuguu UNDAUGCC G CUGUUACC GGCACAUU G CCACAGGA naggenna a coecocon eennnecc e coconna ccuoucac e caauguge SAUADUCU G CUUDAAUG GCUUUAAU G CCUUUAUA CUUUAUAU G CAUGCAUA AUAUGCAU G CAUACAAG Substrate 1034 1068 1020 1050 1058 Pos 112 169 192 315 374 387 410 417 420 425 468 518 527 538 569 596 687 795 798 911 94 61

4195	4196	4197	4198	4199	4200	4201	4202	4203	4204	4205	4206	4207	4208	4209	4210	4211	4212	4213	4214	4215	4216	4217	4218	4219	4220	4221	4222	4223	4224	4225	4226	4227	4228
GAGAAAGU	AACGGGGU	AUAGACCA	AAACACUU	GUCAGCAA	GCUGAUGG	AUGCGCUG	AGAGGAGA	GGUAUGGA	GGCUAGGA	AAAACAAG	GAGCAAAA	ACGACAGA	GGCAGAGC	AGCCAUGG	ACAGCCUA	AGCACAGC	GUAGGAUC	GCCGACGG	GGGAUUCA	98000099	GGUAGAGC	GGGCGGUA	GGAGAAGC	GCCCCGUG	GUAAAGAG	ACAGACGG	AGAUGAGA	ACACGGUC	GAAGUGCA	AGAGGUGA	GACGUGCA	GUUCACGG	AGGUUCCU
UAAGUUGG GCcgaaagGCGaGuCaaGGuCu GAGAAAGU	UUGCCGAG GCcgaaagGCGaGuCaaGGuCu	GCcgaaagGCGaGuCaaGGuCu	GCcgaaagGCGaGuCaaGGuCu	GCcgaaagGCGaGuCaaGGuCu	GCcgaaagGCGaGuCaaGGuCu GCUGAUGG	SUUCCACS GCcgaagGCGaGuCaaGGuCu AUGCGCUG	UGGAJUCGG GCcgaaagGCGaGuCaaGGuCu AGAGGAGA	GAGUUCCG GCcgaaagGCGaGuCaaGGuCu	GCoganagGCGaGuCaaGGuCu	GCcgaaagGCGaGuCaaGGuCu	GCcgaaagGCGaGuCaaGGuCu GAGCAAAA	CGGGAGAG GCcgaaagGCGaGuCaaGGuCu ACGACAGA	UAUAUUUG GCcgaaagGCGaGuCaaGGuCu GGGAGAGC	CAGCCUAG GCcgaaagGCGaGuCaaGGuCu AGCCAUGG	GUUGGCAG GCcgaaagGCGaGuCaaGGuCu ACAGCCUA	CCAGUUGG GCcgaaagGCGaGuCaaGGuCu	ACGUCCCG GCcgaaagGCGaGuCaaGGuCu	GCcgaaagGCGaGuCaaGGuCu	GCcgaaagGCGaGuCaaGGuCu GGGAUUCA	GCCCCAAG GCcgaaagGCGaGuCaaGGuCu GGCCCCGG	GAAGCGGG GCcgaaagGCGaGuCaaGGuCu GGUAGAGC	CGGAGAAG GCcgaaagGCGaGuCaaGGuCu GGGCGGUA	ACAAUAGG GCcgaaagGCGaGuCaaGGuCu	GAGAGGUG GCcgaaagGCGaGuCaaGGuCu	GCcgaaagGCGaGuCaaGGuCu	UGAGAAGG GCcgaaagGCGaGuCaaGGuCu ACAGACGG	CGGUCCGG GCcgaaagGCGaGuCaaGGuCu AGAUGAGA	GCGAAGUG GCcgaaagGCGaGuCaaGGuCu ACACGGUC	AGGUGAAG GCcgaaagGCGaGuCaaGGuCu GAAGUGCA	GCcgaaagGCGaGuCaaGGuCu	GCcgaaagGCGaGuCaaGGuCu	GCcgaaagGCGaGuCaaGGuCu	ACCUUGGG GCcgaaagGCGaGuCaaGGuCu AGGUUCCU
UAAGUUGG GC	UUGCCGAG GC	ACACUUGG GC	UGCGUCAG GC	GGGGGUUG GC	CACGCAUG GC	GUUCCACG GC	UGGAUCGG GC	GAGUUCCG GC	AAAACAAG GC	GCUGCGAG GC	Accudedug ac	CGGGAGAG GC	UAUAUUUG GC	CAGCCUAG GC	GUUGGCAG GC	CCAGUUGG GC	ACGUCCCG GC	GGAUUCAG GC	GUCGUCCG GC	GCCCCAAG GC	GAAGCGGG GC	CGGAGAAG GC	ACAAUAGG GC	GAGAGGUG GC	GGAGUCCG GC	UGAGAAGG GC	ceeuccee ec	GCGAAGUG GC	AGGUGAAG GC	GCGACGUG GC	UCUCCAUG GC	ccuanaga ac	ACCUUGGG GC
1486	1488	1489	1490	1492	1493	1494	1495	1497	1498	1499	1500	1502	1503	1504	1505	1506	1507	1508	1510	1512	1513	1514	1515	1517	1518	1519	1520	1521	1522	1523	1524	1526	1527
ACUUUCUC G CCAACUUA	ACCCCGUU G CUCGGCAA	UGGUCUAU G CCAAGUGU	AAGUGUUU G CUGACGCA	UUGCUGAC G CAACCCCC	CCAUCAGC G CAUGCGUG	CAGOGCAU G CGUGGAAC	ucuccucu a ccaaucca	O	UCCUAGCC G CUUGUUUU	condonno a cocacado	UUUUGCUC G CAGCAGGU	nandende a chancade	GCUCUCCC G CAAAUAUA	CCAUGGCU G CUAGGCUG	UAGGCUGU G CUGCCAAC	GCUGUGCU G CCAACUGG	GAUCCUAC G CGGGACGU	ccenceec e cnevance	UGAAUCCC G CGGACGAC	ccacaca a consegac	GCUCUACO G CCCGCUUC	UACCGCCC G CUUCUCCG	GCUUCUCC G CCUAUUGU	CACGGGGC G CACCUCUC	CUCUUDAC G OGGACUCC	ccancnan a ccuncuca	UCUCAUCU G CCGGACCG	GACCGUGU G CACUUCGC	DECACUUC G CUUCACCU	ucaccueu e caceucee	USCACGUC G CAUGGAGA	CCGUGAAC G CCCACAGG	AGGAACCU G CCCAAGGU
1103	1155	1177	1188	1194	1234	1238	1262	1275	1290	1299	1303	1349	1321	1382	1392	1395	1411	1442	1452	1474	1489	1493	1201	1528	1542	1559	1571	1583	1590	1601	1608	1628	1642

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1654	O	1528	CUCUUAUG GCcgaaagGCGaGuCaaGGuCu AAGACCUU	4229
1818	AGCACCAU G CAACUUUU	1533	AAAAGUUG GCcgaaagGCGaGuCaaGGuCu AUGGUGCU	4230
5881	ucaccucu e ccuaauca	1534	UGAUUAGG GCcgaaagGCGaGuCaaGGuCu AGAGGUGA	4231
1883	caageugu g cenngggu	1535	ACCCAAGG GCcgaaagGCGaGuCaaGGuCu ACAGCUUG	4232
1959	ucununu e courcuea	1537	UCAGAAGG GCcgaaagGCGaGuCaaGGuCu AAAAAAGA	4233
2002	UCGACACC G CCUCUGCU	1541	AGCAGAGG GCcgaaagGCGaGuCaaGGuCu GGUGUCGA	4234
2008	cceccucu e cucuenau	1542	AUACAGAG GCcgaaagGCGaGuCaaGGuCu AGAGGCGG	4235
2282	GUGGAUJC G CACUCCUC	1548	GAGGAGUG GCcgaaagGCGaGuCaaGGuCu GAAUCCAC	4236
2293	CUCCUCCU G CAUAUAGA	1549	UCUAUAUG GCcgaaagGCGaGuCaaGGuCu AGGAGGAG	4237
2311	CACCAAAU G CCCCUAUC	1550	GAUAGGG GCcgaaagGCGaGuCaaGGuCu AUUUGGUG	4238
2388	ACUCCCUC G CCUCGCAG	1552	CUGCGAGG GCcgaaagGCGaGuCaaGGuCu GAGGGAGU	4239
2393	cuceccuc e casacsaa	1553	UUCGUCUG GCcgaaagGCGaGuCaaGGuCu GAGGCGAG	4240
2412	UCUCAAUC G CCGCGUCG	1555	CGACGCGG GCcgaaagGCGaGuCaaGGuCu GAUUGAGA	4241
2415	CAAUCGCC G CGUCGCAG	1556	CUGCGACG GCcgaaagGCGaGuCaaGGuCu GGCGAUUG	4242
2420	GCCGCGUC G CAGAAGAU	1557	AUCUUCUG GCcgaaagGCGaGuCaaGGuCu GACGCGGC	4243
2514	GGUACCUU G CUUUNAUC	1558	GAUUAAAG GCcgaaagGCGaGuCaaGGuCu AAGGUACC	4244
2560	AUUCAUUU G CAGGAGGA	1560	UCCUCCUG GCcgaaagGCGaGuCaaGGuCu AAAUGAAU	4245
2641	UNAACUAU G CCUGCUAG	1563	CUAGCAGG GCcgaaagGCGaGuCaaGGuCu AUAGUUAA	4246
2645	CUAUGCCU G CUAGGUUU	1564	AAACCUNG GCcgaaagGCGaGuCaaGGuCu AGGCNUAG	4247
2677	AAAUAUUU G CCCUUAGA	1565	UCUAAGGG GCcgaaagGCGaGuCaaGGuCu AAAUAUUU	4248
2740	UUCCAGAC G CGACAUUA	1566	UNAUGUCG GCcgaaagGCGaGuCaaGGuCu GUCUGGAA	4249
2804	CACGUAGC G CCUCAUUU	1568	AAAUGAGG GCcgaaagGCGaGuCaaGGuCu GCUACGUG	4250
2814	CUCAUTUU G CGGGUCAC	1569	GUGACCCG GCcgaaagGCGaGuCaaGGuCu AAAAUGAG	4251
2946	UGGACCCU G CAUUCAAA	1572	UUUGAAUG GCcgaaagGCGaGuCaaGGuCu AGGGUCCA	4252
2990	CUCAACCC G CACAAGGA	1573	UCCUUGUG GCcgaaagGCGaGuCaaGGuCu GGGUUGAG	4253
3012	GGCCGGAC G CCAACAAG	1574	CUUGUUGG GCcgaaagGCGaGuCaaGGuCu GUCCGGCC	4254
3090	GCCCUCAC G CUCAGGGC	1575	GCCCUGAG GCcgaaagGCGaGuCaaGGuCu GUGAGGGC	4255
3113	ACAACUGU G CCAGCAGC	1576	GCUGCUGG GCcgaaagGCGaGuCaaGGuCu ACAGUUGU	4256
3132	cuccuccu e ccuccacc	1577	GGUGGAGG GCcgaaagGCGaGuCaaGGuCu AGGAGGAG	4257
51	AGGGCCCU G UACUTUCC	1578	GGAAAGUA GCcgaaagGCGaGuCaaGGuCu AGGGCCCU	4258
106	AGAAUACU G UCUCUGCC	1579	GGCAGAGA GCcgaaagGCGaGuCaaGGuCu AGUAUUCU	4259
148	GGGACCCU G UACCGAAC	1580	GUUCGGUA GCcgaaagGCGaGuCaaGGuCu AGGGUCCC	4260
198	CUGCUCGU G UUACAGGC	1581	GCCUGUAA GCcgaaagGCGaGuCaaGGuCu ACGAGCAG	4261
219	UUUUUCUU G UUGACAAA	1582	UJUGUCAA GCcgaaagGCGaGuCaaGGuCu AAGAAAAA	4262

1390	GCUAGGCU G UGCUGCCA	1617	UGGCAGCA GCcgaaagGCGaGuCaaGGuCu AGCCUAGC	4297
1425	CGUCCUUU G UUUACGUC	1618	GACGUAAA GCcgaaagGCGaGuCaaGGuCu AAAGGACG	4298
1508	CGCCUAUU G UACCGACC	1619	GGUCGGUA GCcgaaagGCGaGuCaaGGuCu AAUAGGCG	4299
1557	ccccenca e neccanca	1620	AGAAGGCA GCcgaaagGCGaGuCaaGGuCu AGACGGGG	4300
1581	CGGACCGU G UGCACUUC	1621	GAAGUGCA GCcgaaagGCGaGuCaaGGuCu ACGGUCCG	4301
1684	UCAGCAAU G UCAACGAC	1622	GUCGUUGA GCcgaaagGCGaGuCaaGGuCu AUUGCUGA	4302
1719	CAAAGACU G UGUGUUUA	1623	UAAACACA GCcgaaagGCGaGuCaaGGuCu AGUCUUUG	4303
1721	AAGACUGU G UGUUUAAU	1624	AUUAAACA GCcgaaagGCGaGuCaaGGuCu ACAGUCUU	4304
1723	GACUGUGU G UUUAAUGA	1625	UCAUUAAA GCcgaaagGCGaGuCaaGGuCu ACACAGUC	4305
1772	AGGUCUUU G UACUAGGA	1626	UCCUAGUA GCcgaaagGCGaGuCaaGGuCu AAAGACCU	4306
1785	AGGAGGCU G UAGGCAUA	1627	UAUGCCUA GCcgaaagGCGaGuCaaGGuCu AGCCUCCU	4307
1801	AAAUUGGU G UGUUCACC	1628	GGUGAACA GCcgaaagGCGaGuCaaGGuCu ACCAAUUU	4308
1803	AUUGGUGU G UUCACCAG	1629	CUGGUGAA GCcgaaagGCGaGuCaaGGuCu ACACCAAU	4309
1850	CAUCUCAU G UUCAUGUC	1630	GACAUGAA GCcgaaagGCGaGuCaaGGuCu AUGAGAUG	4310
1856	AUGUICAU G UCCUACUG	1631	CAGUAGGA GCcgaaagGCGaGuCaaGGuCu AUGAACAU	4311
1864	GUCCUACU G UUCAAGCC	1632	GGCUUGAA GCCgaaagGCGaGuCaaGGuCu AGUAGGAC	4312
1881	uccaageu e ueceuuse	1633	CCAAGGCA GCcgaaagGCGaGuCaaGGuCu AGCUUGGA	4313
1939	GAGCUUCU G UGGAGUUA	1634	UNACUCCA GCcgaaagGCGaGuCaaGGuCu AGAAGCUC	4314
2013	UCUGCUCU G UAUCAGGG	1635	CCCCGAUA GCcgaaagGCGaGuCaaGGuCu AGAGCAGA	4315
2045	GGAACAUU G UUCACCUC	1636	GAGGUGAA GCcgaaagGCGaGuCaaGGuCu AAUGUUCC	4316
2082	GCUAUUCU G UGUUGGGG	1637	CCCCAACA GCcgaaagGCGaGuCaaGGuCu AGAAUAGC	4317
2084	UAUUCUGU G UUGGGGUG	1638	CACCCCAA GCcgaaagGCGaGuCaaGGuCu ACAGAAUA	4318
2167	UCAGCUAU G UCAACGUU	1639	AACGUUGA GCcgaaagGCGaGuCaaGGuCu AUAGCUGA	4319
2205	CAACUAUU G UGGUUUCA	1640	UGAAACCA GCcgaaagGCGaGuCaaGGuCu AAUAGUUG	4320
2222	CAUTUCCU G UCUTACUU	1641	AAGUAAGA GCcgaaagGCGaGuCaaGGuCu AGGAAAUG	4321
2245	GAGAAACU G UUCUUGAA	1642	UUCAAGAA GCcgaaagGCGaGuCaaGGuCu AGUUUCUC	4322
2262	UAUUUGGU G UCUUUUGG	1643	CCAAAAGA GCcgaaagGCGaGuCaaGGuCu ACCAAAUA	4323
2274	UNUGGAGU G UGGAUUCG	1644	CGAAUCCA GCcgaaagGCGaGuCaaGGuCu ACUCCAAA	4324
2344	AAACUACU G UUGUUAGA	1645	UCUPACAA GCcgaaagGCGaGuCaaGGuCu AGUAGUUU	4325
2347	CUACUGUU G UUAGACGA	1646	UCGUCUAA GCcgaaagGCGaGuCaaGGuCu AACAGUAG	4326
2450	AUCUCAAU G UDAGUAUU	1647	ANUACUAA GCcgaaagGCGaGuCaaGGuCu AUUGAGAU	4327
2573	AGGACAUU G UUGAUAGA	1648	UCUAUCAA GCcgaaagGCGaGuCaaGGuCu AAUGUCCU	4328
2583	UGAUAGAU G UAAGCAAU	1649	AUUGCUUA GCcgaaagGCGaGuCaaGGuCu AUCUAUCA	4329
2594	AGCAAUUU G UGGGGCCC	1650	GGGCCCCA GCcgaaagGCGaGuCaaGGuCu AAAUUGCU	4330

4347 4348 4349 4350 4351 4352 4353 4354 4355 4356 4359 4360

AGUCUAGA GCcgaaagGCGaGuCaaGGuCu UCUGUGGU GUCCACCA GCcgaaagGCGaGuCaaGGuCu GAGUCUAG GAAGUCCA GCcgaaaqGCGaGuCaaGGuCu CACGAGUC AAGACACA GCcgaaagGCGaGuCaaGGuCu GGGUGUUC AAUUUUGG GCcgaaagGCGaGuCaaGGuCu CAAGACAC AUTUGGGA GCcgaaagGCGaGuCaaGGuCu UGCGAAUU GUGAGUGA GCcgaaagGCGaGuCaaGGuCu UGGAGAUU AGCGAUAA GCcgaaagGCGaGuCaaGGuCu CAGGACAA AUAAAACG GCcgaaagGCGaGuCaaGGuCu CGCAGACA UGAUAAAA GCcqaaaqGCGaGuCaaGGuCu GCCGCAGA CAGAAGAA GCcgaaagGCGaGuCaaGGuCu CAACAAGA SCAACAUA GCcgaaagGCGaGuCaaGGuCu CUUGAUAG GUCCGGUG GCcgaaagGCGaGuCaaGGuCu UGGUUGUU JGCGAAAG GCcgaaagGCGaGuCaaGGuCu CCAAGAUG 3AGGCCCA GCcgaaagGCGaGuCaaGGuCu UCCCAUAG SACUGAGG GCcgaaagGCGaGuCaaGGuCu CCACUCCC BAAACGGA GCcqaaagGCGaGuCaaGGuCu UGAGGCCC

1668 1669 1670 1672 1674 1677

1671 1673 1675 1676 1678 1679 1680 1681 1682

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ACCACAGA G UCUAGACU CUAGACUC G UGGUGGAC GACUCGUG G UGGACUUC GAACACCC G UGUGUCUU GUGUCUUG G CCAAAAUU AAUTOGCA G UCCCAAAU AAUCUCCA G UCACUCAC unancena a unancaeu UGUCUACA & CAUUUUAU ucueceec e ununauca actualing a uncuncus CUAUCAAG G UAUGUUGC CAUCINGG G CUMOGCA CUAUGGGA G UGGGCCUC GGGAGUGG G CCUCAGUC GGGCCUCA G UCCGUUUC

4357 4358 4361

AGGACAAA GCccaaaaGCGaGuCaaGGuCu GGGCAACA

uennecco e nondocon AACAACCA G CACCGGAC 1683 1684

85 120 196 205 210 248 258 261 295 305 318 332 368 390 392 442 461 472 206 625 648 652 658

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792	THIOSTORIES C CONCOCUE	1685	AAGAGAAA GCCGGaagGCGaGuCaaGGuCu GGACUGAG	4365
3	000000000000000000000000000000000000000	1000	consistence of the same of the	1300
611	UUGGCUCA G UUUACUAG	1687	CUAGUAAA GCcgaaagGCGaGuCaaGGuCu UGAGCCAA	4367
685	GUUDACUA G UGCCAUUU	1688	AAAUGGCA GCcgaaagGCGaGuCaaGGuCu UAGUAAAC	4368
669	unuennew a naemocan	1689	ACGAACCA GCcgaaagGCGaGuCaaGGuCu UGAACAAA	4369
702	GUUCAGUG G UUCGUAGG	1690	CCUACGAA GCcgaaagGCGaGuCaaGGuCu CACUGAAC	4370
206	AGUGGUUC G UAGGGCUU	1691	AAGCCCUA GCcgaaagGCGaGuCaaGGuCu GAACCACU	4371
711	UUCGUAGG G CUUUCCCC	1692	GGGGAAAG GCcgaaagGCGaGuCaaGGuCu CCUACGAA	4372
729	ACUGUCUG G CUUUCAGU	1693	ACUGAAAG GCcgaaagGCGaGuCaaGGuCu CAGACAGU	4373
736	GGCUUUCA G UUAUAUGG	1694	CCAUAUNA GCcgaaagGCGaGuCaaGGuCu UGNAAGCC	4374
753	AUGAUGUG G UUUUGGGG	1695	CCCCAAAA GCcgaaagGCGaGuCaaGGuCu CACAUCAU	4375
762	nonneege e connenco	1696	AGACUUGG GCcgaaagGCGaGuCaaGGuCu CCCCAAAA	4376
167	GGGGCCAA G UCUGUACA	1691	UGUACAGA GCcgaaagGCGaGuCaaGGuCu UUGGCCCC	4377
785	CAUCUUGA G UCCCUUUA	1698	UAAAGGGA GCcgaaagGCGaGuCaaGGuCu UCAAGAUG	4378
826	GUCUTUGG G UNUACAUT	1699	AAUGUAUA GCcgaaagGCGaGuCaaGGuCu CCAAAGAC	4379
898	AAUUGGGA G UUGGGGCA	1700	UGCCCCAA GCcgaaagGCGaGuCaaGGuCu UCCCAAUU	4380
904	GAGUUGGG G CACAUUGC	1701	GCAAUGUG GCcgaaagGCGaGuCaaGGuCu CCCAACUC	4381
971	GUAAACAG G CCUAUUGA	1702	UCAAUAGG GCcgaaagGCGaGuCaaGGuCu CUGUUUAC	4382
987	AUUGGAAA G UAUGUCAA	1703	UUGACAUA GCcgaaagGCGaGuCaaGGuCu UUUCCAAU	4383
1006	AAUUGUGG G UCUUUUGG	1704	CCAAAAGA GCcgaaagGCGaGuCaaGGuCu CCACAAUU	4384
1016	cumuded e unueccec	1705	GCGGCAAA GCcgaaagGCGaGuCaaGGuCu CCCAAAAG	4385
1080	GCAUACAA G CAAAACAG	1706	CUGUUUUG GCcgaaagGCGaGuCaaGGuCu UUGUAUGC	4386
1089	CAAAACAG G CUUUUACU	1707	AGUAAAAG GCcgaaagGCGaGuCaaGGuCu CUGUUUUG	4387
1116	CUUACAAG G CCUUUCUA	1708	UAGAAAGG GCcgaaagGCGaGuCaaGGuCu CUUGUAAG	4388
1126	CUUUCUAA G UAAACAGU	1709	ACUGUTUA GCcgaaagGCGaGuCaaGGuCu UUAGAAAG	4389
1133	AGUAAACA G UAUGUGAA	1710	UUCACAUA GCcgaaagGCGaGuCaaGGuCu UGUUUACU	4390
1152	UNUACCCC G UNGCUCGG	1711	CCGAGCAA GCcgaaagGCGaGuCaaGGuCu GGGGUAAA	4391
1160	gundence G	1712	GGCCGUUG GCcgaaagGCGaGuCaaGGuCu CGAGCAAC	4392
1166	CGGCAACG G CCUGGUCU	1713	AGACCAGG GCcgaaagGCGaGuCaaGGuCu CGUJGCCG	4393
1171	ACGGCCUG G UCUAUGCC	1714	GGCAUAGA GCcgaaagGCGaGuCaaGGuCu CAGGCCGU	4394
1182	UAUGCCAA G UGUUUGCU	1715	AGCAAACA GCcgaaagGCGaGuCaaGGuCu UUGGCAUA	4395
1207	CCCCACUG G UUGGGGCU	1716	AGCCCCAA GCcgaaagGCGaGuCaaGGuCu CAGUGGGG	4396
1213		4141	UGGCCAAG GCcgaaagGCGaGuCaaGGuCu CCCAACCA	4397
1218	GGGGCUUG G CCAUAGGC	1718	GCCUAUGG GCcgaaagGCGaGuCaaGGuCu CAAGCCCC	4398

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1223		1/13	GCOGADISG GCCGaaagaccaacaccac CDADGGCC	4333
1232	GGCCAUCA G	1720	CGCAUGCG GCcgaaagGCGaGuCaaGGuCu UGAUGGCC	4400
1240	GCGCAUGC G UGGAACCU	1721	AGGUUCCA GCcgaaagGCGaGuCaaGGuCu GCAUGCGC	4401
1287	AACUCCUA G CCGCUUGU	1722	ACAAGOOG GCcgaaagGCGaGuCaaGGuCu UAGGAGUU	4402
1306	UGCUCGCA G CAGGUCUG	1723	CAGACCUG GCcgaaagGCGaGuCaaGGuCu UGCGAGCA	4403
1310	CGCAGCAG G UCUGGGGC	1724	GCCCCAGA GCcgaaagGCGaGuCaaGGuCu CUGCUGCG	4404
1317	GGUCUGGG G CAAAACUC	1725	GAGUIUUG GCcgaaagGCGaGuCaaGGuCu CCCAGACC	4405
1347	AUTCUGUC G UGCUCUCC	1726	GGAGAGCA GCcgaaagGCGaGuCaaGGuCu GACAGAAU	4406
1379	UUUCCAUG G CUGCUAGG	1727	CCUAGCAG GCcgaaagGCGaGuCaaGGuCu CAUGGAAA	4407
1387	ecuecuae e cueuecue	1728	CAGCACAG GCcgaaagGCGaGuCaaGGuCu CUAGCAGC	4408
1418	CGCGGGAC G UCCUUUGU	1729	ACAAAGGA GCcgaaagGCGaGuCaaGGuCu GUCCCGCG	4409
1431	UNGUUUAC G UCCCGUCG	1730	CGACOGGA GCcgaaagGCGaGuCaaGGuCu GUAAACAA	4410
1436	UACGUCCC G UCGCCGCU	1731	AGOGCCGA GCcgaaagGCGaGuCaaGGuCu GGGACGUA	4411
1440	UCCCGUCG G CGCUGAAU	1732	AUUCAGCG GCcgaaagGCGaGuCaaGGuCu CGACGGGA	4412
1471	cucceas a coscunas	1733	CCAAGCGG GCcgaaagGCGaGuCaaGGuCu CCCGGGAG	4413
1481	OGCUUGGG G CUCUACOG	1734	CGGUAGAG GCcgaaagGCGaGuCaaGGuCu CCCAAGCG	4414
1517	UACCGACC G UCCACGGG	1735	CCCGUGGA GCcgaaagGCGaGuCaaGGuCu GGUCGGUA	4415
1526	UCCACGGG G CGCACCUC	1736	GAGGUGCG GCcgaaagGCGaGuCaaGGuCu CCCGUGGA	4416
1553	GACTUCCCC G UCUGUGCC	1737	GGCACAGA GCcgaaagGCGaGuCaaGGuCu GGGGAGUC	4417
1579	GCCGGACC G UGUGCACU	1738	AGUGCACA GCcgaaagGCGaGuCaaGGuCu GGUCCGGC	4418
1605	CUCUGCAC G UCSCAUGG	1739	CCAUGCGA GCcgaaagGCGaGuCaaGGuCu GUGCAGAG	4419
1622	AGACCACC G UGAACGCC	1740	GGCGUUCA GCcgaaagGCGaGuCaaGGuCu GGUGGUCU	4420
1649	_	1741	AUGCAAGA GCcgaaagGCGaGuCaaGGuCu CUUGGGCA	4421
1679	GACUUUCA G CAAUGUCA	1742	UGACAUUG GCcgaaagGCGaGuCaaGGuCu UGAAAGUC	4422
1703	ACCUUGAG G CAUACUUC	1743	GAAGUAUG GCcgaaagGCGaGuCaaGGuCu CUCAAGGU	4423
1732	UUUAAUGA G UGGGAGGA	1744	UCCUCCCA GCcgaaagGCGaGuCaaGGuCu UCAUUAAA	4424
1741	UGGCAGGA G UUGGGGGA	1745	UCCCCCAA GCcgaaagGCGaGuCaaGGuCu UCCUCCCA	4425
1754	GGGAGGAG G UUAGGUUA	1746	UAACCUAA GCcgaaagGCGaGuCaaGGuCu CUCCUCCC	4426
1759	GAGGUUAG G UUAAAGGU	1747	ACCUUDAA GCcgaaagGCGaGuCaaGGuCu CUAACCUC	4427
1766	GGUUAAAG G UCUUUGUA	1748	UACAAAGA GCcgaaagGCGaGuCaaGGuCu CUUUAACC	4428
1782	ACUAGGAG G CUGUAGGC	1749	GCCUACAG GCcgaaagGCGaGuCaaGGuCu CUCCUAGU	4429
1789	GGCUGUAG G CAUAAAUU	1750	AAUUUAUG GCcgaaagGCGaGuCaaGGuCu CUACAGCC	4430
1799	Ľ	1751	UGAACACA GCcgaaagGCGaGuCaaGGuCu CAAUUUAU	4431
1811	GUUCACCA G CACCAUGC	1752	GCAUGGUG GCcgaaagGCGaGuCaaGGuCu UGGUGAAC	4432

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Occupant Controlled Contr	1870	CUGUUCAA G CCUCCAAG	1753	CUUGGAGG GCcgaaagGCGaGuCaaGGuCu UUGAACAG	4433
UCUNOSADI 6 USCOUNDED 1755	1878	GCCUCCAA G CUGUGCCU	1754	AGGCACAG GCcgaaagGCGaGuCaaGGuCu UUGGAGGC	4434
CUUDAGAGO (1756 AUDRACCC (175	1890	O	1755	CAAAGCCA GCcgaaagGCGaGuCaaGGuCu CCAAGGCA	4435
AUTORACCE G UNIDADAO 1755	1893	O	1756	CCCCAAAG GCcgaaagGCGaGuCaaGGuCu CACCCAAG	4436
AUUTOGAG C ULUNAAGA 1755 AUUTOGAG C ULUCUUCU 1756 GUCUULAA U UUCUCCCC 1766 GUCUULAA U UUCUCCCC 1766 GUCUULAA U UUCUCCCA 1765 GUCUULAA U UUCUCCCA 1765 GUCUULAA U UUCUCCCA 1765 GUCUULAA U UUCUCCCA 1766 GUGUULCG C ULUAUUCU 1766 UGAACUAC G CAUCUCCC 1766 GUGUULCG C ULUAUUCU 1766 GUGUULCG C ULUAUUCU 1776 GUGUULCG C ULUAUUCU 1777 AUUTUCCA U UUCUCCAU 1777 AUUTUCCA U UUCUCCAU 1777 AUUTUCCA U UUCUCCAU 1777 AUUTUCCA U UUCUCCAU 1776 AUUTUCCA U UUCUCCAU 1777 AUUTUCCA U UUCUCCAU 1777 AUUTUCCA U UUCUCCAU 1777 AUUTUCCA U UUCUCCAU 1776 AUUTUCCA U UUCUCCAU 1776 AUUTUCCA U UUCUCCAU 1777 AUUTUCCA U UUCUCCAU 1776 AUUTUCCA U UUCUCCAU 1777 AUUTUCCA U UUCUCCAU 1776 AUUTUCCA U UUCUCCAU 1776 AUUTUCCAU U 1776 AUUTUCCAU U 1776 AUUTUCCAU 17	1901	O	1757		4437
AMUNDAR G CURCIOUS 1755 HUCORGOSG G COUDAGA 1765 ACCOUNAGA G UNCUCCOS 1762 COCACCAG G CANCOUS 1765 GGACACAG G CANCOUS 1765 GGACACAG G CANCOUS 1765 GGACACAG G CANCOUS 1765 GGACACAG G CANCOUS 1766 GGACACAG G CANCOUS 1766 GGACACAG G CANCOUS 1766 GGACACAG G CANCOUS 1776 GGACACAG G CANCOUS 1776 AUGUSTOR G CANCOUS 1776 AGANANUM G UNGUCAU 1777 ACUNDOS G CANCOCC 1778 ACACAGAG G UNGCACU 1777 ACACAGAGG G CONGOCC 1778 ACACAGAGG G CONG	1917	AUUGACCC G UNUAAAGA	1758	UCUUUAUA GCcgaaagGCGaGuCaaGGuCu GGGUCAAU	4438
UCCUMING UNIVERSE	1933	AAUUUGGA G CUUCUGUG	1759	CACAGAAG GCcgaaagGCGaGuCaaGGuCu UCCAAAUU	4439
AUCOGOGO G COCUNADA O 1761 GCCULLARA G UDICOCORA DECALLOCADO G DACIDORO DECALDOCO G DACIDORO DECALDOCORO	1944	UCUGUGGA G UDACUCUC	1760	GAGAGUAA GCcgaaagGCGaGuCaaGGuCu UCCACAGA	4440
ACCOMANG CUCCOGA 1765	2023		1761	CUCUAAGG GCcgaaagGCGaGuCaaGGuCu CCCCCGAU	4441
ACCIONAGE G CAUCIONES 1765 CONCICION G CAUDICUM 1765 GIGURIOLES G CAUDICUM 1765 GIGURIOLES G CAUDICUM 1765 GIGURIOLES G CAUDICUM 1767 GIGURIOLES G GAUDICUM 1767 GIGURIOLES G GAUDICUM 1767 GIGURIOLES G GAUDICUM 1776 AUDICUM C CAUDICUM 1776 AUDICUM G CAUDICUM 1777 AUDICUM G GAUDICUM 1776 CUMULOS G GAUDICUM 1776 AUDICUM G GAUDICUM 1776 CUMULOS G GAUDICUM 1776 AUDICUM G GAUDICUM 1776 AUDICUM G GAUDICUM 1776 AUDICUM G GAUDICUM 1776 AUDICUM G GAUDICUM 1778	2031	GCCUUAGA G UCUCCGGA	1762	UCCGGAGA GCcgaaagGCGaGuCaaGGuCu UCUAAGGC	4442
CONTUCTOR CANACIDA 1764	2062	O	1763	CCUGAGUG GCcgaaagGCGaGuCaaGGuCu CGUAUGGU	4443
UNAGORA G CUNTUCUS 1765 UNAGORA G CUNTUCUS 1765 UNAGORA G CONTUCUS 1765 UNAGORA G CONTUCUS 1765 UNAGORA G CONTUCUS 1765 UNAGORA G UNAG	2070	GCACUCAG G CAAGCUAU	1764	AUAGCUUG GCcgaaagGCGaGuCaaGGuCu CUGAGUGC	4444
Occasiona University Univ	2074	UCAGGCAA G CUAUUCUG	1765	CAGAAUAG GCcgaaagGCGaGuCaaGGuCu UUGCCUGA	4445
UGGANGUA G UNANUGAN 1767 UGGANGUA G UNGGANGUA G	2090	GUGUUGGG G UGAGUUGA	1766	UCAACUCA GCcgaaagGCGaGuCaaGGuCu CCCAACAC	4446
UAANUUR C CANCURS 1768	2094	O	1767	UUCAUCAA GCcgaaagGCGaGuCaaGGuCu UCACCCCA	4447
CCACCUGG G UGGGAAGG 1776 GOUGGAAL O LOUGGAGG 1777 AGANCA C CAUCCAGG 1777 AGANCA C CAUCCAGG 1777 AGANCA C CAUCCAGG 1777 AGANCA C CAUCCAGG 1777 AGANCAGG C CAUCCAGG 1777 AGANCAGG G UGGGAAGA 1776 AGANCAGG G UGGGAAGA 1776 AGANCAGG G CAUCCAGG 1778 AGANCAGG G CAUCCAGG 1778 AGANCAGG G CAUCCAGG 1778 AGANCAGGG G GUGGAAGA 1778 AGANCAGGG G GUGGCAGG 1778 AGANCAGGG G GUGGAGGG 1778 AGANCAGGG G GUGGAGGG 1778 AGANCAGGG G GUGGAGGG 1778 AGANCAGGG G GUGGAGGG 1778 AGANCAGGG G GUGGGG 1778 AGANCAGGG G GUGGAGGG 1778 AGANCAGGG G GUGGGG 1778 AGANCAGGG G G GUGGGG 1778 AGANCAGG G G GUGGGG 1778 AGANCAGGG G G GGGGGG 1778 AGANCAGGG G G GGGGGG 1778 AGANCAGGG G G G GGGGGG 1778 AGANCA	2107	v	1768	CCAGGUGG GCcgaaagGCGaGuCaaGGuCu UAGAUUCA	4448
Address Control	2116		1769	ACUUCCCA GCcgaaagGCGaGuCaaGGuCu CCAGGUGG	4449
Advances a cytochesia Advances a consultation of consultation of consultation of cytochesia and	2123	GGUGGGAA G UAAUUUGG	1770	CCAPAUJA GCcgaaagGCGaGuCaaGGuCu UUCCCACC	4450
AUTHORIUS G VOCACION AUTHORIUS G CONTROL G CUINGUICA 1773	2140	AAGAUCCA G CAUCCAGG	1771	CCUGGAUG GCcgaaagGCGaGuCaaGGuCu UGGAUCUU	4451
AUMAUNA G UGAGOLAN 2773 AGURGICA, G UGARANA 2774 AUGUCA, G UGARANA 2777 AUGUCA, G UGARANA 2777 AUGUCA, G UGARANA 2777 AUGUCA, G UGARANA 2777 AUGUCA, G UGAGOLA 2777 AGURGA, G UGCCCUA 2778 AGARAGO, G UCCCCUA 2778 AGAGOLA, G UGCCCUA 2778 AGAGOLA, G UCCCUA 277	2155	O	1772	GCUGACUA GCcgaaagGCGaGuCaaGGuCu UAAUUCCC	4452
AURIOLOS G CUCIDADAS DI AURIOLOS DE AURIOLOS G CUCIDADAS DI AURIOLOS G CUCIDADAS DI AURIOLOS G CUCIDADAS DI AURIOLOS G CUCIDADAS DI AURIOLOS G CUCIDADOS G CUCIDADOS G CONGRADAS G CONGRAD	2158	O	1773	AUAGCUGA GCcgaaagGCGaGuCaaGGuCu UACUAAUU	4453
MUNICACA G UNIVARIAND 1775	2162	O	1774	UGACAUAG GCCgaaagGCGaGuCaaGGuCu UGACUACU	4454
UANDAGO & CUDADADA 1776 CURJUDUS G UUDCACAU 1777 CURJUDUS G CORDADAC 1778 CURJUDUS G CORDADAC 1779 CURJUDUS G CORDADAC 1779 CURJUDUS G CORDADAC 1779 CURJUDUS G CORDADAC 1782 CARAGEON G UUCCCUMG 1784	2173	O	1775	CAUAUUAA GCcgaaagGCGaGuCaaGGuCu GUUGACAU	4455
CHAUGUGG G UGUCACAU ACUUUUGG G CRAGAAAC AAUANUUG G UGUCAUU 1779 CUUUGGG G UGUCAUU 1779 CASAACAG G UGCCUAG AAACCAG G UCCCUAG AAACCAG G UCCCUAG AAACCAG G UCCCUAG AAACCAG G UCCCUAG AAACCAG G UCCCAG AAA	2183	nvanance e convava	1776	UUUUUAGG GCcgaaagGCGaGuCaaGGuCu CCAUAUUA	4456
ADMINING G CRABAAC 1778 ADMINING G UNICOTUT 1779 CUITIDIGAS G UNICOTUT 1779 CARAGORA G UNICOTUT 1760 AGACCING O UNICOTUT 1760 AGACCING O UNICOTUT 1778 CARAGORA G UNICOTUT 1778 CARAGORA G UNICOTUT 1778 CARAGORA G UNICOTUT 1778	2208	CUAUUGUG G UUUCACAU	1777	AUGUGAAA GCcgaaagGCGaGuCaaGGuCu CACAAUAG	4457
ANDMUNG UNICULUUU 1779 AAAAAAA CICcgaaagGCGaaCcaaccaaccaaccaaccaaccaaccaaccaacca	2235		1778	GUUUCUCG GCcgaaagGCGaGuCaaGGuCu CCAAAAGU	4458
COUNDIDADA U USUGRAUU 7.1900 AMUCOCON G COEgoanagiCONGUICARAGOAU ACADAGNIG G DEGITICOC 7.1721 COUNCECHO G COEgoanagiCONGUICARAGOAU ACACCANIG G UCCCUUDO 7.1722 CUINGECHO G COEgoanagiCONGUICARAGOAU ACACCANIG G UCCCUUDO 7.1723 CAUNDIAGA G COEgoanagiCONGUICARAGOAU AUGUCOCOC G UCCCUANA 7.784 AUGUCOR AG COEgoanagiCONGUICARAGOAU ACADAULM 0 HUNICOUT 7.785 AAADAMAU, G COEgoanagiCONGUICARAGOAU CAUNDIAGOAU 1 VAUNICOUT 7.786 AUGUCOCO, G COEGOANAGICORAGOAU CAUNDIAGOAU 1 VAUNICOUT 7.786 AUGUCOCO, G COEGOANAGICORAGOAU CAUNDIAGOAU 1 VAUNICOUT 7.786 AUGUCOCO, G COEGOANAGICORAGOAU COEGOANAGICO 7.786 AUGUCOUT 7.786 AUGUCOCO, G COEGOANAGICORAGOAU COEGOANAGICO 7.786 AUGUCOUT 7.786 AUGUCOCO, G COEGOANAGICO 7.786 AUGUCOUT 7.786 AUGU	2260	AAUAUUUG G UGUCUUUU	1779	AAAAGACA GCcgaaagGCGaGuCaaGGuCu CAAAUAUU	4459
ACCAMANG G CAGGILCCC 1781 AGAGGGAG G UCCCCUMG 1782 AGACGAGA G UCCCAMA 1783 AUCGCGG G UCCCAGAA 1784 CAAUGUMA G UNGCAGAT 1786 CAAUGUMA G UNGCAGAAA 1786	2272	o	1780	AAUCCACA GCcgaaagGCGaGuCaaGGuCu UCCAAAAG	4460
AGAGGCAG G UCCCCUAG 1782 AGAGGAGG G UCCCCUAG 1783 AUGGCGG G UGCCAAU 1784 CAAUGUUG G UAUUCCUU 1785 CAAUGUUG G UAUUCCUU 1786	2360	O	1781	GGGACCUG GCcgaaagGCGaGuCaaGGuCu CUCUUCGU	4461
AGACGAAG G UCUCAAUC 1783 AUGGCGC G UGGCAGAA 1784 CAAUGUUA G UAUUCCUU 1785 CACAUAAG UGGGAAAC 1786	2364	AGAGGCAG G UCCCCUAG	1782	CUAGGGGA GCcgaaagGCGaGuCaaGGuCu CUGCCUCU	4462
AUCGCCGC G UCGCAGAA 1784 CAAUGUUA G UAUUCCUU 1785 CACAUAAG G UGGGAAAC 1786	2403	AGACGAAG G UCUCAAUC	1783	GAUUGAGA GCcgaaagGCGaGuCaaGGuCu CUUCGUCU	4463
CACAUGUUA G UNGGAAAC 1786 GUUUCCCA GCGGAAAGGGCGAGUCAAGGAUCA CACAUAAG G UNGGAAAC 1786 GUUUCCCA GCGGAAAGGGCGAGUCAAGGGCAA	2417	AUCGCCGC G UCGCAGAA	1784	UUCUGCGA GCcgaaagGCGaGuCaaGGuCu GCGGCGAU	4464
CACAUAAG G UGGGAAAC 1786	2454	ღ	1785	AAGGAAUA GCcgaaagGCGaGuCaaGGuCu UAACAUUG	4465
	2474	O	1786	GUUUCCCA GCcgaaagGCGaGuCaaGGuCu CUUAUGUG	4466

2491	UUVACGGG G CUUUAUUC	1787	GAAUAAAG GCcgaaagGCGaGuCaaGGuCu CCCGUAAA	4467
2507	CUUCUACG G DACCUUGC	1788	GCAAGGUA GCcgaaagGCGaGuCaaGGuCu CGUAGAAG	4468
2530	CCUAAAUG G CAAACUCC	1789	GGAGUUUG GCcgaaagGCGaGuCaaGGuCu CAUUUAGG	4469
2587	AGAUGUAA G CAAUUUGU	1790	ACAAAUUG GCcgaaagGCGaGuCaaGGuCu UUACAUCU	4470
2599	UUUGUGGG G CCCCUUAC	1791	GUAAGGGG GCcgaaagGCGaGuCaaGGuCu CCCACAAA	4471
5609	CCCUUACA G UAAAUGAA	1792	UUCAUUUA GCcgaaagGCGaGuCaaGGuCu UGUAAGGG	4472
2650	ccugcuag g ununaucc	1793	GGAUAAAA GCcgaaagGCGaGuCaaGGuCu CUAGCAGG	4473
2701	AUCAAACC G UAUUAUCC	1794	GGNUAAUA GCcgaaagGCGaGuCaaGGuCu GGUUUGAU	4474
2713	UNUCCAGA G UNUGUAGU	1795	ACUACAUA GCogaaagGCGaGuCaaGGuCu UCUGGAUA	4475
2720	AGUAUGUA G UUAAUCAU	1796	AUGAUDAA GCcgaaagGCGaGuCaaGGuCu UACAUACU	4476
2768	UNUGGAAG G CGGGGAUC	1797	GAUCCCCG GCcgaaagGCGaGuCaaGGuCu CUUCCAAA	4477
2791	AAAAGAGA G UCCACACG	1798	CGUGUGGA GCcgaaagGCGaGuCaaGGuCu UCUCUUUU	4478
2799	GUCCACAC G DAGCGCCU	1799	AGGCGCUA GCcgaaagGCGaGuCaaGGuCu GUGUGGAC	4479
2802	CACACGUA G CGCCUCAU	1800	AUGAGGCG GCcgaaagGCGaGuCaaGGuCu UACGUGUG	4480
2818	UUUUGCGG G UCACCAUA	1801	UAUGGUGA GCcgaaagGCGaGuCaaGGuCu CCGCAAAA	4481
2848	GAUCUACA G CAUGGGAG	1802	CUCCCAUG GCcgaaagGCGaGuCaaGGuCu UGUAGAUC	4482
2857	CAUGGGAG G UUGGUCUU	1803	AAGACCAA GCcgaaagGCGaGuCaaGGuCu CUCCCAUG	4483
2861	GGAGGUUG G UCUUCCAA	1804	UUGGAAGA GCcgaaagGCGaGuCaaGGuCu CAACCUCC	4484
2881	UCGAAAAG G CAUGGGGA	1805	UCCCCAUG GCcgaaagGCGaGuCaaGGuCu CUUUUCGA	4485
2936	GAUCAUCA G UNGGACCC	1806	GGGUCCAA GCcgaaagGCGaGuCaaGGuCu UGAUGAUC	4486
2955	CAUUCAAA G CCAACUCA	1807	UGAGUUGG GCcgaaagGCGaGuCaaGGuCu UUUGAAUG	4487
2964	CCAACUCA G UNAAUCCA	1808	UGGAUUUA GCcgaaagGCGaGuCaaGGuCu UGAGUUGG	4488
3008	GACAACUG G CCGGACGC	1809	GCGUCCGG GCcgaaagGCGaGuCaaGGuCu CAGUUGUC	4489
3021	CCAACAAG G UGGGAGUG	1810	CACUCCCA GCcgaaagGCGaGuCaaGGuCu CUUGJUGG	4490
3027	ACCUGGGA G UGGGAGCA	1811	UGCUCCCA GCcgaaagGCGaGuCaaGGuCu UCCCACCU	4491
3033	GAGUGGGA G CAUUCGGG	1812	CCCGAAUG GCcgaaagGCGaGuCaaGGuCu UCCCACUC	4492
3041	GCAUUCGG G CCAGGGUU	1813	AACOCUGG GCogaaagGCGaGuCaaGGuCu CCGAAUGC	4493
3047	вавссива в пислессе	1814	GGGGUGAA GCcgaaagGCGaGuCaaGGuCu CCUGGCCC	4494
3077	cuanuage a negracco	1815	GGGCUCCA GCcgaaagGCGaGuCaaGGuCu CCCAACAG	4495
3082	GGGGUGGA G CCCUCACG	1816	CGUGAGGG GCcgaaagGCGaGuCaaGGuCu UCCACCCC	4496
3097	CGCUCAGG G CCUACUCA	1817	UGAGUAGG GCcgaaagGCGaGuCaaGGuCu CCUGAGCG	4497
3117	cususcea s easenceu	1818	AGGAGCUG GCcgaaagGCGaGuCaaGGuCu UGGCACAG	4498
3120	UGCCAGCA G CUCCUCCU	1819	AGGAGGAG GCcgaaagGCGaGuCaaGGuCu UGCUGGCA	4499
3146	ACCAAUGG G CAGUCAGG	1820	CCUGACUG GCcgaaagGCGaGuCaaGGuCu CGAUUGGU	4500

Table 40

3149	AAUCGGCA G UCAGGAAG	1821	CUUCCUGA GCcgaaagGCGaGuCaaGGuCu UGCCGAUU	4501
158	3158 UCAGGAAG G CAGCCUAC	1822	GUAGGCUG GCcgaaagGCGaGuCaaGGuCu CUUCCUGA	4502
161	3161 GGAAGGCA G CCUACUCC	1823	GGAGUAGG GCcgaaagGCGaGuCaaGGuCu UGCCUUCC	4503
2204	0.000,400 0 0.00000000	3	THE PERSON NAMED IN COLUMN TO PERSON NAMED I	1

Input Sequence = AP100308. Cut Site = YG/M or UG/U. Stem Length = 8 . Core Sequence = GCogaaagGCGaGCaaGGuCaAF100308 (Hepatitis B virus strain 2-18, 3215 bp)

Table 41

Table 41: Human HBV DNAzyme and Substrate Sequence

Pos	Substrate	Seq ID	DNAzyme	Rz Seq
508	CAACCAGC A CCGGACCA	833	TGGTCCGG GGCTAGCTACAACGA GCTGGTTG	4505
1632	GAACGCCC A CAGGAACC	1096	GGTTCCTG GGCTAGCTACAACGA GGGCGTTC	4506
2992	CAACCCGC A CAAGGACA	1376	TGTCCTTG GGCTAGCTACAACGA GCGGGTTG	4507
61	ACUUUCCU G CUGGUGGC	1448	GCCACCAG GGCTAGCTACAACGA AGGAAAGT	4508
94	UGAGCCCU G CUCAGAAU	1450	ATTCTGAG GGCTAGCTACAACGA AGGGCTCA	4509
112	CUGUCUCU G CCAUAUCG	1451	CGATATGG GGCTAGCTACAACGA AGAGACAG	4510
169	AGAACAUC G CAUCAGGA	1454	TCCTGATG GGCTAGCTACAACGA GATGTTCT	4511
192	GGACCCCU G CUCGUGUU	1455	AACACGAG GGCTAGCTACAACGA AGGGGTCC	4512
315	CAAAAUUC G CAGUCCCA	1457	TGGGACTG GGCTAGCTACAACGA GAATTTTG	4513
374	UGGUUAUC G CUGGAUGU	1458	ACATCCAG GGCTAGCTACAACGA GATAACCA	4514
387	AUGUGUCU G CGGCGUUU	1459	AAACGCCG GGCTAGCTACAACGA AGACACAT	4515
410	CUUCCUCU G CAUCCUGC	1460	GCAGGATG GGCTAGCTACAACGA AGAGGAAG	4516
417	UGCAUCCU G CUGCUAUG	1461	CATAGCAG GGCTAGCTACAACGA AGGATGCA	4517
420	AUCCUGCU G CUAUGCCU	1462	AGGCATAG GGCTAGCTACAACGA AGCAGGAT	4518
425	GCUGCUAU G CCUCAUCU	1463	AGATGAGG GGCTAGCTACAACGA ATAGCAGC	4519
468	GGUAUGUU G CCCGUUUG	1464	CAAACGGG GGCTAGCTACAACGA AACATACC	4520
518	CGGACCAU G CAAAACCU	1465	AGGTTTTG GGCTAGCTACAACGA ATGGTCCG	4521
527	CAAAACCU G CACAACUC	1466	GAGTTGTG GGCTAGCTACAACGA AGGTTTTG	4522
538	CAACUCCU G CUCAAGGA	1467	TCCTTGAG GGCTAGCTACAACGA AGGAGTTG	4 5 2 3
569	CUCAUGUU G CUGUACAA	1468	TTGTACAG GGCTAGCTACAACGA AACATGAG	4524
596	CGGAAACU G CACCUGUA	1469	TACAGGTG GGCTAGCTACAACGA AGTTTCCG	4525
631	GGGCUUUC G CAAAAUAC	1470	GTATTTTG GGCTAGCTACAACGA GAAAGCCC	4526
687	UUACUAGU G CCAUUUGU	1471	ACAAATGG GGCTAGCTACAACGA ACTAGTAA	4527
795	CCCUUUAU G CCGCUGUU	1474	AACAGCGG GGCTAGCTACAACGA ATAAAGGG	4528
798	UUUAUGCC G CUGUUACC	1475	GGTAACAG GGCTAGCTACAACGA GGCATAAA	4529
911	GGCACAUU G CCACAGGA	1476	TCCTGTGG GGCTAGCTACAACGA AATGTGCC	4530
1020	UGGGGUUU G CCGCCCCU	1479	AGGGGCGG GGCTAGCTACAACGA AAACCCCA	4531
1023	GGUUUGCC G CCCCUUUC	1480	GAAAGGG GGCTAGCTACAACGA GGCAAACC	4532
1034	CCUUUCAC G CAAUGUGG	1481	CCACATTG GGCTAGCTACAACGA GTGAAAGG	4533
1050	GAUAUUCU G CUUUAAUG	1482	CATTAAAG GGCTAGCTACAACGA AGAATATC	4534
1058	GCUUUAAU G CCUUUAUA	1483	TATAAAGG GGCTAGCTACAACGA ATTAAAGC	4535
1068	CUUUAUAU G CAUGCAUA	1484	TATGCATG GGCTAGCTACAACGA ATATAAAG	4536
1072	AUAUGCAU G CAUACAAG	1485	CTTGTATG GGCTAGCTACAACGA ATGCATAT	4537
1103	ACUUUCUC G CCAACUUA	1486	TAAGTTGG GGCTAGCTACAACGA GAGAAAGT	4538
1155	ACCCCGUU G CUCGGCAA	1488	TTGCCGAG GGCTAGCTACAACGA AACGGGGT	4539
1177	UGGUCUAU G CCAAGUGU	1489	ACACTTGG GGCTAGCTACAACGA ATAGACCA	4540
1188	AAGUGUUU G CUGACGCA	1490	TGCGTCAG GGCTAGCTACAACGA AAACACTT	4541
1194	UUGCUGAC G CAACCCCC	1492	GGGGGTTG GGCTAGCTACAACGA GTCAGCAA	4542
1234	CCAUCAGC G CAUGCGUG CAGCGCAU G CGUGGAAC	1493 1494	CACGCATG GGCTAGCTACAACGA GCTGATGG	4543
1238	UCUCCUCU G CCGAUCCA		GTTCCACG GGCTAGCTACAACGA ATGCGCTG	4544
1262	UCUCCUCU G CCGAUCCA UCCAUACC G CGGAACUC	1495	TGGATCGG GGCTAGCTACAACGA AGAGGAGA GAGTTCCG GGCTAGCTACAACGA GGTATGGA	4545
1275	UCCUAGCC G CGGAACUC	1497		4546
			AAAACAAG GGCTAGCTACAACGA GGCTAGGA	4547
1299	CUUGUUUU G CUCGCAGC	1499	GCTGCGAG GGCTAGCTACAACGA AAAACAAG	4548
1303	UUUUGCUC G CAGCAGGU	1500	ACCTGCTG GGCTAGCTACAACGA GAGCAAAA	4549
1349	UCUGUCGU G CUCUCCCG	1502	CGGGAGAG GGCTAGCTACAACGA ACGACAGA	4550
1357	GCUCUCCC G CAAAUAUA	1503	TATATTTG GGCTAGCTACAACGA GGGAGAGC	4551

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1382	CCAUGGCU G CUAGGCUG	1504	CAGCCTAG GGCTAGCTACAACGA AGCCATGG	4552
1392	UAGGCUGU G CUGCCAAC	1505	GTTGGCAG GGCTAGCTACAACGA ACAGCCTA	4553
1395	GCUGUGCU G CCAACUGG	1506	CCAGTTGG GGCTAGCTACAACGA AGCACAGC	4554
1411	GAUCCUAC G CGGGACGU	1507	ACGTCCCG GGCTAGCTACAACGA GTAGGATC	4555
1442	CCGUCGGC G CUGAAUCC	1508	GGATTCAG GGCTAGCTACAACGA GCCGACGG	4556
1452	UGAAUCCC G CGGACGAC	1510	GTCGTCCG GGCTAGCTACAACGA GGGATTCA	4557
1474	CCGGGGCC G CUUGGGGC	1512	GCCCCAAG GGCTAGCTACAACGA GGCCCCGG	4558
1489	GCUCUACC G CCCGCUUC	1513	GAAGCGGG GGCTAGCTACAACGA GGTAGAGC	4559
1493	UACCGCCC G CUUCUCCG	1514	CGGAGAAG GGCTAGCTACAACGA GGGCGGTA	4560
1501	GCUUCUCC G CCUAUUGU	1515	ACAATAGG GGCTAGCTACAACGA GGAGAAGC	4561
1528	CACGGGGC G CACCUCUC	1517	GAGAGGTG GGCTAGCTACAACGA GCCCCGTG	4562
1542	CUCUUUAC G CGGACUCC	1518	GGAGTCCG GGCTAGCTACAACGA GTAAAGAG	4563
1559	CCGUCUGU G CCUUCUCA	1519	TGAGAAGG GGCTAGCTACAACGA ACAGACGG	4564
1571	UCUCAUCU G CCGGACCG	1520	CGGTCCGG GGCTAGCTACAACGA AGATGAGA	4565
1583	GACCGUGU G CACUUCGC	1521	GCGAAGTG GGCTAGCTACAACGA ACACGGTC	4566
1590	UGCACUUC G CUUCACCU	1522	AGGTGAAG GGCTAGCTACAACGA GAAGTGCA	4567
1601	UCACCUCU G CACGUCGC	1523	GCGACGTG GGCTAGCTACAACGA AGAGGTGA	4568
1608	UGCACGUC G CAUGGAGA	1524	TCTCCATG GGCTAGCTACAACGA GACGTGCA	4569
1628	CCGUGAAC G CCCACAGG	1526	CCTGTGGG GGCTAGCTACAACGA GTTCACGG	4570
1642	AGGAACCU G CCCAAGGU	1527	ACCTTGGG GGCTAGCTACAACGA AGGTTCCT	4571
1654	AAGGUCUU G CAUAAGAG	1528	CTCTTATG GGCTAGCTACAACGA AAGACCTT	4572
1818	AGCACCAU G CAACUUUU	1533	AAAAGTTG GGCTAGCTACAACGA ATGGTGCT	4573
1835	UCACCUCU G CCUAAUCA	1534	TGATTAGG GGCTAGCTACAACGA AGAGGTGA	4574
1883	CAAGCUGU G CCUUGGGU	1535	ACCCAAGG GGCTAGCTACAACGA ACAGCTTG	4575
1959	UCUUUUUU G CCUUCUGA	1537	TCAGAAGG GGCTAGCTACAACGA AAAAAAGA	4576
2002	UCGACACC G CCUCUGCU	1541	AGCAGAGG GGCTAGCTACAACGA GGTGTCGA	4577
2008	CCGCCUCU G CUCUGUAU	1542	ATACAGAG GGCTAGCTACAACGA AGAGGCGG	4578
2282	GUGGAUUC G CACUCCUC	1548	GAGGAGTG GGCTAGCTACAACGA GAATCCAC	4579
2293	CUCCUCCU G CAUAUAGA	1549	TCTATATG GGCTAGCTACAACGA AGGAGGAG	4580
2311	CACCAAAU G CCCCUAUC	1550	GATAGGGG GGCTAGCTACAACGA ATTTGGTG	4581
2388	ACUCCCUC G CCUCGCAG	1552	CTGCGAGG GGCTAGCTACAACGA GAGGGAGT	4582
2393	CUCGCCUC G CAGACGAA	1553	TTCGTCTG GGCTAGCTACAACGA GAGGCGAG	4583
2412	UCUCAAUC G CCGCGUCG	1555	CGACGCGG GGCTAGCTACAACGA GATTGAGA	4584
2415	CAAUCGCC G CGUCGCAG	1556	CTGCGACG GGCTAGCTACAACGA GGCGATTG	4585
2420	GCCGCGUC G CAGAAGAU	1557	ATCTTCTG GGCTAGCTACAACGA GACGCGGC	4586
2514	GGUACCUU G CUUUAAUC	1558	GATTAAAG GGCTAGCTACAACGA AAGGTACC	4587
2560	AUUCAUUU G CAGGAGGA	1560	TCCTCCTG GGCTAGCTACAACGA AAATGAAT	4588
2641	UUAACUAU G CCUGCUAG	1563	CTAGCAGG GGCTAGCTACAACGA ATAGTTAA	4589
2645	CUAUGCCU G CUAGGUUU	1564	AAACCTAG GGCTAGCTACAACGA AGGCATAG	4590
2677	AAAUAUUU G CCCUUAGA	1565	TCTAAGGG GGCTAGCTACAACGA AAATATTT	4591
2740	UUCCAGAC G CGACAUUA	1566	TAATGTCG GGCTAGCTACAACGA GTCTGGAA	4592
2804	CACGUAGO G COUCAUUU	1568	AAATGAGG GGCTAGCTACAACGA GCTACGTG	4593
2814	CUCAUUUU G CGGGUCAC	1569	GTGACCCG GGCTAGCTACAACGA AAAATGAG	4594
2946	UGGACCCU G CAUUCAAA	1572	TTTGAATG GGCTAGCTACAACGA AGGGTCCA	4595
2990	CUCAACCC G CACAAGGA	1573	TCCTTGTG GGCTAGCTACAACGA GGGTTGAG	4596
3012	GGCCGGAC G CCAACAAG	1574	CTTGTTGG GGCTAGCTACAACGA GTCCGGCC	4597
3090	GCCCUCAC G CUCAGGGC	1575	GCCCTGAG GGCTAGCTACAACGA GTGAGGGC	4598
3113	ACAACUGU G CCAGCAGC	1576	GCTGCTGG GGCTAGCTACAACGA ACAGTTGT	4599
3132	CUCCUCCU G CCUCCACC	1577	GGTGGAGG GGCTAGCTACAACGA AGGAGGAG	4600
51	AGGGCCCU G UACUUUCC	1578	GGAAAGTA GGCTAGCTACAACGA AGGGCCCT	4601
106	AGAAUACU G UCUCUGCC	1579	GGCAGAGA GGCTAGCTACAACGA AGTATTCT	4602
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Table 41

148	GGGACCCU G UACCGAAC	1580	GTTCGGTA GGCTAGCTACAACGA AGGGTCCC	4603
198	CUGCUCGU G UUACAGGC	1581	GCCTGTAA GGCTAGCTACAACGA ACGAGCAG	4604
219	UUUUUCUU G UUGACAAA	1582	TTTGTCAA GGCTAGCTACAACGA AAGAAAAA	4605
297	ACACCCGU G UGUCUUGG	1583	CCAAGACA GGCTAGCTACAACGA ACGGGTGT	4606
299	ACCCGUGU G UCUUGGCC	1584	GGCCAAGA GGCTAGCTACAACGA ACACGGGT	4607
347	ACCAACCU G UUGUCCUC	1585	GAGGACAA GGCTAGCTACAACGA AGGTTGGT	4608
350	AACCUGUU G UCCUCCAA	1586	TTGGAGGA GGCTAGCTACAACGA AACAGGTT	4609
362	UCCAAUUU G UCCUGGUU	1587	AACCAGGA GGCTAGCTACAACGA AAATTGGA	4610
381	CGCUGGAU G UGUCUGCG	1588	CGCAGACA GGCTAGCTACAACGA ATCCAGCG	4611
383	CUGGAUGU G UCUGCGGC	1589	GCCGCAGA GGCTAGCTACAACGA ACATCCAG	4612
438	AUCUUCUU G UUGGUUCU	1590	AGAACCAA GGCTAGCTACAACGA AAGAAGAT	4613
465	CAAGGUAU G UUGCCCGU	1591	ACGGGCAA GGCTAGCTACAACGA ATACCTTG	4614
476	GCCCGUUU G UCCUCUAA	1592	TTAGAGGA GGCTAGCTACAACGA AAACGGGC	4615
555	ACCUCUAU G UUUCCCUC	1593	GAGGGAAA GGCTAGCTACAACGA ATAGAGGT	4616
566	UCCCUCAU G UUGCUGUA	1594	TACAGCAA GGCTAGCTACAACGA ATGAGGGA	4617
572	AUGUUGCU G UACAAAAC	1595	GTTTTGTA GGCTAGCTACAACGA AGCAACAT	4618
602	CUGCACCU G UAUUCCCA	1596	TGGGAATA GGCTAGCTACAACGA AGGTGCAG	4619
694	UGCCAUUU G UUCAGUGG	1597	CCACTGAA GGCTAGCTACAACGA AAATGGCA	4620
724	CCCCCACU G UCUGGCUU	1598	AAGCCAGA GGCTAGCTACAACGA AGTGGGGG	4621
750	UGGAUGAU G UGGUUUUG	1599	CAAAACCA GGCTAGCTACAACGA ATCATCCA	4622
771	CCAAGUCU G UACAACAU	1600	ATGTTGTA GGCTAGCTACAACGA AGACTTGG	4623
801	AUGCCGCU G UUACCAAU	1601	ATTGGTAA GGCTAGCTACAACGA AGCGGCAT	4624
818	UUUCUUUU G UCUUUGGG	1602	CCCAAAGA GGCTAGCTACAACGA AAAAGAAA	4625
888	UGGGAUAU G UAAUUGGG	1603	CCCAATTA GGCTAGCTACAACGA ATATCCCA	4626
927	AACAUAUU G UACAAAAA	1604	TTTTGTA GGCTAGCTACAACGA AATATGTT	4627
944	AUCAAAAU G UGUUUUAG	1605	CTAAAACA GGCTAGCTACAACGA ATTTTGAT	4628
946	CAAAAUGU G UUUUAGGA	1606	TCCTAAAA GGCTAGCTACAACGA ACATTTTG	4629
963	AACUUCCU G UAAACAGG	1607	CCTGTTTA GGCTAGCTACAACGA AGGAAGTT	4630
991	GAAAGUAU G UCAACGAA	1608	TTCGTTGA GGCTAGCTACAACGA ATACTTTC	4631
1002	AACGAAUU G UGGGUCUU	1609	AAGACCCA GGCTAGCTACAACGA AATTCGTT	4632
1039	CACGCAAU G UGGAUAUU	1610	AATATCCA GGCTAGCTACAACGA ATTGCGTG	4633
1137	AACAGUAU G UGAACCUU	1611	AAGGITCA GGCTAGCTACAACGA ATACTGTT	4634
1184	UGCCAAGU G UUUGCUGA	1612	TCAGCAAA GGCTAGCTACAACGA ACTTGGCA	4635
1251	GAACCUUU G UGUCUCCU	1613	AGGAGACA GGCTAGCTACAACGA AAAGGTTC	4636
1253	ACCUUUGU G UCUCCUCU	1614	AGAGGAGA GGCTAGCTACAACGA ACAAAGGT	4637
1294	AGCCGCUU G UUUUGCUC	1615	GAGCAAAA GGCTAGCTACAACGA AAGCGGCT	4638
1344	ACAAUUCU G UCGUGCUC	1616	GAGCACGA GGCTAGCTACAACGA AGAATTGT	4639
1390	GCUAGGCU G UGCUGCCA	1617	TGGCAGCA GGCTAGCTACAACGA AGCCTAGC	4640
1425	CGUCCUUU G UUUACGUC	1618	GACGTAAA GGCTAGCTACAACGA AAAGGACG	4641
1508	CGCCUAUU G UACCGACC	1619	GGTCGGTA GGCTAGCTACAACGA AATAGGCG	4642
1557	CCCCGUCU G UGCCUUCU	1620	AGAAGGCA GGCTAGCTACAACGA AGACGGGG	4643
1581	CGGACCGU G UGCACUUC	1621	GAAGTGCA GGCTAGCTACAACGA ACGGTCCG	4644
1684	UCAGCAAU G UCAACGAC	1622	GTCGTTGA GGCTAGCTACAACGA ATTGCTGA	4645
1719	CAAAGACU G UGUGUUUA	1623	TAAACACA GGCTAGCTACAACGA AGTCTTTG	4646
1721	AAGACUGU G UGUUUAAU	1624	ATTAAACA GGCTAGCTACAACGA ACAGTCTT	4647
1723	GACUGUGU G UUUAAUGA	1625	TCATTAAA GGCTAGCTACAACGA ACACAGTC	4648
1772	AGGUCUUU G UACUAGGA	1626	TCCTAGTA GGCTAGCTACAACGA AAAGACCT	4649
1785	AGGAGGCU G UAGGCAUA	1627	TATGCCTA GGCTAGCTACAACGA AGCCTCCT	4650
1801	AAAUUGGU G UGUUCACC	1628	GGTGAACA GGCTAGCTACAACGA ACCAATTT	4651
1803	AUUGGUGU G UUCACCAG	1629	CTGGTGAA GGCTAGCTACAACGA ACACCAAT	4652
1850	CAUCUCAU G UUCAUGUC	1630	GACATGAA GGCTAGCTACAACGA ATGAGATG	4653

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1856	AUGUUCAU G UCCUACUG	1631	CAGTAGGA GGCTAGCTACAACGA ATGAACAT	4654
1864	GUCCUACU G UUCAAGCC	1632	GGCTTGAA GGCTAGCTACAACGA AGTAGGAC	4655
1881	UCCAAGCU G UGCCUUGG	1633	CCAAGGCA GGCTAGCTACAACGA AGCTTGGA	4656
1939	GAGCUUCU G UGGAGUUA	1634	TAACTCCA GGCTAGCTACAACGA AGAAGCTC	4657
2013	UCUGCUCU G UAUCGGGG	1635	CCCCGATA GGCTAGCTACAACGA AGAGCAGA	4658
2045	GGAACAUU G UUCACCUC	1636	GAGGTGAA GGCTAGCTACAACGA AATGTTCC	4659
2082	GCUAUUCU G UGUUGGGG	1637	CCCCAACA GGCTAGCTACAACGA AGAATAGC	4660
2084	UAUUCUGU G UUGGGGUG	1638	CACCCCAA GGCTAGCTACAACGA ACAGAATA	4661
2167	UCAGCUAU G UCAACGUU	1639	AACGTTGA GGCTAGCTACAACGA ATAGCTGA	4662
2205	CAACUAUU G UGGUUUCA	1640	TGAAACCA GGCTAGCTACAACGA AATAGTTG	4663
2222	CAUUUCCU G UCUUACUU	1641	AAGTAAGA GGCTAGCTACAACGA AGGAAATG	4664
2245	GAGAAACU G UUCUUGAA	1642	TTCAAGAA GGCTAGCTACAACGA AGTTTCTC	4665
2262	UAUUUGGU G UCUUUUGG	1643	CCAAAAGA GGCTAGCTACAACGA ACCAAATA	4666
2274	UUUGGAGU G UGGAUUCG	1644	CGAATCCA GGCTAGCTACAACGA ACTCCAAA	4667
2344	AAACUACU G UUGUUAGA	1645	TCTAACAA GGCTAGCTACAACGA AGTAGTTT	4668
2347	CUACUGUU G UUAGACGA	1646	TCGTCTAA GGCTAGCTACAACGA AACAGTAG	4669
2450	AUCUCAAU G UUAGUAUU	1647	AATACTAA GGCTAGCTACAACGA ATTGAGAT	4670
2573	AGGACAUU G UUGAUAGA	1648	TCTATCAA GGCTAGCTACAACGA AATGTCCT	4671
2583	UGAUAGAU G UAAGCAAU	1649	ATTGCTTA GGCTAGCTACAACGA ATCTATCA	4672
2594	AGCAAUUU G UGGGGCCC	1650	GGGCCCCA GGCTAGCTACAACGA AAATTGCT	4673
2663	AUCCCAAU G UUACUAAA	1651	TTTAGTAA GGCTAGCTACAACGA ATTGGGAT	4674
2717	CAGAGUAU G UAGUUAAU	1652	ATTAACTA GGCTAGCTACAACGA ATACTCTG	4675
2901	AUCUUUCU G UCCCCAAU	1653	ATTGGGGA GGCTAGCTACAACGA AGAAAGAT	4676
3071	GGGGGACU G UUGGGGUG	1654	CACCCCAA GGCTAGCTACAACGA AGTCCCCC	4677
3111	UCACAACU G UGCCAGCA	1655	TGCTGGCA GGCTAGCTACAACGA AGTTGTGA	4678
40	AUCCCAGA G UCAGGGCC	1656	GGCCCTGA GGCTAGCTACAACGA TCTGGGAT	4679
46	GAGUCAGG G CCCUGUAC	1657	GTACAGGG GGCTAGCTACAACGA CCTGACTC	4680
65	UCCUGCUG G UGGCUCCA	1658	TGGAGCCA GGCTAGCTACAACGA CAGCAGGA	4681
68	UGCUGGUG G CUCCAGUU	1659	AACTGGAG GGCTAGCTACAACGA CACCAGCA	4682
74	UGGCUCCA G UUCAGGAA	1660	TTCCTGAA GGCTAGCTACAACGA TGGAGCCA	4683
85	CAGGAACA G UGAGCCCU	1661	AGGGCTCA GGCTAGCTACAACGA TGTTCCTG	4684
89	AACAGUGA G CCCUGCUC	1662	GAGCAGGG GGCTAGCTACAACGA TCACTGTT	4685
120	GCCAUAUC G UCAAUCUU	1663	AAGATTGA GGCTAGCTACAACGA GATATGGC	4686
196	CCCUGCUC G UGUUACAG	1664	CTGTAACA GGCTAGCTACAACGA GAGCAGGG	4687
205	UGUUACAG G CGGGGUUU	1665	AAACCCCG GGCTAGCTACAACGA CTGTAACA	4688
210	CAGGCGGG G UUUUUCUU	1666	AAGAAAAA GGCTAGCTACAACGA CCCGCCTG	4689
248	ACCACAGA G UCUAGACU	1667	AGTCTAGA GGCTAGCTACAACGA TCTGTGGT	4690
258	CUAGACUC G UGGUGGAC	1668	GTCCACCA GGCTAGCTACAACGA GAGTCTAG	4691
261	GACUCGUG G UGGACUUC	1669	GAAGTCCA GGCTAGCTACAACGA CACGAGTC	4692
295	GAACACCC G UGUGUCUU	1670	AAGACACA GGCTAGCTACAACGA GGGTGTTC	4693
305	GUGUCUUG G CCAAAAUU	1671	AATTTTGG GGCTAGCTACAACGA CAAGACAC	4694
318	AAUUCGCA G UCCCAAAU	1672	ATTTGGGA GGCTAGCTACAACGA TGCGAATT	4695
332	AAUCUCCA G UCACUCAC	1673	GTGAGTGA GGCTAGCTACAACGA TGGAGATT	4696
368	UUGUCCUG G UUAUCGCU	1674	AGCGATAA GGCTAGCTACAACGA CAGGACAA	4697
390	UGUCUGCG G CGUUUUAU	1675	ATAAAACG GGCTAGCTACAACGA CGCAGACA	4698
392	UCUGCGGC G UUUUAUCA	1676	TGATAAAA GGCTAGCTACAACGA GCCGCAGA	4699
442	OCUUGUUG G UUCUUCUG	1677	CAGAAGAA GGCTAGCTACAACGA CAACAAGA	4700
461	CUAUCAAG G UAUGUUGC	1678	GCAACATA GGCTAGCTACAACGA CTTGATAG	4701
472	UGUUGCCC G UUUGUCCU	1679	AGGACAAA GGCTAGCTACAACGA GGGCAACA	4702
506	AACAACCA G CACCGGAC	1680	GTCCGGTG GGCTAGCTACAACGA TGGTTGTT	4703
625	CAUCUUGG G CUUUCGCA	1681	TGCGAAAG GGCTAGCTACAACGA CCAAGATG	4704

Table 41

648	CUAUGGGA G UGGGCCUC	1682	GAGGCCCA GGCTAGCTACAACGA TCCCATAG	4705
652	GGGAGUGG G CCUCAGUC	1683	GACTGAGG GGCTAGCTACAACGA CCACTCCC	4705
658	GGGCCUCA G UCCGUUUC	1684	GAAACGGA GGCTAGCTACAACGA TGAGGCCC	4707
662	CUCAGUCC G UNICUCUN	1685	AAGAGAAA GGCTAGCTACAACGA GGACTGAG	4708
672	UUCUCUUG G CUCAGUUU	1686	AAACTGAG GGCTAGCTACAACGA CAAGAGAA	4709
677	UUGGCUCA G UUUACUAG	1687	CTAGTAAA GGCTAGCTACAACGA TGAGCCAA	4710
685	GUUUACUA G UGCCAUUU	1688	AAATGGCA GGCTAGCTACAACGA TGAGCCAA	4711
699	UUUGUUCA G UGGUUCGU	1689	ACGAACCA GGCTAGCTACAACGA TAGTAAAC ACGAACCA GGCTAGCTACAACGA TGAACAAA	4711
702	GUUCAGUG G UUCGUAGG	1690	CCTACGAA GGCTAGCTACAACGA TGAACAAA	4712
				4714
706	AGUGGUUC G UAGGGCUU	1691	AAGCCCTA GGCTAGCTACAACGA GAACCACT	
711	UUCGUAGG G CUUUCCCC	1692	GGGGAAAG GGCTAGCTACAACGA CCTACGAA	4715
729	ACUGUCUG G CUUUCAGU	1693	ACTGAAAG GGCTAGCTACAACGA CAGACAGT	4716
736	GGCUUUCA G UUAUAUGG	1694	CCATATAA GGCTAGCTACAACGA TGAAAGCC	4717
753	AUGAUGUG G UUUUGGGG	1695	CCCCAAAA GGCTAGCTACAACGA CACATCAT	4718
762	UUUUGGGG G CCAAGUCU	1696	AGACTTGG GGCTAGCTACAACGA CCCCAAAA	4719
767	GGGGCCAA G UCUGUACA	1697	TGTACAGA GGCTAGCTACAACGA TTGGCCCC	4720
785	CAUCUUGA G UCCCUUUA	1698	TAAAGGGA GGCTAGCTACAACGA TCAAGATG	4721
826	GUCUUUGG G UAUACAUU	1699	AATGTATA GGCTAGCTACAACGA CCAAAGAC	4722
898	AAUUGGGA G UUGGGGCA	1700	TGCCCCAA GGCTAGCTACAACGA TCCCAATT	4723
904	GAGUUGGG G CACAUUGC	1701	GCAATGTG GGCTAGCTACAACGA CCCAACTC	4724
971	GUAAACAG G CCUAUUGA	1702	TCAATAGG GGCTAGCTACAACGA CTGTTTAC	4725
987	AUUGGAAA G UAUGUCAA	1703	TTGACATA GGCTAGCTACAACGA TTTCCAAT	4726
1006	AAUUGUGG G UCUUUUGG	1704	CCAAAAGA GGCTAGCTACAACGA CCACAATT	4727
1016	CUUUUGGG G UUUGCCGC	1705	GCGGCAAA GGCTAGCTACAACGA CCCAAAAG	4728
1080	GCAUACAA G CAAAACAG	1706	CTGTTTTG GGCTAGCTACAACGA TTGTATGC	4729
1089	CAAAACAG G CUUUUACU	1707	AGTAAAAG GGCTAGCTACAACGA CTGTTTTG	4730
1116	CUUACAAG G CCUUUCUA	1708	TAGAAAGG GGCTAGCTACAACGA CTTGTAAG	4731
1126	CUUUCUAA G UAAACAGU	1709	ACTGTTTA GGCTAGCTACAACGA TTAGAAAG	4732
1133	AGUAAACA G UAUGUGAA	1710	TTCACATA GGCTAGCTACAACGA TGTTTACT	4733
1152	UUUACCCC G UUGCUCGG	1711	CCGAGCAA GGCTAGCTACAACGA GGGGTAAA	4734
1160	GUUGCUCG G CAACGGCC	1712	GGCCGTTG GGCTAGCTACAACGA CGAGCAAC	4735
1166	CGGCAACG G CCUGGUCU	1713	AGACCAGG GGCTAGCTACAACGA CGTTGCCG	4736
1171	ACGGCCUG G UCUAUGCC	1714	GGCATAGA GGCTAGCTACAACGA CAGGCCGT	4737
1182	UAUGCCAA G UGUUUGCU	1715	AGCAAACA GGCTAGCTACAACGA TTGGCATA	4738
1207	CCCCACUG G UUGGGGCU	1716	AGCCCCAA GGCTAGCTACAACGA CAGTGGGG	4739
1213	UGGUUGGG G CUUGGCCA	1717	TGGCCAAG GGCTAGCTACAACGA CCCAACCA	4740
1218	GGGGCUUG G CCAUAGGC	1718	GCCTATGG GGCTAGCTACAACGA CAAGCCCC	4741
1225	GGCCAUAG G CCAUCAGC	1719	GCTGATGG GGCTAGCTACAACGA CTATGGCC	4742
1232	GGCCAUCA G CGCAUGCG	1720	CGCATGCG GGCTAGCTACAACGA TGATGGCC	4743
1240	GCGCAUGC G UGGAACCU	1721	AGGTTCCA GGCTAGCTACAACGA GCATGCGC	4744
1287	AACUCCUA G CCGCUUGU	1722	ACAAGCGG GGCTAGCTACAACGA TAGGAGTT	4745
1306	UGCUCGCA G CAGGUCUG	1723	CAGACCTG GGCTAGCTACAACGA TGCGAGCA	4746
1310	CGCAGCAG G UCUGGGGC	1724	GCCCCAGA GGCTAGCTACAACGA CTGCTGCG	4747
1317	GGUCUGGG G CAAAACUC	1725	GAGTTTTG GGCTAGCTACAACGA CCCAGACC	4748
1347	AUUCUGUC G UGCUCUCC	1726	GGAGAGCA GGCTAGCTACAACGA GACAGAAT	4749
1379	UUUCCAUG G CUGCUAGG	1727	CCTAGCAG GGCTAGCTACAACGA CATGGAAA	4750
1387	GCUGCUAG G CUGUGCUG	1728	CAGCACAG GGCTAGCTACAACGA CTAGCAGC	4751
1418	CGCGGGAC G UCCUUUGU	1729	ACAAAGGA GGCTAGCTACAACGA GTCCCGCG	4752
1431	UUGUUUAC G UCCCGUCG	1730	CGACGGGA GGCTAGCTACAACGA GTAAACAA	4753
1436	UACGUCCC G UCGGCGCU	1731	AGCGCCGA GGCTAGCTACAACGA GGGACGTA	4754
1440	UCCCGUCG G CGCUGAAU	1732	ATTCAGCG GGCTAGCTACAACGA CGACGGGA	4755

Table 41

1471	CUCCCGGG G CCGCUUGG	1733	CCAAGCGG GGCTAGCTACAACGA CCCGGGAG	4756
1481	CGCUUGGG G CUCUACCG	1734	CGGTAGAG GGCTAGCTACAACGA CCCAAGCG	4757
1517	UACCGACC G UCCACGGG	1735	CCCGTGGA GGCTAGCTACAACGA GGTCGGTA	4758
1526	UCCACGGG G CGCACCUC	1736	GAGGTGCG GGCTAGCTACAACGA CCCGTGGA	4759
1553	GACUCCCC G UCUGUGCC	1737	GGCACAGA GGCTAGCTACAACGA GGGGAGTC	4760
1579	GCCGGACC G UGUGCACU	1738	AGTGCACA GGCTAGCTACAACGA GGTCCGGC	4761
1605	CUCUGCAC G UCGCAUGG	1739	CCATGCGA GGCTAGCTACAACGA GTGCAGAG	4762
1622	AGACCACC G UGAACGCC	1740	GGCGTTCA GGCTAGCTACAACGA GGTGGTCT	4763
1649	UGCCCAAG G UCUUGCAU	1741	ATGCAAGA GGCTAGCTACAACGA CTTGGGCA	4764
1679	GACUUUCA G CAAUGUCA	1742	TGACATTG GGCTAGCTACAACGA TGAAAGTC	4765
1703	ACCUUGAG G CAUACUUC	1743	GAAGTATG GGCTAGCTACAACGA CTCAAGGT	4766
1732	UUUAAUGA G UGGGAGGA	1744	TCCTCCCA GGCTAGCTACAACGA TCATTAAA	4767
1741	UGGGAGGA G UUGGGGGA	1745	TCCCCCAA GGCTAGCTACAACGA TCCTCCCA	4768
1754	GGGAGGAG G UUAGGUUA	1746	TAACCTAA GGCTAGCTACAACGA CTCCTCCC	4769
1759	GAGGUUAG G UUAAAGGU	1747	ACCTTTAA GGCTAGCTACAACGA CTAACCTC	4770
1766	GGUUAAAG G UCUUUGUA	1748	TACAAAGA GGCTAGCTACAACGA CTTTAACC	4771
1782	ACUAGGAG G CUGUAGGC	1749	GCCTACAG GGCTAGCTACAACGA CTCCTAGT	4772
1789	GGCUGUAG G CAUAAAUU	1750	AATTTATG GGCTAGCTACAACGA CTACAGCC	4773
1799	AUAAAUUG G UGUGUUCA	1751	TGAACACA GGCTAGCTACAACGA CAATTTAT	4774
1811	GUUCACCA G CACCAUGC	1752	GCATGGTG GGCTAGCTACAACGA TGGTGAAC	4775
1870	CUGUUCAA G CCUCCAAG	1753	CTTGGAGG GGCTAGCTACAACGA TTGAACAG	4776
1878	GCCUCCAA G CUGUGCCU	1754	AGGCACAG GGCTAGCTACAACGA TTGGAGGC	4777
1890	UGCCUUGG G UGGCUUUG	1755	CAAAGCCA GGCTAGCTACAACGA CCAAGGCA	4778
1893	CUUGGGUG G CUUUGGGG	1756	CCCCAAAG GGCTAGCTACAACGA CACCCAAG	4779
1901	GCUUUGGG G CAUGGACA	1757	TGTCCATG GGCTAGCTACAACGA CCCAAAGC	4780
1917	AUUGACCC G UAUAAAGA	1758	TCTTTATA GGCTAGCTACAACGA GGGTCAAT	4781
1933	AAUUUGGA G CUUCUGUG	1759	CACAGAAG GGCTAGCTACAACGA TCCAAATT	4782
1944	UCUGUGGA G UUACUCUC	1760	GAGAGTAA GGCTAGCTACAACGA TCCACAGA	4783
2023	AUCGGGG G CCUUAGAG	1761	CTCTAAGG GGCTAGCTACAACGA CCCCCGAT	4784
2031	GCCUUAGA G UCUCCGGA	1762	TCCGGAGA GGCTAGCTACAACGA TCTAAGGC	4785
2062	ACCAUACG G CACUCAGG	1763	CCTGAGTG GGCTAGCTACAACGA CGTATGGT	4786
2070	GCACUCAG G CAAGCUAU	1764	ATAGCTTG GGCTAGCTACAACGA CTGAGTGC	4787
2074	UCAGGCAA G CUAUUCUG	1765	CAGAATAG GGCTAGCTACAACGA TTGCCTGA	4788
2090	GUGUUGGG G UGAGUUGA	1766	TCAACTCA GGCTAGCTACAACGA CCCAACAC	4789
2094	UGGGGUGA G UUGAUGAA	1767	TTCATCAA GGCTAGCTACAACGA TCACCCCA	4790
2107	UGAAUCUA G CCACCUGG	1768	CCAGGTGG GGCTAGCTACAACGA TAGATTCA	4791
2116	CCACCUGG G UGGGAAGU	1769	ACTTCCCA GGCTAGCTACAACGA CCAGGTGG	4792
2123	GGUGGGAA G UAAUUUGG	1770	CCAAATTA GGCTAGCTACAACGA TTCCCACC	4793
2140	AAGAUCCA G CAUCCAGG	1771	CCTGGATG GGCTAGCTACAACGA TGGATCTT	4794
2155	GGGAAUUA G UAGUCAGC	1772	GCTGACTA GGCTAGCTACAACGA TAATTCCC	4795
2158	AAUUAGUA G UCAGCUAU	1773	ATAGCTGA GGCTAGCTACAACGA TACTAATT	4796
2162	AGUAGUCA G CUAUGUCA	1774	TGACATAG GGCTAGCTACAACGA TGACTACT	4797
2173	AUGUCAAC G UUAAUAUG	1775	CATATTAA GGCTAGCTACAACGA GTTGACAT	4798
2183	UAAUAUGG G CCUAAAAA	1776	TTTTTAGG GGCTAGCTACAACGA CCATATTA	4799
2208	CUAUUGUG G UUUCACAU	1777	ATGTGAAA GGCTAGCTACAACGA CACAATAG	4800
2235	ACUUUUGG G CGAGAAAC	1778	GTTTCTCG GGCTAGCTACAACGA CCAAAAGT	4801
2260	AAUAUUUG G UGUCUUUU	1779	AAAAGACA GGCTAGCTACAACGA CAAATATT	4802
2272	CUUUUGGA G UGUGGAUU	1780	AATCCACA GGCTAGCTACAACGA TCCAAAAG	4803
2360	ACGAAGAG G CAGGUCCC	1781	GGGACCTG GGCTAGCTACAACGA CTCTTCGT	4804
2364	AGAGGCAG G UCCCCUAG	1782	CTAGGGGA GGCTAGCTACAACGA CTGCCTCT	4805
2403	AGACGAAG G UCUCAAUC	1783	GATTGAGA GGCTAGCTACAACGA CTTCCTCT	4806
2403	AGACGAMG G UCUCAAUC	1/03	GRITOMOM OGCIMOCIMCAMCOM CITCOTCT	1000

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2417	AUCGCCGC G UCGCAGAA	1784	TTCTGCGA GGCTAGCTACAACGA GCGGCGAT	4807
2454	CAAUGUUA G UAUUCCUU	1785	AAGGAATA GGCTAGCTACAACGA TAACATTG	4808
2474	CACAUAAG G UGGGAAAC	1786	GTTTCCCA GGCTAGCTACAACGA CTTATGTG	4809
2491	UUUACGGG G CUUUAUUC	1787	GAATAAAG GGCTAGCTACAACGA CCCGTAAA	4810
2507	CUUCUACG G UACCUUGC	1788	GCAAGGTA GGCTAGCTACAACGA CGTAGAAG	4811
2530	CCUAAAUG G CAAACUCC	1789	GGAGTTTG GGCTAGCTACAACGA CATTTAGG	4812
2587	AGAUGUAA G CAAUUUGU	1790	ACAAATTG GGCTAGCTACAACGA TTACATCT	4813
2599	UUUGUGGG G CCCCUUAC	1791	GTAAGGGG GGCTAGCTACAACGA CCCACAAA	4814
2609	CCCUUACA G UAAAUGAA	1792	TTCATTTA GGCTAGCTACAACGA TGTAAGGG	4815
2650	CCUGCUAG G UUUUAUCC	1793	GGATAAAA GGCTAGCTACAACGA CTAGCAGG	4816
2701	AUCAAACC G UAUUAUCC	1794	GGATAATA GGCTAGCTACAACGA GGTTTGAT	4817
2713	UAUCCAGA G UAUGUAGU	1795	ACTACATA GGCTAGCTACAACGA TCTGGATA	4818
2720	AGUAUGUA G UUAAUCAU	1796	ATGATTAA GGCTAGCTACAACGA TACATACT	4819
2768	UUUGGAAG G CGGGGAUC	1797	GATCCCCG GGCTAGCTACAACGA CTTCCAAA	4820
2791	AAAAGAGA G UCCACACG	1798	CGTGTGGA GGCTAGCTACAACGA TCTCTTTT	4821
2799	GUCCACAC G UAGCGCCU	1799	AGGCGCTA GGCTAGCTACAACGA GTGTGGAC	4822
2802	CACACGUA G CGCCUCAU	1800	ATGAGGCG GGCTAGCTACAACGA TACGTGTG	4823
2818	UUUUGCGG G UCACCAUA	1801	TATGGTGA GGCTAGCTACAACGA CCGCAAAA	4824
2848	GAUCUACA G CAUGGGAG	1802	CTCCCATG GGCTAGCTACAACGA TGTAGATC	4825
2857	CAUGGGAG G UUGGUCUU	1803	AAGACCAA GGCTAGCTACAACGA CTCCCATG	4826
2861	GGAGGUUG G UCUUCCAA	1804	TTGGAAGA GGCTAGCTACAACGA CAACCTCC	4827
2881	UCGAAAAG G CAUGGGGA	1805	TCCCCATG GGCTAGCTACAACGA CTTTTCGA	4828
2936	GAUCAUCA G UUGGACCC	1806	GGGTCCAA GGCTAGCTACAACGA TGATGATC	4829
2955	CAUUCAAA G CCAACUCA	1807	TGAGTTGG GGCTAGCTACAACGA TTTGAATG	4830
2964	CCAACUCA G UAAAUCCA	1808	TGGATTTA GGCTAGCTACAACGA TGAGTTGG	4831
3005	GACAACUG G CCGGACGC	1809	GCGTCCGG GGCTAGCTACAACGA CAGTTGTC	4832
3021	CCAACAAG G UGGGAGUG	1810	CACTCCCA GGCTAGCTACAACGA CTTGTTGG	4833
3027	AGGUGGGA G UGGGAGCA	1811	TGCTCCCA GGCTAGCTACAACGA TCCCACCT	4834
3033	GAGUGGGA G CAUUCGGG	1812	CCCGAATG GGCTAGCTACAACGA TCCCACTC	4835
3041	GCAUUCGG G CCAGGGUU	1813	AACCCTGG GGCTAGCTACAACGA CCGAATGC	4836
3047	GGGCCAGG G UUCACCCC	1814	GGGGTGAA GGCTAGCTACAACGA CCTGGCCC	4837
3077	CUGUUGGG G UGGAGCCC	1815	GGGCTCCA GGCTAGCTACAACGA CCCAACAG	4838
3082	GGGGUGGA G CCCUCACG	1816	CGTGAGGG GGCTAGCTACAACGA TCCACCCC	4839
3097	CGCUCAGG G CCUACUCA	1817	TGAGTAGG GGCTAGCTACAACGA CCTGAGCG	4840
3117	CUGUGCCA G CAGCUCCU	1818	AGGAGCTG GGCTAGCTACAACGA TGGCACAG	4841
3120	UGCCAGCA G CUCCUCCU	1819	AGGAGGAG GGCTAGCTACAACGA TGCTGGCA	4842
3146	ACCAAUCG G CAGUCAGG	1820	CCTGACTG GGCTAGCTACAACGA CGATTGGT	4843
3149	AAUCGGCA G UCAGGAAG	1821	CTTCCTGA GGCTAGCTACAACGA TGCCGATT	4844
3158	UCAGGAAG G CAGCCUAC	1822	GTAGGCTG GGCTAGCTACAACGA CTTCCTGA	4845
3161	GGAAGGCA G CCUACUCC	1823	GGAGTAGG GGCTAGCTACAACGA TGCCTTCC	4846
3204	AUCCUCAG G CCAUGCAG	1824	CTGCATGG GGCTAGCTACAACGA CTGAGGAT	4847
10	ACUCCACC A CUUUCCAC	1825	GTGGAAAG GGCTAGCTACAACGA GGTGGAGT	4848
17	CACUUUCC A CCAAACUC	1826	GAGTTTGG GGCTAGCTACAACGA GGAAAGTG	4849
22	UCCACCAA A CUCUUCAA	1827	TTGAAGAG GGCTAGCTACAACGA TTGGTGGA	4850
32	UCUUCAAG A UCCCAGAG	1828	CTCTGGGA GGCTAGCTACAACGA CTTGAAGA	4851
53	GGCCCUGU A CUUUCCUG	1829	CAGGAAAG GGCTAGCTACAACGA ACAGGGCC	4852
82	GUUCAGGA A CAGUGAGC	1830	GCTCACTG GGCTAGCTACAACGA TCCTGAAC	4853
101	UGCUCAGA A UACUGUCU	1831	AGACAGTA GGCTAGCTACAACGA TCTGAGCA	4854
103	CUCAGAAU A CUGUCUCU	1832	AGAGACAG GGCTAGCTACAACGA ATTCTGAG	4855
115	UCUCUGCC A UAUCGUCA	1833	TGACGATA GGCTAGCTACAACGA GGCAGAGA	4856
117	UCUGCCAU A UCGUCAAU	1834	ATTGACGA GGCTAGCTACAACGA ATGGCAGA	4857

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124	UAUCGUCA A UCUUAUCG	1835	CGATAAGA GGCTAGCTACAACGA TGACGATA	4858
129	UCAAUCUU A UCGAAGAC	1836	GTCTTCGA GGCTAGCTACAACGA AAGATTGA	4859
136	UAUCGAAG A CUGGGGAC	1837	GTCCCCAG GGCTAGCTACAACGA CTTCGATA	4860
143	GACUGGGG A CCCUGUAC	1838	GTACAGGG GGCTAGCTACAACGA CCCCAGTC	4861
150	GACCCUGU A CCGAACAU	1839	ATGTTCGG GGCTAGCTACAACGA ACAGGGTC	4862
155	UGUACCGA A CAUGGAGA	1840	TCTCCATG GGCTAGCTACAACGA TCGGTACA	4863
157	UACCGAAC A UGGAGAAC	1841	GTTCTCCA GGCTAGCTACAACGA GTTCGGTA	4864
164	CAUGGAGA A CAUCGCAU	1842	ATGCGATG GGCTAGCTACAACGA TCTCCATG	4865
166	UGGAGAAC A UCGCAUCA	1843	TGATGCGA GGCTAGCTACAACGA GTTCTCCA	4866
171	AACAUCGC A UCAGGACU	1844	AGTCCTGA GGCTAGCTACAACGA GCGATGTT	4867
177	GCAUCAGG A CUCCUAGG	1845	CCTAGGAG GGCTAGCTACAACGA CCTGATGC	4868
186	CUCCUAGG A CCCCUGCU	1846	AGCAGGGG GGCTAGCTACAACGA CCTAGGAG	4869
201	CUCGUGUU A CAGGCGGG	1847	CCCGCCTG GGCTAGCTACAACGA AACACGAG	4870
223	UCUUGUUG A CAAAAAUC	1848	GATTTTTG GGCTAGCTACAACGA CAACAAGA	4871
229	UGACAAAA A UCCUCACA	1849	TGTGAGGA GGCTAGCTACAACGA TTTTGTCA	4872
235	AAAUCCUC A CAAUACCA	1850	TGGTATTG GGCTAGCTACAACGA GAGGATTT	4873
238	UCCUCACA A UACCACAG	1851	CTGTGGTA GGCTAGCTACAACGA TGTGAGGA	4874
240	CUCACAAU A CCACAGAG	1852	CTCTGTGG GGCTAGCTACAACGA ATTGTGAG	4875
243	ACAAUACC A CAGAGUCU	1853	AGACTCTG GGCTAGCTACAACGA GGTATTGT	4876
254	GAGUCUAG A CUCGUGGU	1854	ACCACGAG GGCTAGCTACAACGA CTAGACTC	4877
265	CGUGGUGG A CUUCUCUC	1855	GAGAGAAG GGCTAGCTACAACGA CCACCACG	4878
275	UUCUCUCA A UUUUCUAG	1856	CTAGAAAA GGCTAGCTACAACGA TGAGAGAA	4879
289	UAGGGGGA A CACCCGUG	1857	CACGGGTG GGCTAGCTACAACGA TCCCCCTA	4880
291	GGGGGAAC A CCCGUGUG	1858	CACACGGG GGCTAGCTACAACGA GTTCCCCC	4881
311	UGGCCAAA A UUCGCAGU	1859	ACTGCGAA GGCTAGCTACAACGA TTTGGCCA	4882
325	AGUCCCAA A UCUCCAGU	1860	ACTGGAGA GGCTAGCTACAACGA TTGGGACT	4883
335	CUCCAGUC A CUCACCAA	1861	TTGGTGAG GGCTAGCTACAACGA GACTGGAG	4884
339	AGUCACUC A CCAACCUG	1862	CAGGTTGG GGCTAGCTACAACGA GAGTGACT	4885
343	ACUCACCA A CCUGUUGU	1863	ACAACAGG GGCTAGCTACAACGA TGGTGAGT	4886
358	GUCCUCCA A UUUGUCCU	1864	AGGACAAA GGCTAGCTACAACGA TGGAGGAC	4887
371	UCCUGGUU A UCGCUGGA	1865	TCCAGCGA GGCTAGCTACAACGA AACCAGGA	4888
379	AUCGCUGG A UGUGUCUG	1866	CAGACACA GGCTAGCTACAACGA CCAGCGAT	4889
397	GGCGUUUU A UCAUCUUC	1867	GAAGATGA GGCTAGCTACAACGA AAAACGCC	4890
400	GUUUUAUC A UCUUCCUC	1868	GAGGAAGA GGCTAGCTACAACGA GATAAAAC	4891
412	UCCUCUGC A UCCUGCUG	1869	CAGCAGGA GGCTAGCTACAACGA GCAGAGGA	4892
423	CUGCUGCU A UGCCUCAU	1870	ATGAGGCA GGCTAGCTACAACGA AGCAGCAG	4893
430	UAUGCCUC A UCUUCUUG	1871	CAAGAAGA GGCTAGCTACAACGA GAGGCATA	4894
452	UCUUCUGG A CUAUCAAG	1872	CTTGATAG GGCTAGCTACAACGA CCAGAAGA	4895
455	UCUGGACU A UCAAGGUA	1873	TACCTTGA GGCTAGCTACAACGA AGTCCAGA	4896
463	AUCAAGGU A UGUUGCCC	1874	GGGCAACA GGCTAGCTACAACGA ACCTTGAT	4897
484	GUCCUCUA A UUCCAGGA	1875	TCCTGGAA GGCTAGCTACAACGA TAGAGGAC	4898
492	AUUCCAGG A UCAUCAAC	1876	GTTGATGA GGCTAGCTACAACGA CCTGGAAT	4899
495	CCAGGAUC A UCAACAAC	1877	GTTGTTGA GGCTAGCTACAACGA GATCCTGG	4900
499	GAUCAUCA A CAACCAGC	1878	GCTGGTTG GGCTAGCTACAACGA TGATGATC	4901
502	CAUCAACA A CCAGCACC	1879	GGTGCTGG GGCTAGCTACAACGA TGTTGATG	4902
513	AGCACCGG A CCAUGCAA	1880	TTGCATGG GGCTAGCTACAACGA CCGGTGCT	4903
516	ACCGGACC A UGCAAAAC	1881	GTTTTGCA GGCTAGCTACAACGA GGTCCGGT	4904
523	CAUGCAAA A CCUGCACA	1882	TGTGCAGG GGCTAGCTACAACGA TTTGCATG	4905
529	AAACCUGC A CAACUCCU	1883	AGGAGTTG GGCTAGCTACAACGA GCAGGTTT	4906
532	CCUGCACA A CUCCUGCU	1884	AGCAGGAG GGCTAGCTACAACGA TGTGCAGG	4907
547	CUCAAGGA A CCUCUAUG	1885	CATAGAGG GGCTAGCTACAACGA TCCTTGAG	4908
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553	GAACCUCU A UGUUUCCC	1886	GGGAAACA GGCTAGCTACAACGA AGAGGTTC	4909
564	UUUCCCUC A UGUUGCUG	1887	CAGCAACA GGCTAGCTACAACGA GAGGGAAA	4910
574	GUUGCUGU A CAAAACCU	1888	AGGTTTTG GGCTAGCTACAACGA ACAGCAAC	4911
579	UGUACAAA A CCUACGGA	1889	TCCGTAGG GGCTAGCTACAACGA TTTGTACA	4912
583	CAAAACCU A CGGACGGA	1890	TCCGTCCG GGCTAGCTACAACGA AGGTTTTG	4913
587	ACCUACGG A CGGAAACU	1891	AGTTTCCG GGCTAGCTACAACGA CCGTAGGT	4914
593	GGACGGAA A CUGCACCU	1892	AGGTGCAG GGCTAGCTACAACGA TTCCGTCC	4915
598	GAAACUGC A CCUGUAUU	1893	AATACAGG GGCTAGCTACAACGA GCAGTTTC	4916
604	GCACCUGU A UUCCCAUC	1894	GATGGGAA GGCTAGCTACAACGA ACAGGTGC	4917
610	GUAUUCCC A UCCCAUCA	1895	TGATGGGA GGCTAGCTACAACGA GGGAATAC	4918
615	CCCAUCCC A UCAUCUUG	1896	CAAGATGA GGCTAGCTACAACGA GGGATGGG	4919
618	AUCCCAUC A UCUUGGGC	1897	GCCCAAGA GGCTAGCTACAACGA GATGGGAT	4920
636	UUCGCAAA A UACCUAUG	1898	CATAGGTA GGCTAGCTACAACGA TTTGCGAA	4921
638	CGCAAAAU A CCUAUGGG	1899	CCCATAGG GGCTAGCTACAACGA ATTTTGCG	4922
642	AAAUACCU A UGGGAGUG	1900	CACTCCCA GGCTAGCTACAACGA AGGTATTT	4923
681	CUCAGUUU A CUAGUGCC	1901	GGCACTAG GGCTAGCTACAACGA AAACTGAG	4924
690	CUAGUGCC A UUUGUUCA	1902	TGAACAAA GGCTAGCTACAACGA GGCACTAG	4925
721	UUUCCCCC A CUGUCUGG	1903	CCAGACAG GGCTAGCTACAACGA GGGGGAAA	4926
739	UUUCAGUU A UAUGGAUG	1904	CATCCATA GGCTAGCTACAACGA AACTGAAA	4927
741	UCAGUUAU A UGGAUGAU	1905	ATCATCCA GGCTAGCTACAACGA ATAACTGA	4928
745	UUAUAUGG A UGAUGUGG	1906	CCACATCA GGCTAGCTACAACGA CCATATAA	4929
748	UAUGGAUG A UGUGGUUU	1907	AAACCACA GGCTAGCTACAACGA CATCCATA	4930
773	AAGUCUGU A CAACAUCU	1908	AGATGTTG GGCTAGCTACAACGA ACAGACTT	4931
776	UCUGUACA A CAUCUUGA	1909	TCAAGATG GGCTAGCTACAACGA TGTACAGA	4932
778	UGUACAAC A UCUUGAGU	1910	ACTCAAGA GGCTAGCTACAACGA GTTGTACA	4933
793	GUCCCUUU A UGCCGCUG	1911	CAGCGGCA GGCTAGCTACAACGA AAAGGGAC	4934
804	CCGCUGUU A CCAAUUUU	1912	AAAATTGG GGCTAGCTACAACGA AACAGCGG	4935
808	UGUUACCA A UUUUCUUU	1913	AAAGAAAA GGCTAGCTACAACGA TGGTAACA	4936
828	CUUUGGGU A UACAUUUA	1914	TAAATGTA GGCTAGCTACAACGA ACCCAAAG	4937
830	UUGGGUAU A CAUUUAAA	1915	TTTAAATG GGCTAGCTACAACGA ATACCCAA	4938
832	GGGUAUAC A UUUAAACC	1916	GGTTTAAA GGCTAGCTACAACGA GTATACCC	4939
838	ACAUUUAA A CCCUCACA	1917	TGTGAGGG GGCTAGCTACAACGA TTAAATGT	4940
844	AAACCCUC A CAAAACAA	1918	TTGTTTTG GGCTAGCTACAACGA GAGGGTTT	4941
849	CUCACAAA A CAAAAAGA	1919	TCTTTTG GGCTAGCTACAACGA TTTGTGAG	4942
857	ACAAAAAG A UGGGGAUA	1920	TATCCCCA GGCTAGCTACAACGA CTTTTTGT	4943
863	AGAUGGGG A UAUUCCCU	1921	AGGGAATA GGCTAGCTACAACGA CCCCATCT	4944
865	AUGGGGAU A UUCCCUUA	1922	TAAGGGAA GGCTAGCTACAACGA ATCCCCAT	4945
874	UUCCCUUA A CUUCAUGG	1923	CCATGAAG GGCTAGCTACAACGA TAAGGGAA	4946
879	UUAACUUC A UGGGAUAU	1924	ATATCCCA GGCTAGCTACAACGA GAAGTTAA	4947
884	UUCAUGGG A UAUGUAAU	1925	ATTACATA GGCTAGCTACAACGA CCCATGAA	4948
886	CAUGGGAU A UGUAAUUG	1926	CAATTACA GGCTAGCTACAACGA ATCCCATG	4949
891	GAUAUGUA A UUGGGAGU	1927	ACTCCCAA GGCTAGCTACAACGA TACATATC	4950
906	GUUGGGGC A CAUUGCCA	1928	TGGCAATG GGCTAGCTACAACGA GCCCCAAC	4951
908	UGGGGCAC A UUGCCACA	1929	TGTGGCAA GGCTAGCTACAACGA GTGCCCCA	4952
914	ACAUUGCC A CAGGAACA	1930	TGTTCCTG GGCTAGCTACAACGA GGCAATGT	4953
920	CCACAGGA A CAUAUUGU	1931	ACAATATG GGCTAGCTACAACGA TCCTGTGG	4954
922	ACAGGAAC A UAUUGUAC	1932	GTACAATA GGCTAGCTACAACGA GTTCCTGT	4955
924	AGGAACAU A UUGUACAA	1933	TTGTACAA GGCTAGCTACAACGA ATGTTCCT	4956
929	CAUAUUGU A CAAAAAAU	1934	ATTTTTG GGCTAGCTACAACGA ACAATATG	4957
936	UACAAAAA A UCAAAAUG	1935	CATTTGA GGCTAGCTACAACGA TTTTTGTA	4958
942	AAAUCAAA A UGUGUUUU		AAAACACA GGCTAGCTACAACGA TTTGATTT	4959
942	AAAUCAAA A UGUGUUUU	1936	AAAACACA GGCTAGCTACAACGA TTTGATTT	4959

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956	UUUAGGAA A CUUCCUGU	1937	ACAGGAAG GGCTAGCTACAACGA TTCCTAAA	4960
967	UCCUGUAA A CAGGCCUA	1938	TAGGCCTG GGCTAGCTACAACGA TTACAGGA	4961
975	ACAGGCCU A UUGAUUGG	1939	CCAATCAA GGCTAGCTACAACGA AGGCCTGT	4962
979	GCCUAUUG A UUGGAAAG	1940	CTTTCCAA GGCTAGCTACAACGA CAATAGGC	4963
989	UGGAAAGU A UGUCAACG	1941	CGTTGACA GGCTAGCTACAACGA ACTTTCCA	4964
995	GUAUGUCA A CGAAUUGU	1942	ACAATTCG GGCTAGCTACAACGA TGACATAC	4965
999	GUCAACGA A UUGUGGGU	1943	ACCCACAA GGCTAGCTACAACGA TCGTTGAC	4966
1032	CCCCUUUC A CGCAAUGU	1944	ACATTGCG GGCTAGCTACAACGA GAAAGGGG	4967
1037	UUCACGCA A UGUGGAUA	1945	TATCCACA GGCTAGCTACAACGA TGCGTGAA	4968
1043	CAAUGUGG A UAUUCUGC	1946	GCAGAATA GGCTAGCTACAACGA CCACATTG	4969
1045	AUGUGGAU A UUCUGCUU	1947	AAGCAGAA GGCTAGCTACAACGA ATCCACAT	4970
1056	CUGCUUUA A UGCCUUUA	1948	TAAAGGCA GGCTAGCTACAACGA TAAAGCAG	4971
1064	AUGCCUUU A UAUGCAUG	1949	CATGCATA GGCTAGCTACAACGA AAAGGCAT	4972
1066	GCCUUUAU A UGCAUGCA	1950	TGCATGCA GGCTAGCTACAACGA ATAAAGGC	4973
1070	UUAUAUGC A UGCAUACA	1951	TGTATGCA GGCTAGCTACAACGA GCATATAA	4974
1074	AUGCAUGC A UACAAGCA	1952	TGCTTGTA GGCTAGCTACAACGA GCATGCAT	4975
1076	GCAUGCAU A CAAGCAAA	1953	TTTGCTTG GGCTAGCTACAACGA ATGCATGC	4976
1085	CAAGCAAA A CAGGCUUU	1954	AAAGCCTG GGCTAGCTACAACGA TTTGCTTG	4977
1095	AGGCUUUU A CUUUCUCG	1955	CGAGAAAG GGCTAGCTACAACGA AAAAGCCT	4978
1107	UCUCGCCA A CUUACAAG	1956	CTTGTAAG GGCTAGCTACAACGA TGGCGAGA	4979
1111	GCCAACUU A CAAGGCCU	1957	AGGCCTTG GGCTAGCTACAACGA AAGTTGGC	4980
1130	CUAAGUAA A CAGUAUGU	1958	ACATACTG GGCTAGCTACAACGA TTACTTAG	4981
1135	UAAACAGU A UGUGAACC	1959	GGTTCACA GGCTAGCTACAACGA ACTGTTTA	4982
1141	GUAUGUGA A CCUUUACC	1960	GGTAAAGG GGCTAGCTACAACGA TCACATAC	4983
1147	GAACCUUU A CCCCGUUG	1961	CAACGGGG GGCTAGCTACAACGA AAAGGTTC	4984
1163	GCUCGGCA A CGGCCUGG	1962	CCAGGCCG GGCTAGCTACAACGA TGCCGAGC	4985
1175	CCUGGUCU A UGCCAAGU	1963	ACTTGGCA GGCTAGCTACAACGA AGACCAGG	4986
1192	GUUUGCUG A CGCAACCC	1964	GGGTTGCG GGCTAGCTACAACGA CAGCAAAC	4987
1197	CUGACGCA A CCCCCACU	1965	AGTGGGGG GGCTAGCTACAACGA TGCGTCAG	4988
1203	CAACCCCC A CUGGUUGG	1966	CCAACCAG GGCTAGCTACAACGA GGGGGTTG	4989
1221	GCUUGGCC A UAGGCCAU	1967	ATGGCCTA GGCTAGCTACAACGA GGCCAAGC	4990
1228	CAUAGGCC A UCAGCGCA	1968	TGCGCTGA GGCTAGCTACAACGA GGCCTATG	4991
1236	AUCAGCGC A UGCGUGGA	1969	TCCACGCA GGCTAGCTACAACGA GCGCTGAT	4992
1245	UGCGUGGA A CCUUUGUG	1970	CACAAAGG GGCTAGCTACAACGA TCCACGCA	4993
1266	CUCUGCCG A UCCAUACC	1971	GGTATGGA GGCTAGCTACAACGA CGGCAGAG	4994
1270	GCCGAUCC A UACCGCGG	1972	CCGCGGTA GGCTAGCTACAACGA GGATCGGC	4995
1272	CGAUCCAU A CCGCGGAA	1973	TTCCGCGG GGCTAGCTACAACGA ATGGATCG	4996
1280	ACCGCGGA A CUCCUAGC	1974	GCTAGGAG GGCTAGCTACAACGA TCCGCGGT	4997
1322	GGGGCAAA A CUCAUCGG	1975	CCGATGAG GGCTAGCTACAACGA TTTGCCCC	4998
1326	CAAAACUC A UCGGGACU	1976	AGTCCCGA GGCTAGCTACAACGA GAGTTTTG	4999
1332	UCAUCGGG A CUGACAAU	1977	ATTGTCAG GGCTAGCTACAACGA CCCGATGA	5000
1336	CGGGACUG A CAAUUCUG	1978	CAGAATTG GGCTAGCTACAACGA CAGTCCCG	5001
1339	GACUGACA A UUCUGUCG	1979	CGACAGAA GGCTAGCTACAACGA TGTCAGTC	5002
1361	UCCCGCAA A UAUACAUC	1980	GATGTATA GGCTAGCTACAACGA TTGCGGGA	5003
1363	CCGCAAAU A UACAUCAU	1981	ATGATGTA GGCTAGCTACAACGA ATTTGCGG	5004
1365	GCAAAUAU A CAUCAUUU	1982	AAATGATG GGCTAGCTACAACGA ATATTTGC	5005
1367	AAAUAUAC A UCAUUUCC	1983	GGAAATGA GGCTAGCTACAACGA GTATATTT	5006
1370	UAUACAUC A UUUCCAUG	1984	CATGGAAA GGCTAGCTACAACGA GATGTATA	5007
1376	UCAUUUCC A UGGCUGCU	1985	AGCAGCCA GGCTAGCTACAACGA GGAAATGA	5008
1399	UGCUGCCA A CUGGAUCC	1986	GGATCCAG GGCTAGCTACAACGA TGGCAGCA	5009
1404	CCAACUGG A UCCUACGC	1987	GCGTAGGA GGCTAGCTACAACGA CCAGTTGG	5010

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1409	UGGAUCCU A CGCGGGAC	1988	GTCCCGCG GGCTAGCTACAACGA AGGATCCA	5011
1416	UACGCGGG A CGUCCUUU	1989	AAAGGACG GGCTAGCTACAACGA CCCGCGTA	5012
1429	CUUUGUUU A CGUCCCGU	1990	ACGGGACG GGCTAGCTACAACGA AAACAAAG	5013
1447	GGCGCUGA A UCCCGCGG	1991	CCGCGGGA GGCTAGCTACAACGA TCAGCGCC	5014
1456	UCCCGCGG A CGACCCCU	1992	AGGGGTCG GGCTAGCTACAACGA CCGCGGGA	5015
1459	CGCGGACG A CCCCUCCC	1993	GGGAGGGG GGCTAGCTACAACGA CGTCCGCG	5016
1486	GGGGCUCU A CCGCCCGC	1994	GCGGGCGG GGCTAGCTACAACGA AGAGCCCC	5017
1505	CUCCGCCU A UUGUACCG	1995	CGGTACAA GGCTAGCTACAACGA AGGCGGAG	5018
1510	CCUAUUGU A CCGACCGU	1996	ACGGTCGG GGCTAGCTACAACGA ACAATAGG	5019
1514	UUGUACCG A CCGUCCAC	1997	GTGGACGG GGCTAGCTACAACGA CGGTACAA	5020
1521	GACCGUCC A CGGGGCGC	1998	GCGCCCCG GGCTAGCTACAACGA GGACGGTC	5021
1530	CGGGCGC A CCUCUCUU	1999	AAGAGAGG GGCTAGCTACAACGA GCGCCCCG	5022
1540	CUCUCUUU A CGCGGACU	2000	AGTCCGCG GGCTAGCTACAACGA AAAGAGAG	5023
1546	UUACGCGG A CUCCCCGU	2001	ACGGGGAG GGCTAGCTACAACGA CCGCGTAA	5024
1567	GCCUUCUC A UCUGCCGG	2002	CCGGCAGA GGCTAGCTACAACGA GAGAAGGC	5025
1576	UCUGCCGG A CCGUGUGC	2003	GCACACGG GGCTAGCTACAACGA CCGGCAGA	5026
1585	CCGUGUGC A CUUCGCUU	2004	AAGCGAAG GGCTAGCTACAACGA GCACACGG	5027
1595	UUCGCUUC A CCUCUGCA	2005	TGCAGAGG GGCTAGCTACAACGA GAAGCGAA	5028
1603	ACCUCUGC A CGUCGCAU	2006	ATGCGACG GGCTAGCTACAACGA GCAGAGGT	5029
1610	CACGUCGC A UGGAGACC	2007	GGTCTCCA GGCTAGCTACAACGA GCGACGTG	5030
1616	GCAUGGAG A CCACCGUG	2008	CACGGTGG GGCTAGCTACAACGA CTCCATGC	5031
1619	UGGAGACC A CCGUGAAC	2009	GTTCACGG GGCTAGCTACAACGA GGTCTCCA	5032
1626	CACCGUGA A CGCCCACA	2010	TGTGGGCG GGCTAGCTACAACGA TCACGGTG	5033
1638	CCACAGGA A CCUGCCCA	2011	TGGGCAGG GGCTAGCTACAACGA TCCTGTGG	5034
1656	GGUCUUGC A UAAGAGGA	2012	TCCTCTTA GGCTAGCTACAACGA GCAAGACC	5035
1664	AUAAGAGG A CUCUUGGA	2013	TCCAAGAG GGCTAGCTACAACGA CCTCTTAT	5036
1672	ACUCUUGG A CUUUCAGC	2014	GCTGAAAG GGCTAGCTACAACGA CCAAGAGT	5037
1682	UUUCAGCA A UGUCAACG	2015	CGTTGACA GGCTAGCTACAACGA TGCTGAAA	5038
1688	CAAUGUCA A CGACCGAC	2016	GTCGGTCG GGCTAGCTACAACGA TGACATTG	5039
1691	UGUCAACG A CCGACCUU	2017	AAGGTCGG GGCTAGCTACAACGA CGTTGACA	5040
1695	AACGACCG A CCUUGAGG	2018	CCTCAAGG GGCTAGCTACAACGA CGGTCGTT	5041
1705	CUUGAGGC A UACUUCAA	2019	TTGAAGTA GGCTAGCTACAACGA GCCTCAAG	5042
1707	UGAGGCAU A CUUCAAAG	2020	CTTTGAAG GGCTAGCTACAACGA ATGCCTCA	5043
1716	CUUCAAAG A CUGUGUGU	2021	ACACACAG GGCTAGCTACAACGA CTTTGAAG	5044
1728	UGUGUUUA A UGAGUGGG	2022	CCCACTCA GGCTAGCTACAACGA TAAACACA	5045
1774	GUCUUUGU A CUAGGAGG	2023	CCTCCTAG GGCTAGCTACAACGA ACAAAGAC	5046
1791	CUGUAGGC A UAAAUUGG	2024	CCAATITA GGCTAGCTACAACGA GCCTACAG	5047
1795	AGGCAUAA A UUGGUGUG	2025	CACACCAA GGCTAGCTACAACGA TTATGCCT	5048
1807	GUGUGUUC A CCAGCACC	2026	GGTGCTGG GGCTAGCTACAACGA GAACACAC	5049
1813	UCACCAGC A CCAUGCAA	2027	TTGCATGG GGCTAGCTACAACGA GCTGGTGA	5050
1816	CCAGCACC A UGCAACUU	2028	AAGTTGCA GGCTAGCTACAACGA GGTGCTGG	5051
1821	ACCAUGCA A CUUUUUCA	2029	TGAAAAG GGCTAGCTACAACGA TGCATGGT	5052
1829	ACUUUUUC A CCUCUGCC	2030	GGCAGAGG GGCTAGCTACAACGA GAAAAAGT	5053
1840	UCUGCCUA A UCAUCUCA	2031	TGAGATGA GGCTAGCTACAACGA TAGGCAGA	5054
1843	GCCUAAUC A UCUCAUGU	2032	ACATGAGA GGCTAGCTACAACGA GATTAGGC	5055
1848	AUCAUCUC A UGUUCAUG	2033	CATGAACA GGCTAGCTACAACGA GAGATGAT	5056
1854	UCAUGUUC A UGUCCUAC	2034	GTAGGACA GGCTAGCTACAACGA GAACATGA	5057
1861	CAUGUCCU A CUGUUCAA	2035	TTGAACAG GGCTAGCTACAACGA AGGACATG	5058
1903	UUUGGGGC A UGGACAUU	2036	AATGTCCA GGCTAGCTACAACGA GCCCCAAA	5059
1907	GGGCAUGG A CAUUGACC	2037	GGTCAATG GGCTAGCTACAACGA CCATGCCC	5060
1909	GCAUGGAC A UUGACCCG	2038	CGGGTCAA GGCTAGCTACAACGA GTCCATGC	5061
1909	GUAUGGAC A UUGACCCG	2038	CGGGTCAA GGCTAGCTACAACGA GTCCATGC	5061

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1913	GGACAUUG A CCCGUAUA	2039	TATACGGG GGCTAGCTACAACGA CAATGTCC	5062
1919	UGACCCGU A UAAAGAAU	2040	ATTCTTTA GGCTAGCTACAACGA ACGGGTCA	5063
1926	UAUAAAGA A UUUGGAGC	2041	GCTCCAAA GGCTAGCTACAACGA TCTTTATA	5064
1947	GUGGAGUU A CUCUCUUU	2042	AAAGAGAG GGCTAGCTACAACGA AACTCCAC	5065
1967	GCCUUCUG A CUUCUUUC	2043	GAAAGAAG GGCTAGCTACAACGA CAGAAGGC	. 5066
1981	UUCCUUCU A UUCGAGAU	2044	ATCTCGAA GGCTAGCTACAACGA AGAAGGAA	5067
1988	UAUUCGAG A UCUCCUCG	2045	CGAGGAGA GGCTAGCTACAACGA CTCGAATA	5068
1997	UCUCCUCG A CACCGCCU	2046	AGGCGGTG GGCTAGCTACAACGA CGAGGAGA	5069
1999	UCCUCGAC A CCGCCUCU	2047	AGAGGCGG GGCTAGCTACAACGA GTCGAGGA	5070
2015	UGCUCUGU A UCGGGGGG	2048	CCCCCCGA GGCTAGCTACAACGA ACAGAGCA	5071
2040	UCUCCGGA A CAUUGUUC	2049	GAACAATG GGCTAGCTACAACGA TCCGGAGA	5072
2042	UCCGGAAC A UUGUUCAC	2050	GTGAACAA GGCTAGCTACAACGA GTTCCGGA	5073
2049	CAUUGUUC A CCUCACCA	2051	TGGTGAGG GGCTAGCTACAACGA GAACAATG	5074
2054	UUCACCUC A CCAUACGG	2052	CCGTATGG GGCTAGCTACAACGA GAGGTGAA	5075
2057	ACCUCACC A UACGGCAC	2053	GTGCCGTA GGCTAGCTACAACGA GGTGAGGT	5076
2059	CUCACCAU A CGGCACUC	2054	GAGTGCCG GGCTAGCTACAACGA ATGGTGAG	5077
2064	CAUACGGC A CUCAGGCA	2055	TGCCTGAG GGCTAGCTACAACGA GCCGTATG	5078
2077	GGCAAGCU A UUCUGUGU	2056	ACACAGAA GGCTAGCTACAACGA AGCTTGCC	5079
2098	GUGAGUUG A UGAAUCUA	2057	TAGATTCA GGCTAGCTACAACGA CAACTCAC	5080
2102	GUUGAUGA A UCUAGCCA	2058	TGGCTAGA GGCTAGCTACAACGA TCATCAAC	5081
2110	AUCUAGCC A CCUGGGUG	2059	CACCCAGG GGCTAGCTACAACGA GGCTAGAT	5082
2126	GGGAAGUA A UUUGGAAG	2060	CTTCCAAA GGCTAGCTACAACGA TACTTCCC	5083
2135	UUUGGAAG A UCCAGCAU	2061	ATGCTGGA GGCTAGCTACAACGA CTTCCAAA	5084
2142	GAUCCAGC A UCCAGGGA	2062	TCCCTGGA GGCTAGCTACAACGA GCTGGATC	5085
2151	UCCAGGGA A UUAGUAGU	2063	ACTACTAA GGCTAGCTACAACGA TCCCTGGA	5086
2165	AGUCAGCU A UGUCAACG	2064	CGTTGACA GGCTAGCTACAACGA AGCTGACT	5087
2171	CUAUGUCA A CGUUAAUA	2065	TATTAACG GGCTAGCTACAACGA TGACATAG	5088
2177	CAACGUUA A UAUGGGCC	2066	GGCCCATA GGCTAGCTACAACGA TAACGTTG	5089
2179	ACGUUAAU A UGGGCCUA	2067	TAGGCCCA GGCTAGCTACAACGA ATTAACGT	5090
2191	GCCUAAAA A UCAGACAA	2068	TTGTCTGA GGCTAGCTACAACGA TTTTAGGC	5091
2196	AAAAUCAG A CAACUAUU	2069	AATAGTTG GGCTAGCTACAACGA CTGATTTT	5092
2199	AUCAGACA A CUAUUGUG	2070	CACAATAG GGCTAGCTACAACGA TGTCTGAT	5093
2202	AGACAACU A UUGUGGUU	2071	AACCACAA GGCTAGCTACAACGA AGTTGTCT	5094
2213	GUGGUUUC A CAUUUCCU	2072	AGGAAATG GGCTAGCTACAACGA GAAACCAC	5095
2215	GGUUUCAC A UUUCCUGU	2073	ACAGGAAA GGCTAGCTACAACGA GTGAAACC	5096
2227	CCUGUCUU A CUUUUGGG	2074	CCCAAAAG GGCTAGCTACAACGA AAGACAGG	5097
2242	GGCGAGAA A CUGUUCUU	2075	AAGAACAG GGCTAGCTACAACGA TTCTCGCC	5098
2253	GUUCUUGA A UAUUUGGU	2076	ACCAAATA GGCTAGCTACAACGA TCAAGAAC	5099
2255	UCUUGAAU A UUUGGUGU	2077	ACACCAAA GGCTAGCTACAACGA ATTCAAGA	5100
2278	GAGUGUGG A UUCGCACU	2078	AGTGCGAA GGCTAGCTACAACGA CCACACTC	5101
2284	GGAUUCGC A CUCCUCCU	2079	AGGAGGAG GGCTAGCTACAACGA GCGAATCC	5102
2295	CCUCCUGC A UAUAGACC	2080	GGTCTATA GGCTAGCTACAACGA GCAGGAGG	5103
2297	UCCUGCAU A UAGACCAC	2081	GTGGTCTA GGCTAGCTACAACGA ATGCAGGA	5104
2301	GCAUAUAG A CCACCAAA	2082	TTTGGTGG GGCTAGCTACAACGA CTATATGC	5105
2304	UAUAGACC A CCAAAUGC	2083	GCATTTGG GGCTAGCTACAACGA GGTCTATA	5106
2309	ACCACCAA A UGCCCCUA	2084	TAGGGGCA GGCTAGCTACAACGA TTGGTGGT	5107
2317	AUGCCCCU A UCUUAUCA	2085	TGATAAGA GGCTAGCTACAACGA AGGGGCAT	5108
2322	CCUAUCUU A UCAACACU	2086	AGTGTTGA GGCTAGCTACAACGA AAGATAGG	5109
2326	UCUUAUCA A CACUUCCG	2087	CGGAAGTG GGCTAGCTACAACGA TGATAAGA	5110
2328	UUAUCAAC A CUUCCGGA	2088	TCCGGAAG GGCTAGCTACAACGA GTTGATAA	5111
2338	UUCCGGAA A CUACUGUU	2089	AACAGTAG GGCTAGCTACAACGA TTCCGGAA	5112

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2341	CGGAAACU A CUGUUGUU	2090	AACAACAG GGCTAGCTACAACGA AGTTTCCG	5113
2352	GUUGUUAG A CGAAGAGG	2091	CCTCTTCG GGCTAGCTACAACGA CTAACAAC	5114
2380	GAAGAAGA A CUCCCUCG	2092	CGAGGGAG GGCTAGCTACAACGA TCTTCTTC	5115
2397	CCUCGCAG A CGAAGGUC	2093	GACCITCG GGCTAGCTACAACGA CTGCGAGG	5116
2409	AGGUCUCA A UCGCCGCG	2094	CGCGGCGA GGCTAGCTACAACGA TGAGACCT	5117
2427	CGCAGAAG A UCUCAAUC	2095	GATTGAGA GGCTAGCTACAACGA CTTCTGCG	5118
2433	AGAUCUCA A UCUCGGGA	2096	TCCCGAGA GGCTAGCTACAACGA TGAGATCT	5119
2442	UCUCGGGA A UCUCAAUG	2097	CATTGAGA GGCTAGCTACAACGA TCCCGAGA	5120
2448	GAAUCUCA A UGUUAGUA	2098	TACTAACA GGCTAGCTACAACGA TGAGATTC	5121
2456	AUGUUAGU A UUCCUUGG	2099	CCAAGGAA GGCTAGCTACAACGA ACTAACAT	5122
2465	UUCCUUGG A CACAUAAG	2100	CTTATGTG GGCTAGCTACAACGA CCAAGGAA	5123
2467	CCUUGGAC A CAUAAGGU	2101	ACCTTATG GGCTAGCTACAACGA GTCCAAGG	5124
2469	UUGGACAC A UAAGGUGG	2102	CCACCTTA GGCTAGCTACAACGA GTGTCCAA	5125
2481	GGUGGGAA A CUUUACGG	2103	CCGTAAAG GGCTAGCTACAACGA TTCCCACC	5126
2486	GAAACUUU A CGGGGCUU	2104	AAGCCCCG GGCTAGCTACAACGA AAAGTTTC	5127
2496	GGGGCUUU A UUCUUCUA	2105	TAGAAGAA GGCTAGCTACAACGA AAAGCCCCC	5128
2504	AUUCUUCU A CGGUACCU	2106	AGGTACCG GGCTAGCTACAACGA AGAAGAAT	5129
2509	UCUACGGU A CCUUGCUU	2107	AAGCAAGG GGCTAGCTACAACGA ACCGTAGA	5130
2520	UUGCUUUA A UCCUAAAU	2108	ATTTAGGA GGCTAGCTACAACGA TAAAGCAA	5131
2527	AAUCCUAA A UGGCAAAC	2109	GTTTGCCA GGCTAGCTACAACGA TTAGGATT	5132
2534	AAUGGCAA A CUCCUUCU	2110	AGAAGGAG GGCTAGCTACAACGA TTGCCATT	5133
2550	UUUUCCUG A CAUUCAUU	2111	AATGAATG GGCTAGCTACAACGA CAGGAAAA	5134
2552	UUCCUGAC A UUCAUUUG	2112	CAAATGAA GGCTAGCTACAACGA GTCAGGAA	5135
2556	UGACAUUC A UUUGCAGG	2113	CCTGCAAA GGCTAGCTACAACGA GAATGTCA	5136
2568	GCAGGAGG A CAUUGUUG	2114	CAACAATG GGCTAGCTACAACGA CCTCCTGC	5137
2570	AGGAGGAC A UUGUUGAU	2115	ATCAACAA GGCTAGCTACAACGA GTCCTCCT	5138
2577	CAUUGUUG A UAGAUGUA	2116	TACATCTA GGCTAGCTACAACGA CAACAATG	5139
2581	GUUGAUAG A UGUAAGCA	2117	TGCTTACA GGCTAGCTACAACGA CTATCAAC	5140
2590	UGUAAGCA A UUUGUGGG	2118	CCCACAAA GGCTAGCTACAACGA TGCTTACA	5141
2606	GGCCCCUU A CAGUAAAU	2119	ATTTACTG GGCTAGCTACAACGA AAGGGGCC	5142
2613	UACAGUAA A UGAAAACA	2120	TGTTTTCA GGCTAGCTACAACGA TTACTGTA	5143
2619	AAAUGAAA A CAGGAGAC	2121	GTCTCCTG GGCTAGCTACAACGA TTTCATTT	5144
2626	AACAGGAG A CUUAAAUU	2122	AATTTAAG GGCTAGCTACAACGA CTCCTGTT	5145
2632	AGACUUAA A UUAACUAU	2123	ATAGTTAA GGCTAGCTACAACGA TTAAGTCT	5146
2636	UUAAAUUA A CUAUGCCU	2124	AGGCATAG GGCTAGCTACAACGA TAATTTAA	5147
2639	AAUUAACU A UGCCUGCU	2125	AGCAGGCA GGCTAGCTACAACGA AGTTAATT	5148
2655	UAGGUUUU A UCCCAAUG	2126	CATTGGGA GGCTAGCTACAACGA AAAACCTA	5149
2661	UUAUCCCA A UGUUACUA	2127	TAGTAACA GGCTAGCTACAACGA TGGGATAA	5150
2666	CCAAUGUU A CUAAAUAU	2128	ATATTTAG GGCTAGCTACAACGA AACATTGG	5151
2671	GUUACUAA A UAUJUGCC	2129	GGCAAATA GGCTAGCTACAACGA TTAGTAAC	5152
2673	UACUAAAU A UUUGCCCU	2130	AGGGCAAA GGCTAGCTACAACGA ATTTAGTA	5153
2685	GCCCUUAG A UAAAGGGA	2131	TCCCTTTA GGCTAGCTACAACGA CTAAGGGC	5154
2693	AUAAAGGG A UCAAACCG	2132	CGGTTTGA GGCTAGCTACAACGA CCCTTTAT	5155
2698	GGGAUCAA A CCGUAUUA	2133	TAATACGG GGCTAGCTACAACGA TTGATCCC	5156
2703	CAAACCGU A UUAUCCAG	2134	CTGGATAA GGCTAGCTACAACGA ACGGTTTG	5157
2706	ACCGUAUU A UCCAGAGU	2135	ACTOTIGA GGCTAGCTACAACGA AATACGGT	5158
2715	UCCAGAGU A UGUAGUUA	2136	TAACTACA GGCTAGCTACAACGA ACTCTGGA	5159
2724	UGUAGUUA A UCAUUACU	2137	AGTAATGA GGCTAGCTACAACGA TAACTACA	5160
2727	AGUUAAUC A UUACUUCC	2138	GGAAGTAA GGCTAGCTACAACGA GATTAACT	5160
2730	UAAUCAUU A CUUCCAGA	2139	TCTGGAAG GGCTAGCTACAACGA GATTAACT	5162
2738	ACUUCCAG A CGCGACAU	2140	ATGTCGCG GGCTAGCTACAACGA CTGGAAGT	5162
2/38	ACCOUNT A COUGACAU	2140	ATOTOGO GOCTAGOTACAACGA CTGGAAGT	2163

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2743	CAGACGCG A CAUUAUUU	2141	AAATAATG GGCTAGCTACAACGA CGCGTCTG	5164
2745	GACGCGAC A UUAUUUAC	2142	GTAAATAA GGCTAGCTACAACGA GTCGCGTC	5165
2748	GCGACAUU A UUUACACA	2143	TGTGTAAA GGCTAGCTACAACGA AATGTCGC	5166
2752	CAUUAUUU A CACACUCU	2144	AGAGTGTG GGCTAGCTACAACGA AAATAATG	5167
2754	UUAUUUAC A CACUCUUU	2145	AAAGAGTG GGCTAGCTACAACGA GTAAATAA	5168
2756	AUUUACAC A CUCUUUGG	2146	CCAAAGAG GGCTAGCTACAACGA GTGTAAAT	5169
2774	AGGCGGGG A UCUUAUAU	2147	ATATAAGA GGCTAGCTACAACGA CCCCGCCT	5170
2779	GGGAUCUU A UAUAAAAG	2148	CTTTTATA GGCTAGCTACAACGA AAGATCCC	5171
2781	GAUCUUAU A UAAAAGAG	2149	CTCTTTTA GGCTAGCTACAACGA ATAAGATC	5172
2795	GAGAGUCC A CACGUAGC	2150	GCTACGTG GGCTAGCTACAACGA GGACTCTC	5173
2797	GAGUCCAC A CGUAGCGC	2151	GCGCTACG GGCTAGCTACAACGA GTGGACTC	5174
2809	AGCGCCUC A UUUUGCGG	2152	CCGCAAAA GGCTAGCTACAACGA GAGGCGCT	5175
2821	UGCGGGUC A CCAUAUUC	2153	GAATATGG GGCTAGCTACAACGA GACCCGCA	5176
2824	GGGUCACC A UAUUCUUG	2154	CAAGAATA GGCTAGCTACAACGA GGTGACCC	5177
2826	GUCACCAU A UUCUUGGG	2155	CCCAAGAA GGCTAGCTACAACGA ATGGTGAC	5178
2836	UCUUGGGA A CAAGAUCU	2156	AGATOTTG GGCTAGCTACAACGA TCCCAAGA	5179
2841	GGAACAAG A UCUACAGC	2157	GCTGTAGA GGCTAGCTACAACGA CTTGTTCC	5180
2845	CAAGAUCU A CAGCAUGG	2158	CCATGCTG GGCTAGCTACAACGA AGATCTTG	5181
2850	UCUACAGC A UGGGAGGU	2159	ACCTCCCA GGCTAGCTACAACGA GCTGTAGA	5182
2870	UCUUCCAA A CCUCGAAA	2160	TTTCGAGG GGCTAGCTACAACGA TTGGAAGA	5183
2883	GAAAAGGC A UGGGGACA	2161	TGTCCCCA GGCTAGCTACAACGA GCCTTTTC	5184
2889	GCAUGGGG A CAAAUCUU	2162	AAGATTTG GGCTAGCTACAACGA CCCCATGC	5185
2893	GGGGACAA A UCUUUCUG	2163	CAGAAAGA GGCTAGCTACAACGA TTGTCCCC	5186
2908	UGUCCCCA A UCCCCUGG	2164	CCAGGGGA GGCTAGCTACAACGA TGGGGACA	5187
2918	CCCCUGGG A UUCUUCCC	2165	GGGAAGAA GGCTAGCTACAACGA CCCAGGGG	5188
2929	CUUCCCCG A UCAUCAGU	2166	ACTGATGA GGCTAGCTACAACGA CGGGGAAG	5189
2932	CCCCGAUC A UCAGUUGG	2167	CCAACTGA GGCTAGCTACAACGA GATCGGGG	5190
2941	UCAGUUGG A CCCUGCAU	2168	ATGCAGGG GGCTAGCTACAACGA CCAACTGA	5191
2948	GACCCUGC A UUCAAAGC	2169	GCTTTGAA GGCTAGCTACAACGA GCAGGGTC	5192
2959	CAAAGCCA A CUCAGUAA	2170	TTACTGAG GGCTAGCTACAACGA TGGCTTTG	5193
2968	CUCAGUAA A UCCAGAUU	2171	AATCTGGA GGCTAGCTACAACGA TTACTGAG	5194
2974	AAAUCCAG A UUGGGACC	2172	GGTCCCAA GGCTAGCTACAACGA CTGGATTT	5195
2980	AGAUUGGG A CCUCAACC	2173	GGTTGAGG GGCTAGCTACAACGA CCCAATCT	5196
2986	GGACCUCA A CCCGCACA	2174	TGTGCGGG GGCTAGCTACAACGA TGAGGTCC	5197
2998	GCACAAGG A CAACUGGC	2175	GCCAGTTG GGCTAGCTACAACGA CCTTGTGC	5198
3001	CAAGGACA A CUGGCCGG	2176	CCGGCCAG GGCTAGCTACAACGA TGTCCTTG	5199
3010	CUGGCCGG A CGCCAACA	2177	TGTTGGCG GGCTAGCTACAACGA CCGGCCAG	5200
3016	GGACGCCA A CAAGGUGG	2178	CCACCTTG GGCTAGCTACAACGA TGGCGTCC	5201
3035	GUGGGAGC A UUCGGGCC	2179	GGCCCGAA GGCTAGCTACAACGA GCTCCCAC	5202
3051	CAGGGUUC A CCCCUCCC	2180	GGGAGGG GGCTAGCTACAACGA GAACCCTG	5203
3061	CCCUCCCC A UGGGGGAC	2181	GTCCCCCA GGCTAGCTACAACGA GGGGAGGG	5204
3068	CAUGGGG A CUGUUGGG	2182	CCCAACAG GGCTAGCTACAACGA CCCCCATG	5205
3088	GAGCCCUC A CGCUCAGG	2183	CCTGAGCG GGCTAGCTACAACGA GAGGGCTC	5206
3101	CAGGGCCU A CUCACAAC	2184	GTTGTGAG GGCTAGCTACAACGA AGGCCCTG	5207
3105	GCCUACUC A CAACUGUG	2185	CACAGTTG GGCTAGCTACAACGA GAGTAGGC	5208
3108	UACUCACA A CUGUGCCA	2186	TGGCACAG GGCTAGCTACAACGA TGTGAGTA	5209
3138	CUGCCUCC A CCAAUCGG	2187	CCGATTGG GGCTAGCTACAACGA GGAGGCAG	5210
3142	CUCCACCA A UCGGCAGU	2188	ACTGCCGA GGCTAGCTACAACGA TGGTGGAG	5211
3165	GGCAGCCU A CUCCCUUA	2189	TAAGGGAG GGCTAGCTACAACGA AGGCTGCC	5212
3173	ACUCCCUU A UCUCCACC	2190	GGTGGAGA GGCTAGCTACAACGA AAGGGAGT	5213
3179	UUAUCUCC A CCUCUAAG	2191	CTTAGAGG GGCTAGCTACAACGA GGAGATAA	5214

Table 41

3190	UCUAAGGG A CACUCAUC	2192	GATGAGTG GGCTAGCTACAACGA CCCTTAGA	5215
3192	UAAGGGAC A CUCAUCCU	2193	AGGATGAG GGCTAGCTACAACGA GTCCCTTA	5216
3196	GGACACUC A UCCUCAGG	2194	CCTGAGGA GGCTAGCTACAACGA GAGTGTCC	5217
3207	CUCAGGCC A UGCAGUGG	2195	CCACTGCA GGCTAGCTACAACGA GGCCTGAG	5218

Input Sequence = AF100308. Cut Site = YG/M or UG/U. Stem Length = 8 . Core Sequence = GGCTAGCTACAACGA AF100308 (Hepatitis B virus strain 2-18, 3215 bp)

Table 42: Human HBV Amberzyme Ribozyme and Substrate Sequence

Rz Seg 5227 5230 5239 5219 5220 5221 5224 5225 5226 5228 5229 5232 5233 5234 5235 5236 5238 5240 5241 5242 5243 5244 5245 5247 AUUCUGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGCUCA CGAUAUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAGACAG CCAGUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCGGG GAUAAGAU UCCUGAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAUGUUCU AACACGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGGUCC AUTUTUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACAAGAA UGGGACUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAAUUUUG ACAUCCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAUAACCA AAACGCCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGACACAU GCAGGAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAGGAAG CAUAGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGAUGCA AGGCAVAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCAGGAU AGAUGAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAGCAGC AGGUUTUG GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AUGGUCCG GAGUUGUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGUUUUG UCCUUGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGAGUUG UNGUACAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACAUGAG SUAUUUUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAAAGCCC ACAAAUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUAGUAA AACCACAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCCAUAU AAGGGACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGAUGUU AACAGCGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAAAGGG SGUAACAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCAUAAA UCCUGUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUGUGCC UUUCCAAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUAGGCC GCCACCAG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AGGAAAGU SCAGGGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUGUUCC UCCAUGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGUACAGG CAAACGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACAUACC UACAGEUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUUUCCG Seq ID 1450 1455 1456 1459 1460 1467 1449 1451 1457 1458 1465 1466 1468 1470 1448 1452 1453 1454 1461 1462 1463 1464 1469 1471 1472 1473 1474 1475 1476 GGACCCCU G CUCGUGUU CANADUUC G CAGUCCCA UGGUDAUC G CUGGAUGU AUGUGUCU G CGGCGUUU GGUAUGUU G CCCGUUUG CGGACCAU G CAAAACCU CAAAACCU G CACAACUC CAACUCCU G CUCAAGGA CUCAUGUU G CUGUACAA CGGAAACU G CACCUGUA GGGCUUUC G CAAAUAC GOCCUAUU G AUUGGAAA ACTUTUCCU G CUGGUGGC GGAACAGU G AGCCCUGC UGAGCCCU G CUCAGAAU CUGUCUCU G CCAUAUCG AUCUIDAUC G AAGACUGG CCUGUACC G AACAUGGA AGAACAUC G CAUCAGGA UUCUUGIIU G ACAAAAU CUUCCUCU G CAUCCUGC uscauceu e euseuaus AUCCUGCU G CUAUGCCU GCUGCUAU G CCUCAUCU UUACUAGU G CCAUTUGU AUAUGGAU G AUGUGGUU AACAUCUU G AGUCCCUU cccuutau e ccecueuu UNUAUGCC G CUGUUACC GCCACAUU G CCACAGGA Substrate 169 192 315 374 410 420 518 878 Pog 83 94 112 132 153 222 387 417 425 468 538 569 296 631 687 747 783 795 798 911

166	AUGUCAAC G AAUUGUGG	1478	CCACAAUU GGAGGAAACUCC CU UCAAGGACAUCGUCGGG GUUGACAU	5249
1020	uegegnin e cegeceen	1479	AGGGGGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AAACCCCA	5250
1023	cennacc e ccccnnc	1480	GAAAGGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCAAACC	5251
1034	CCUUUCAC G CAAUGUGG	1481	CCACAUUG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GUGAAAGG	5252
1050	GAUAUUCU G CUUUAAUG	1482	CAUUAAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAAUAUC	5253
1058	GCUUUAAU G CCUUUAUA	1483	UAUAAAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUUAAAGC	5254
1068	CUUUAUAU G CAUGCAUA	1484	UAUGCAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAUAAAG	5255
1072	AUAUGCAU G CAUACAAG	1485	CUIGUAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGCAUAU	5256
1103	ACUTUCUC G CCAACUUA	1486	UNAGUUGG GGAGGAAACUCC CU UCRAGGACAUCGUCCGGG GAGAAAGU	5257
1139	CAGUAUGU G AACCUUUA	1487	UAAAGGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAUACUG	5258
1155	ACCCCGUU G CUCGGCAA	1488	UDSCCGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACGGGGU	5259
1177	uggucuau g ccaagugu	1489	ACACUUGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AUAGACCA	5260
1188	AAGUGUUU G CUGACGCA	1490	UGCGUCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAACACUU	5261
1191	UGUIUGCU G ACGCAACC	1491	GGUIGCGU GGAGGAAGUCC CU UCAAGGACAUCGUCCGGG AGCAAACA	5262
1194	UUGCUGAC G CAACCCCC	1492	GGGGGUUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUCAGCAA	5263
1234	CCAUCAGC G CAUGCGUG	1493	CACGCAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCUGAUGG	5264
1238	CAGCGCAU G CGUGGAAC	1494	GUUCCACG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AUGCGCUG	5265
1262	UCUCCUCU G CCGAUCCA	1495	UGGAUCGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AGAGGAGA	5266
1265	CCUCUGCC G AUCCAUAC	1496	GUAUGGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCAGAGG	5267
1275	UCCAUACC G CGGAACUC	1497	GAGUUCCE GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGUAUGGA	5268
1290	uccuages a conguun	1498	AAAACAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCUAGGA	5269
1299	CUUGUUM G CUCGCAGC	1499	GCUGCGAG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AAAACAAG	5270
1303	unuuecuc e caecaeeu	1500	ACCUGCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAGCAAAA	5271
1335	UCGGGACU G ACAAUUCU	1501	AGAAUUGU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AGUCCCGA	5272
1349	nonancen e coonecce	1502	CGGGAGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGACAGA	5273
1357	GCUCUCCC G CANAUA	1503	UAUAUTUG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GGGAGAGC	5274
1382	CCAUGGCU G CUAGGCUG	1504	CAGCCUAG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AGCCAUGG	5275
1392	UAGGCUGU G CUGCCAAC	1505	GUUGGCAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAGCCUA	5276
1395	GCUGUGCU G CCAACUGG	1506	CCAGUUGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AGCACAGC	5277
1411	GAUCCUAC G CGGGACGU	1507	ACGUCCCG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GUAGGAUC	5278
1442	CCGUCGGC G CUGAAUCC	1508	GGAUUCAG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GCCGACGG	5279
1445	UCGGCGCU G AAUCCCGC	1509	GCGGGAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCGCCGA	5280
1452	UGAAUCCC G CGGACGAC	1510	GUCGUCCG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GGGAUUCA	5281
1458	CCGCGGAC G ACCCCUCC	1511	GGAGGGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUCCGCGG	5282

1474	CCGGGGCC G CDDGGGGC	1512	GCCCCAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCCCCGG	5283
1489	GCUCUACC G CCCGCUUC	1513	GAAGCGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGUAGAGC	5284
1493	UACCGCCC G CUUCUCCG	1514	CGGAGAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCGGUA	5285
1801	GCUNCINC G CCUAUNGO	1515	ACAAUAGG GGAGGNAACUCC CU UCNAGGACAUCGUCCGGG GGAGAAGC	5286
1513	AUUGUACC G ACCGUCCA	1516	UGGACGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGUACAAU	5287
1528	CACGGGGC G CACCUCUC	1517	GAGAGGUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCCCCGUG	5288
1542	CUCUUDAC G CGGACUCC	1518	GGAGUCCG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GUAAAGAG	5289
1559	ccencuen a ccuncuca	1519	UGAGAAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAGACGG	5290
1571	DCUCAUCU G CCGGACCG	1520	CGGUCCGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AGAUGAGA	5291
1583	GACCAUGU G CACUUCGC	1521	GCGAAGUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACACGGUC	5292
1590	necycnic e chicycci	1522	AGGUGAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAAGUGCA	5293
1601	ucaccucu a caceucec	1523	GCGACGUG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AGAGGUGA	5294
1608	UGCACGUC G CAUGGAGA	1524	UCUCCAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GACGUGCA	5235
1624	ACCACCGU G AACGCCCA	1525	UGGGCGUU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG ACGGUGGU	5296
1628	CCGUGAAC G CCCACAGG	1526	CCUGUGGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GUUCACGG	5297
1642	AGGNACCU G CCCAAGGU	1527	ACCUUGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGUUCCU	5298
1654	AAGGUCUU G CAUAAGAG	1528	CUCUDAUG GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AAGACCUU	5299
1690	AUGUCAAC G ACCGACCU	1529	AGGUCGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUUGACAU	2300
1694	CAACGACC G ACCUUGAG	1530	CUCAAGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGUCGUUG	5301
1700	CCGACCUU G AGGCAUAC	1531	GUAUGCCU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AAGGUCGG	5302
1730	DGUUDAAU G AGUGGGAG	1532	CUCCCACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUUAAACA	5303
1818	AGCACCAU G CAACUUUU	1533	AAAAGUUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGGUGCU	5304
1835	ucaccucu e ccuaauca	1534	UGAUUAGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AGAGGUGA	5305
1883	OPPORTUDE C CONTROCES	1535	ACCCAAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAGCUUG	5306
1912	UGGACAUU G ACCCGUAU	1536	AUACGGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUGUCCA	5307
1959	Monumer a common	1537	UCAGAAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAAAAGA	2308
1966	naccanca e vonacea	1538	AAAGAAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAAGGCA	5309
1985	UUCUAUUC G AGAUCUCC	1539	GGAGAUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAAUAGAA	5310
1996	AUCUCCUC G ACACCGCC	1540	GGCGGUGU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG GAGGAGAU	5311
2002	nceyasca e cononean	1541	AGCAGAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGUGUCGA	5312
2008	CCGCCACA G CACAGAM	1542	AUACAGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGAGGCGG	5313
2092	GUUGGGGU G AGUUGAUG	1543	CAUCAACU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG ACCCCAAC	5314
2097	GGUGAGUU G AUGAAUCU	1544	AGAUUCAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACUCACC	5315
2100	GAGUUGAU G AAUCUAGC	1545	GCUAGAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCAACUC	5316
		The second second		

2237	UUUUGGGC G AGAAACUG	1546	CAGUTUCU GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG GCCCAAAA	5317
2251	CUGUUCUU G AAUAUUUG	1547	CANAUAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGAACAG	5318
2282	GUGGAUUC G CACUCCUC	1548	GAGGAGUG GGAGGAAACUCC CU UCAAGGACAUCGUCGGG GAAUCCAC	5319
2293	CUCCUCCU G CAUAUAGA	1549	UCUAUAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGAGGAG	5320
2311	CACCAAAU G CCCCUAUC	1550	CAUAGGGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AUTUGGUG	5321
2354	UGUUAGAC G AAGAGGCA	1551	UGCCUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUCUAACA	5322
2388	ACUCCCUC G CCUCGCAG	1552	CUSCGAGG GGAGGAAACUCC CU UCAAGGACAUCGUCGGG GAGGGAGU	5323
2393	CUCGCCUC G CAGACGAA	1553	UUCGUCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAGGCGAG	5324
2399	UCGCAGAC G AAGGUCUC	1554	GAGACCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUCUGCGA	5325
2412	neuchane a ceacence	1555	CGACGCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAUUGAGA	5326
2415	CAAUCGCC G CGUCGCAG	1556	CUGCGACG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCGAUUG	5327
2420	GCCGCGUC G CAGAAGAU	1557	AUCUUCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GACGCGGC	5328
2514	COUNTRY C CUUDAUC	1558	GAUUAAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGGUACC	5329
2549	connece e vevnoevo	1559	AUGAAUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGAAAAG	5330
2560	AUDCAUUU G CAGGAGGA	1560	UCCUCCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAUGAAU	5331
2576	ACAUUGUU G AUAGAUGU	1561	ACAUCUAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACAAUGU	5332
2615	CAGUAAAU G AAAACAGG	1562	CCUGUUUU GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG AUJUACUG	5333
2641	UNAACUAU G CCUGCUAG	1563	CUAGCAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAGUUAA	5334
2645	nnneevna e nagennna	1564	SANCCUAG GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AGGCAUAG	5335
2677	AAAUAUUU G CCCUUAGA	1565	UCUAAGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAUAUUU	5336
2740	unccycyc c coycynny	1566	UNAUGUCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUCUGGAA	5337
2742	CCAGACGC G ACAUUAUU	1567	AAUAAUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCGUCUGG	5338
2804	caccunac a concauno	1568	AAAUGAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCUACGUG	5339
2814	COCAUDIU G CGGGUCAC	1569	GUGACCCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAAUGAG	5340
2875	CANACCUC 6 ANABGGCA	1570	DECORDIN GENERANDES EN NOVAMBENCANCENCES GNEROLING	5341
2928	UCUUCCCC G AUCAUCAG	1571	CUGAUGAU GGAGGNAACUCC CU UCAAGGACAUCGUCCGGG GGGGAAAGA	5342
2946	UGGACCCU G CAUUCAAA	1572	UUUGAAUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGUCCA	5343
2990	SUCARCO G CACARGOA	1573	UCCUUGUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGUUGAG	5344
3012	GGCCGGAC G CCAACAAG	1574	CUUGUUGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUCCGGCC	5345
3090	GCCCUCAC G CUCAGGGC	1575	GCCCUGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUGAGGGC	5346
3113	ACAACUGU G CCAGCAGC	9251	GCUGCUGG GGAGGAAACUCC CU UCAAGGACAUCGUCGGG ACAGUUGU	5347
3132	cuecuecu e cenecace	1577	GEUGGAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGAGGAG	5348
51	SOUTH B USCOURCE	1578	GGAAAGUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGCCCU	5349
106	AGANDACU 6 UCUCUGCC	1579	GGCAGAGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUAUUCU	5350

148	GGGACCCU G UACCGAAC	1580	GUUCGGUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGUCCC	5351
198	cuscucsu s unacassc	1581	GCCUGUAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGAGCAG	5352
219	UNUUNCUU G UUGACAAA	1582	UUUGUCAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGAAAAA	5353
297	ACACCCGU G UGUCUUGG	1583	CCAAGACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGGGUGU	5354
599	Acceden e ucungeco	1584	GGCCAAGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACACGGGU	5355
347	ACCAACCU G UUGUCCUC	1585	GAGGACAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGUUGGU	5356
350	AACCUGUU G UCCUCCAA	1586	UUGGAGGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACAGGUU	5357
362	UCCAAUUU G UCCUGGUU	1587	AACCAGGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAUUGGA	5358
381	cecneevn e nencnece	1588	CGCAGACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCCAGCG	5359
383	CUGGAUGU G UCUGCGGC	1589	GCCGCAGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAUCCAG	5360
438	AUCUUCUU G UUGGUUCU	1590	AGAACCAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGAAGAU	5361
465	CAAGGUAU G UUGCCCGU	1591	ACGGGCAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUACCUUG	5362
476	accesum a uccuenaa	1592	UUAGAGGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAACGGGC	5363
555	ACCUCUAU G UUUCCCUC	1593	GAGGGAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAGAGGU	5364
999	ucceucau e unecueua	1594	UACAGCAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGAGGGA	5365
572	AUGUUGCU G UACAAAAC	1595	GUIUUGUA GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG AGCAACAU	5366
602	CUGCACCU G UAUUCCCA	1596	UGGGAAUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGUGCAG	5367
694	UGCCAUTU G UUCAGUGG	1597	CCACUGAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAUGGCA	5368
724	nnoeenon e novocoo	1598	AAGCCAGA GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG AGUCGGGG	5369
750	UGGAUGAU G UGGUUUUG	1599	CAAAACCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUCAUCCA	5370
771	ccaagucu e uacaacau	1600	AUGUUGUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGACUUGG	5371
801	AUGCCGCU G UUACCAAU	1601	AUUGGUAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCGGCAU	5372
818	nancanna e acanaese	1602	CCCAAAGA GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AAAAGAAA	5373
888	UGGGAUAU G UAAUUGGG	1603	CCCAAUUA GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG AUAUCCCA	5374
927	AACAUAUU G UACAAAAA	1604	UUUUUGUA GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AAUAUGUU	5375
944	AUCAAAAU G UGUUUUAG	1605	CURARACA GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AUUUUGAU	5376
946	CAAAAUGU G UUUUAGGA	1606	UCCUAAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAUUUUG	5377
963	AACUUCCU G UAAACAGG	1607	CCUGUUUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGAAGUU	5378
166	GAAAGUAU G UCAACGAA	1608	UUCGUUGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUACUTUC	5379
1002	AACGAAUU G UGGGUCUU	1609	AAGACCCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUUCGUU	5380
1039	CACGCAAU G UGGAUAUU	1610	AAUAUCCA GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG AUUGCGUG	5381
1137	AACAGUAU G UGAACCUU	1611	AAGGUUCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUACUGUU	5382
1184	UGCCAAGU G UUUGCUGA	1612	UCAGCAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUUGGCA	5383
1251	GAACCUUU G UGUCUCCU	1613	AGGAGACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAGGUUC	5384

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1294	AGCCGCUU G UUUUGCUC	1615	GAGCAAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGCGGCU	5386
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1390	GCUAGGCU G UGCUGCCA	1617	UGGCAGCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCCUAGC	5388
1425	COUCCUUT G UTUACGUC	1618	GACGUAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAGGACG	5389
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1557	ccccancn a naccnncn	1620	AGAAGGCA GGAGGAAACUCC CU UCNAGGACAUCGUCCGGG AGACGGGG	5391
1581	COGRECOU G UCCREUUC	1621	GAAGUGCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGGUCCG	5392
1684	UCAGCAAU G UCAACGAC	1622	GUCGUUGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUUGCUGA	5393
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1721	AAGACUGU G UGUUUAAU	1624	AUUAAACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAGUCUU	5395
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1772	AGGUCUUU G UACUAGGA	1626	UCCUAGUA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAGACCU	5397
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1801	AAAUUGGU G UGUUCACC	1628	GGUGAACA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCAAUUU	5399
1803	AUJGGUGU G UUCACCAG	1629	CUGGUGAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACACCAAU	5400
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2274	UNUGGAGU G UGGAUUCG	1644	CGAAUCCA GGAGGAAACUCC CU UCAAGGACAUCGUCGGG ACUCCAAA	5415
2344	AAACUACU G UUGUUAGA	1645	UCUNACNA GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AGUAGUUU	5416
2347	CUACUGUU G UUAGACGA	1646	UCGUCUMA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACAGUAG	5417
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40	AUCCCAGA G UCAGGGCC	1656	GECCCUGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCUGGGAU	5427
46	GAGUCAGG G CCCUGUAC	1657	GUACAGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUGACUC	5428
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4	UGGCUCCA G UUCAGGAA	1660	UUCCUGAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGAGCCA	5431
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68	AACAGUGA G CCCUGCUC	1662	GAGCAGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCACUGUU	5433
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258	CUAGACUC G UGGUGGAC	1668	GUCCACCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAGUCUAG	5439
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332	AAUCUCCA G UCACUCAC	1673	GUGAGUGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGAGAUU	5444
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392	UCUGCGGC G UUUUAUCA	1676	UGAUAAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCCGCAGA	5447
442	исплания в писписия	1677	CAGAAGAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAACAAGA	5448
461	CUAUCAAG G UAUGUUGC	1678	GCAACNUN GGNGGANACUCC CU UCNAGGNCAUCGUCCGGG CUUGAUAG	5449
472	паплассс в пливисси	1679	AGGACAAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGGCAACA	5450
909	AACAACCA G CACCGGAC	1680	GUCCGGUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGUUGUU	5451
625	CAUCUUGG G CUUUCGCA	1681	UGCGAAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAAGAUG	5452
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1870	CUGUUCAA G CCUCCAAG	1753	CUUGGAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGAACAG	5524
1878	eccnecan e cuanecen	1754	AGGCACAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGGAGGC	5525
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1893	cunecene e cumeeee	1756	CCCCAAAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACCCAAG	5527
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1944	UCUGUGGA G UNACUCUC	1760	GAGAGUAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCACAGA	5531
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2090	GUGUUGGG G UGAGUUGA	1766	UCAACUCA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCAACAC	5537
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2173	AUGUCAAC G UDAAUAUG	1775	CAUAUUAA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUUGACAU	5546
2183	UAAUAUGG G CCUAAAAA	1776	UUUUNAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAUAUUA	5547
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2235	ACUUUUGG G CGAGAAAC	1778	GUIUCUCG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAAAAGU	5549
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2791	AAAAGAGA G UCCACACG	1798	CGUGUGGA GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCUCUUUU	5569
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3097	CGCUCAGG G CCUACUCA	1817	UGAGUAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUGAGCG	5588

5589	5590	5591	5592	5593	5594	5655	9655	5597	8655	5599	2600	5601	5602	5603	5604	2605	9099	2607	2608	2609	5610	5611	5612	5613	5614	5615	5616	5617	5618	5619	5620	5621	5622
AGGAGCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGCACAG	AGGAGGAG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCUGGCA	CCUGACUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGAUUGGU	CUUCCUGA GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UGCCGAUU	GUAGGCUG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUUCCUGA	GGAGUAGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCCUUCC	CUGCAUGG GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CUGAGGAU	UCUGGGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGAAGAG	COCUGACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGGAUCU	ACAGGGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGACUCUG	UACAGGG GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGACUCU	GGAGCCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCAGGAA	ACUGGAGO GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCAGCAG	CACUGUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAACUGG	UCACUGUI GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CUGAACUG	ACAGUAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAGCAGG	UCCCCAGU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UUCGAUAA	AGGGUCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUCUUCG	CAGGGUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGUCUUC	ACAGGGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAGUCUU	UACAGGGU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CCCAGUCU	AUGUICUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGUICGG	GAUGUUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUGUUCG	GOGAUGUU GGAGGAAACUCC CU UCAAGGACAUCGUCOGGG UCCAUGUU	UAGGAGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAUGCGA	CUAGGAGU GGAGGANACUCC CU UCAAGGACAUCGUCCGGG CUGAUGCG	CAGGGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAGGAGUC	GCAGGGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUAGGAGU	AACCCCGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUAACAC	ANABACCC GOAGGAACUCC CU UCAAGGACAUCGUCCGGG GCCUGUAA	GAAAAACC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGCCUGUA	AGAAAAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGCCUGU	UCUAGACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUGGUAU	CCACGAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAGACUCU
1818	1819	1820	1821	1822	1823	1824	2196	2197	2198	2199	2200	2201.	2202	2203	2204	2205	2206	2207	2208	5209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222
cueuecca e caecuccu	ဗ	ACCAAUCG G CAGUCAGG	AAUCGGCA G UCAGGAAG	UCAGGAAG G CAGCCUAC	GGAAGGCA G CCUACUCC	AUCCUCAG G CCAUGCAG	CUCUUCAA G AUCCCAGA	AGAUCCCA G AGUCAGGG	CAGAGUCA G GGCCCUGU	AGAGUCAG G GCCCUGUA	noconeco e enegonoc	cuecuseu e ecuccasu	CCAGUUCA G GAACAGUG	CAGUUCAG G AACAGUGA	CCUGCUCA G AAUACUGU	UUAUCGAA G ACUGGGGA	CGAAGACU G GGGACCCU	GNAGACUG G GGACCCUG	AAGACUGG G GACCCUGU	AGACUGGG G ACCCUGUA	CCGAACAU G GAGAACAU	CGAACAUG G AGAACAUC	AACAUGGA G AACAUCGC	UCGCAUCA G GACUCCUA	CGCAUCAG G ACUCCUAG	GACUCCUA G GACCCCUG	ACUCCUAG G ACCCCUGC	GUGUUACA G GCGGGGUU	UNACAGGC G GGGUUUUU	UACAGGCG G GGUUUUUC	ACAGGCGG G GUUUUUCU	AUACCACA G AGUCUAGA	AGAGUCUA G ACTOGUGG
3117	3120	3146	3149	3158	3161	3204	31	38	44	45	64	67	64	80	66	135	139	140	141	142	159	160	162	175	176	184	185	204	207	208	209	246	253

Table 4

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CUCGUGGU G (G GACUUCUC	2224	GAGAAGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCACGAG	5624
ucandane e 7	Actuacucu	2225	AGAGAAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACCACGA	5625
AUTUTUCUA G	G GGGGAACA	2226	UGUUCCCC GGAGGAARCUCC CU UCAAGGACAUCGUCCGGG UAGAAAAU	5626
UUUUCUAG G GGGAACAC	BGGAACAC	2227	GUGUUCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUAGAAAA	5627
UUUCUAGG G GGAACACC	BGAACACC	2228	GGUGUUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUAGAAA	5628
UUCUAGG G GAACACCC	BAACACCC	2229	GGGUGUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCUAGAA	5629
UCUAGGG G AACACCCG	AACACCCG	2230	CGGGUGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCCUAGA	5630
UGUGUCUU G GCCAAAU	SCCANANU	2231	AUTUUGGC GGAGGANACUCC CU UCANGGACAUCGUCCGGG AAGACACA	5631
иливисси в виимисвс	SUUAUCGC	2232	GOGAUAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGACAAA	5632
UNAUCGCU G GAUGUGUC	SAUGUGUC	2233	GACACAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGCGAUAA	5633
UAUCGCUG G AUGUGUCU	AUGUGUCU	2234	AGACACAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGCGAUA	5634
GUGUCUGC G GCGUUUUA	SCGUUUUA	2235	UNANACGO GGAGGANACUCO CU UCAAGGACAUCGUCOGGG GCAGACAC	5635
nocanean e enacanca	suucuucu	2236	AGAAGAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACAAGAA	5636
GUUCUUCU G	GACUAUCA	2237	UGAUAGUC GGAGGANACUCC CU UCAAGGACAUCGUCCGGG AGAAGAAC	5637
UNCUUCUG G ACUAUCAA	ACUAUCAA	2238	UUGAUAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGAAGAA	5638
ACUAUCAA G GUAUGUUG	SUAUGUUG	2239	CAACAUAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGAUAGU	5639
UNAUUCCA G GAUCAUCA	BAUCAUCA	2240	UGAUGAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGAAUUA	5640
AAUUCCAG G AUCAUCAA	AUCAUCAA	2241	UNGAUGAU GGAGGAAACUCC CU UCAAGGACAUCGUCGGG CUGGAAUU	5641
CCAGCACC G GACCAUGC	SACCAUGC	2242	GCAUGGUC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG GGUGCUGG	5642
CAGCACCG G 1	ACCAUGCA	2243	USCAUGGU GEAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGUGCUG	5643
cuecucaa e caaccucu	SAACCUCU	2244	AGAGGUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGAGCAG	5644
UGCUCAAG G AACCUCUA	AACCUCUA	2245	UNGNGGUU GGNGGNAACUCC CU UCAAGGACAUCGUCCGGG CUUGAGCA	5645
AAACCUAC G GACGGAAA	BACGGAAA	2246	UUUCCGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUAGGUUU	5646
AACCUACG G ACGGRAAC	CGGRAAC	2247	GUUUCCGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGUAGGUU	5647
CUACGGAC G O	G GAAACUGC	2248	GCAGUUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUCCGUAG	5648
UACGGACG G A	AAACUGCA	2249	UGCAGUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGUCCGUA	5649
AUCAUCUU G GGCUUUCG	sacuuuce	2250	CGAAAGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGAUGAU	2650
ucaucinia e ecunicec	scuuncec	2251	GCGAAAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAGAUGA	5651
АЛАССПАЛ В ВВАВИВВВ	BGAGUGGG	2252	CCCACUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAGGUAU	5652
UACCUAUG G GAGUGGGC	SAGUGGGC	2253	GCCCACUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUAGGUA	5653
ACCUAUGG G A	AGUGGGCC	2254	GGCCCACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAUAGGU	5654
миссемей в сессисме	SGCCUCAG	2255	CUBAGGCC GBAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUCCCAU	5655
UGGGAGUG G GCCUCAGU	SCCUCAGU	2256	ACUGAGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACUCCCA	2656

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2259 GGAAAGCC
2260 GGGAAAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUACGAAC
2262 ACAUCAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAUAACU
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2270 AUGUAUAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAAGACA
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2276 ACAUAUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGAAGUU
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2285 AUAUGUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUGGCAA
2286 AAUAUGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGUGGCA
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1004 CGA. 1005 GAA. 1013 GGU. 1014 GGC. 1042 GCA. 11159 GCA. 11159 CGU. 1116 UCG. 11110 ACC. 11110 ACC. 11110 ACC. 11111 ACC. 11211 ACC. 1211 ACC. 1211 ACC. 1211 ACC. 1211 ACC. 1211 ACC. 1212 CAC.	CGAAUUGU G GGUCUUUU	2532	AAAAGACC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAAUUCG	5692
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	2000000	2293	CAAAAGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACAAUUC	5693
	genconno e ecenonec	2294	GCAAACCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAAGACC	5694
	sucumme e eemmecc	2295	GGCANACC GGAGGANACUCC CU UCRAGGACAUCGUCCGGG CARAGAC	5695
	nconnote e enonecce	2296	CGGCAAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAAAAGA	9695
	CGCAAUGU G GAUAUUCU	2297	AGAAUAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAUUGCG	5697
	gcaaugus s auatucus	2298	CAGAAUAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACAUUGC	8698
	GCAMAGA G GCUUUUAC	2299	GUAAAAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUUUUGC	5699
	ACUUACAA G GCCUUUCU	2300	AGAAAGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGUAAGU	5700
	ceuticcuc e echaceec	2301	GCCGUUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAGCAACG	5701
	UCGGCAAC G GCCUGGUC	2302	GACCAGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUUGCCGA	5702
	AACGGCCU G GUCUAUGC	2303	GCAUAGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGCCGUU	5703
	ccccvcu e enneeeec	2304	GCCCCAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUGGGGG	5704
Ľ.	CACUGGUU G GGGCUUGG	2305	CCAAGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACCAGUG	5705
_	ACUGGUUG G GCCUUGGC	2306	GCCAAGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAACCAGU	5706
_	cueennae e ecnneecc	2307	GGCCAAGC GGAGGAAACUCC CU UCAAGGACAUCGUCOGGG CCAACCAG	5707
1217 UGG	JGGGGCUU G GCCAUAGG	2308	CCUAUGGC GGAGGAAACUCC CU UCAAGGACAUCGUCOGGG AAGCCCCA	5708
	UGGCCAUA G GCCAUCAG	2309	CUGAUGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAUGGCCA	5709
1242 GCA	GCAUGCGU G GAACCUUU	2310	AAAGGUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACGCAUGC	5710
	CAUGCGUG G AACCUUUG	2311	CAAAGGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACGCAUG	5711
1277 CAU	CAUACCGC G GAACUCCU	2312	AGGAGUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCGGUAUG	5712
_	AUACCGCG G AACUCCUA	2313	UAGGAGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGCGGUAU	5713
	UCGCAGCA G GUCUGGGG	2314	CCCCAGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCUGCGA	5714
1314 GCA	GCAGGUCU G GGGCAAAA	2315	UNUUGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGACCUGC	5715
1315 CAG	CAGGUCUG G GCCAAAAC	2316	GUIUUGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGACCUG	5716
1316 AGG	AGGUCUGG G GCAAAACU	2317	AGUUUUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAGACCU	5717
1329 AAC	AACUCAUC G GGACUGAC	2318	GUCAGUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAUGAGUU	5718
1330 ACU	ACUCAUCE E GACUGACA	2319	UGUCAGUE GGAGGAAACUEC EU UEAAGGACAUEGUEGGG EGAUGAGU	5719
Ш	CUCAUCGG G ACUGACAA	2320	UNSUCAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGAUGAG	5720
Ĺ	AUTUCCAU G GCUGCUAG	2321	CUAGCAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGGAAAU	5721
	adcudeua e ecueuecu	2322	AGCNCAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAGCAGCC	5722
	UGCCAACU G GAUCCUAC	2323	GUAGGAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUUGGCA	5723
1403 GCC	SCCAACUG G AUCCUACG	2324	CGUAGGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGUUGGC	5724

2327 AAGGACGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGCGUAG
2328 UNCAGCGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GACGGGAC
2334 UNGAGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGCGGCC
2335 GUAGAGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAGCGGC
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2337 GUGCGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUGGACGG
2340 GGGGAGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCGUAAAG
2341 CGGGGAGU GGAGGAAACUCC CU UCAAGGACAUCGUCGGG CGCGUAAA
2342 ACAOGGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGCAGAUG
2343 CACACGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGCAGAU
2344 GUGGUCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGCGACG
2346 ACGGUGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCAUGCG
2347 GCAGGUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUGGGCG
2348 GGCAGGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGUGGGC
2349 UGCAAGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGGGCAG
2350 AGAGUCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUAUGCAA
2351 CAAGAGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCUUAUGC
2352 CCAAGAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUCUUAUG
2353 UGAAAGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGAGUCC
2354 CUGAAAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAGAGUC
2355 AAGUAUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCAAGGUC
2356 CACACAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUGAAGU
2357 ACUCCUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUCAUUA
2358 AACUCCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACUCAUU

1736	AUGAGUGG G AGGAGUUG	2359	CAACUCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCACUCAU	5759
1738	GAGUGGGA G GAGUUGGG	2360	CCCAACUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCCACUC	5760
1739	AGUGGGAG G AGUUGGGG	2361	CCCCAACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUCCCACU	5761
1744	GAGGAGUU G GGGGAGGA	2362	UCCUCCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACUCCUC	5762
1745	AGGAGUUG G GGGAGGAG	2363	CUCCUCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAACUCCU	5763
1746	GGAGUUGG G GGAGGAGG	2364	CCUCCUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAACUCC	5764
1747	GAGUUGGG G GAGGAGGU	2365	ACCUCCUC GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG CCCAACUC	5765
1748	AGUUGGGG G AGGAGGUU	2366	AACCUCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCCAACU	2166
1750	UUGGGGGA G GAGGUUAG	2367	CUAACCUC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG UCCCCCAA	5767
1751	UGGGGGAG G AGGUUAGG	2368	CCURACCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUCCCCCA	5768
1753	GGGGAGGA G GUUAGGUU	2369	AACCUAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCUCCCC	5769
1758	GGAGGUUA G GUUAAAGG	2370	CCUUUAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAACCUCC	5770
1765	AGGUUAAA G GUCUUUGU	2371	ACAAAGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUAACCU	5771
1778	UUGUACUA G GAGGCUGU	2372	ACAGCCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAGUACAA	5772
1779	UGUACUAG G AGGCUGUA	2373	UACAGCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUAGUACA	5773
1781	UACUAGGA G GCUGUAGG	2374	CCUACAGO GGAGGAAACUCO CU UCAAGGACAUCGUCOGGG UCCUAGUA	5774
1788	AGGCUGUA G GCAUAAAU	2375	AUTUNUGE GGAGGAAACUCE CU UCAAGGACAUOGUCGGGG UACAGCCU	5775
1798	CAUAAAUU G GUGUGUUC	2376	GAACACAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUUUAUG	5776
1888	nandconn a aenaechn	2377	AAGCCACC GGAGGAAACUCC CU UCAAGGACAUCGUCGGGG AAGGCACA	5777
1889	anaccuna a anaccuna	2378	AAAGCCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAGGCAC	5778
1892	connegen e econnege	2379	CCCAAAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCCAAGG	5779
1898	GUGGCUTU G GGGCAUGG	2380	CCAUGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAGCCAC	5780
1899	UGGCUUUG G GGCAUGGA	2381	UCCAUGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAAGCCA	5781
1900	GGCUUUGG G GCAUGGAC	2382	GUCCAUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAAAGCC	5782
1905	UGGGCCAU G GACAUUGA	2383	UCAAUGUC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG AUGCCCCA	5783
1906	GGGCCAUG G ACAUUGAC	2384	GUCAAUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUGCCCC	5784
1924	CGUADAAA G AAUUUGGA	2385	UCCAAAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUAUACG	5785
1930	AAGAAUUU G GAGCUUCU	2386	AGAAGCUC GGAGGAAACUCC CU UCAAGGACAUCGUCOGGG AAAUUCUU	5786
1931	AGAAUTUG G AGCUUCUG	2387	CAGAAGCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAAUUCU	5787
1941	GCUUCUGU G GAGUUACU	2388	AGUAACUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAGAAGC	5788
1942	CUUCUGUG G AGUUACUC	2389	GAGUAACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACAGAAG	5789
1987	CUAUUCGA G AUCUCCUC	2390	GAGGAGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCGAAUAG	5790
2018	UCUGUAUC G GGGGGCCU	2391	AGGCCCC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG GAUACAGA	5791
2019	CUGUANCG G GGGGCCUU	2392	AAGGCCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGAUACAG	5792

GGCCUUA	2393	UNAGGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGAUACA	5793
GGCCUUAG	2394	CUAAGGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCGAUAC	5794
UAUCGGGG G GCCUUAGA	2395	UCUAAGGC GGAGGAAACUCC CU UCAAGGACAUCGUCOGGG CCCCGAUA	5795
GGGCCUUA G AGUCUCCG	2396	CGGAGACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAAGGCCC	5796
GAGUCUCC G GAACAUUG	2397	CAAUGUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GGAGACUC	5797
AGUCUCCG G AACAUUGU	2398	ACAAUGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGAGACU	5798
GCACUCAG	2399	CUGAGUGO GGAGGAAACUCO CU UCAAGGACAUCGUCOGGG GUAUGGUG	5799
GCAAGCUA	2400	UAGCUUGO GGAGGAAACUCO CU UCAAGGACAUCGUCOGGG UGAGUGCO	5800
UCUGUGUU G GGGUGAGU	2401	ACUCACCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACACAGA	5801
cueuciue e ecueacuu	2402	AACUCACC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAACACAG	5802
UGUGUUGG G GUGAGUUG	2403	CAACUCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAACACA	5803
GGUGGGAA	2404	UUCCCACC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGUGGCU	5804
GUGGGAAG	2405	CUUCCCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGGUGGC	5805
ACCUGGGU G GGAAGUAA	2406	UNACUUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCCAGGU	2806
ceudagua a caaguaau	2407	AUTACUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACCCAGG	5807
CUGGGUGG G AAGUAAUU	2408	AAUUACUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCACCCAG	5808
AGUAAUTU G GAAGAUCC	2409	GGAUCUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAUUACU	5809
GUANTUUG G AAGAUCCA	2410	UGGAUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAAUUAC	5810
AUTUGGAA G AUCCAGCA	2411	UGCUBGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCCAAAU	1185
GGAAUUAG	2412	CUAAUUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGAUGCU	5812
GCAUCCAG G GAAUUAGU	2413	ACUAAUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGGAUGC	5813
CAUCCAGG G AAUUAGUA	2414	UACUAAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUGGAUG	5814
GUUAAUAU G GGCCUAAA	2415	UUUAGGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUAUUAAC	5815
UUAAUAUG G GCCUAAAA	2416	UUUUAGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUAUUAA	5816
AAAAAUCA G ACAACUAU	2417	AUAGUUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAUUUUU	5817
GUUUCACA	2418	UGUGAAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACAAUAGU	5818
UUACUUUU G GGCGAGAA	2419	UUCUCGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAAGUAA	5819
имститив в всемвала	2420	UNUCUCEC GEAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAAAGUA	5820
UUGGGCGA G AAACUGUU	2421	AACAGUUU GGAGGAAACUCC CU UCAAGGACAUCGUCGGG UCGCCCAA	5821
GUGUCUM	2422	AAAGACAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAUAUUC	5822
GAGUGUGG	2423	CCACACUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAAAGACA	5823
SUCCULIUG G AGUGUGGA	2424	UCCACACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAAAGAC	5824
UGGAGUGU G GAUUCGCA	2425	UGCGAAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACACUCCA	5825
GGAGUGUG G AUUCGCAC	2426	GUGCGAAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACACUCC	5826
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2200	STOCKOUT O WINTERSON	2000	CONTRACTOR CONTRACTOR OF THE PROPERTY OF THE P	2003
2300	OGCADADA & ACCACCAA	1757	DOGGOGG GGAGGAGGCC CO OCANGACAOCGGCCGGG DADAGCA	1786
2334	ACACUUCC G GAAACUAC	2428	QUAGUTUC GGAGGNAACUCC CU UCAAGGACAUCGUCCGGG GGAAGUGU	5828
2335	CACUUCCG G AAACUACU	2429	AGUAGUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGAAGUG	5829
2351	UGUUGUUA G ACGAAGAG	2430	CUCUUCGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAACAACA	5830
2357	UAGACGAA G AGGCAGGU	2431	ACCUGACU GGAGGAAACUCA CU UCAAGGACAUCGUCCGGG UUCGUCUA	5831
2359	GACGAAGA G GCAGGUCC	2432	GGACCUGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UCUUCGUC	5832
2363	AAGAGGCA G GUCCCCUA	2433	UAGGGGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCCUCUU	5833
2372	GUCCCCUA G AAGAAGAA	2434	UNCUUCUU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UAGGGGAC	5834
2375	CCCUAGAA G AAGAACUC	2435	GAGUUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCUAGGG	5835
2378	UAGAAGAA G AACUCCCU	2436	AGGGAGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCUUCUA	5836
2396	GCCUCGCA G ACGAAGGU	2437	ACCUDED GEAGGAAACUCE EU UCAAGGACAUCGUCEGGG UGCGAGGE	5837
2402	CAGACGAA G GUCUCAAU	2438	AUUGAGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCGUCUG	5838
2423	GCGUCGCA G AAGAUCUC	2439	GAGAUCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGCGACGC	5839
2426	UCGCAGAA G AUCUCAAU	2440	AUUGAGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCUGCGA	5840
2438	UCAAUCUC G GGAAUCUC	2441	GAGAUUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GAGAUUGA	5841
2439	CAAUCUCG G GAAUCUCA	2442	UGAGAUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGAGAUUG	5842
2440	AAUCUCGG G AAUCUCAA	2443	UUGAGAUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGAGAUU	5843
2463	UAUUCCUU G GACACAUA	2444	UAUGUGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGGAAUA	5844
2464	AUUCCUUG G ACACAUAA	2445	UNAUGUGU GGAGGNAACUCC CU UCAAGGACAUCGUCCGGG CAAGGAAU	5845
2473	ACACAUAA G GUGGGAAA	2446	UUUCCCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUAUGUGU	5846
2476	CAUNAGGU G GGANACUU	2447	AAGUUUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCUUAUG	5847
2477	AUAAGGUG G GAAACUUU	2448	AAAGUUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACCUUAU	5848
2478	UAAGGUGG G AAACUUUA	2449	UAAAGUUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCACCUUA	5849
2488	AACUUUAC G GGCUUUA	2450	UAAAGCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUAAAGUU	5850
2489	ACUUDACG G GGCUUDAU	2451	AUAAAGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGUAAAGU	5851
2490	CUUUNACGG G GCUUUNUU	2452	AAUAAAGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGUAAAG	5852
2506	nannanya e anyaanna	2453	CAAGGUAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GUAGAAGA	5853
2529	UCCUAAAU G GCAAACUC	2454	GAGUUUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUUUAGGA	5854
2563	CAUUUGCA G GAGGACAU	2455	AUGUCCUC GGAGGNANCUCC CU UCAAGGACAUCGUCCGGG UGCAAAUG	5855
2564	AUUUGCAG G AGGACAUU	2456	AAUGUCCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGCAAAU	5856
2566	UUGCAGGA G GACAUUGU	2457	ACAAUGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCUGCAA	5857
2567	UGCAGGAG G ACAUUGUU	2458	AACAAUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUCCUGCA	5858
2580	L	2459	GCUUACAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAUCAACA	5859
2596	CAAUUUGU G GGCCCCU	2460	AGGGGCCC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG ACAAAUUG	5860

2597	AAUUUGUG G GGCCCCUU	2461	AAGGGGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACAAAUU	5861
2598	AUTUGUGG G GCCCCUUA	2462	UNAGGGGC GGAGGNAACUCC CU UCAAGGACAUCGUCCGGG CCACAAAU	5862
2622	UGASACA G GAGACUUA	2463	UAAGUCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGUUUUCA	5863
2623	GANARAGE G AGACUUAA	2464	UNAAGUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGUUUUC	5864
2625	AAACAGGA G ACUURAAU	2465	AUTUDAGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCUGUTU	5865
2649	accnacny a anninync	2466	GAUAAAAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAGCAGGC	2866
2684	USCCCUUA G AUAAAGGG	2467	CCCUUUAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UAAGGGCA	5867
2690	UAGAUAAA G GGAUCAAA	2468	UNUSAUCE GGAGGAAACUCE EU UCAAGGACAUCGUCCGGG UNUAUCUA	5868
2691	AGAUAAAG G GAUCAAAC	2469	GUUUGAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUUUAUCU	5869
2692	GAUAAAGG G AUCAAACC	2470	GGUUUGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUUUAUC	5870
2711	AUUAUCCA G AGUAUGUA	2471	UACAUACU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGAUAAU	5871
2737	UACUUCCA G ACGCGACA	2472	UGUCGCGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGAAGUA	5872
2763	SECOCODO O OVERGEO	2473	COGCOUNC GGAGGAAACUCC OU UCAAGGACAUCGUCCGGG AAAGAGUG	5873
2764	ACUCUUUG G AAGGCGGG	2474	CCCGCCUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAAGAGU	5874
2767	CUUUGGAA G GCGGGGAU	2475	AUCCCCGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUCCAAAG	5875
2770	DEGRAGGE G GEGAUCTU	2476	AAGAUCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCCUUCCA	5876
2771	GGAAGGCG G GGAUCUUA	2477	UAAGAUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGCCUUCC	5877
2772	GAAGGCGG G GAUCUUAU	2478	AUAAGAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCGCCUUC	5878
2773	AAGGCGGG G AUCUUAUA	2479	UAUAAGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCGCCUU	5879
2787	AUAUAAAA G AGAGUCCA	2480	UGGACUCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUUAUAU	5880
2789	AUAAAAGA G AGUCCACA	2481	UGUGGACU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UCUUUUAU	5881
2816	CAUUUUGC G GGUCACCA	2482	UGGUGACC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG GCAAAAUG	5882
2817	AUTUUGCG G GUCACCAU	2483	AUGGUGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGCAAAAU	5883
2832	AUAUUCUU G GGAACAAG	2484	CUUGUUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAGAAUAU	5884
2833	UNUTCUUG G GAACAAGA	2485	UCUUGUUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAGAAUA	5885
2834	AUTOUNGG G AACAAGAU	2486	AUCUUGUU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAAGAAU	5886
2840	GGGAACAA G AUCUACAG	2487	CUGUAGAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGUUCCC	5887
2852	UACAGCAU G GGAGGUUG	2488	CAACCUCC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG AUGCUGUA	5888
2853	ACAGCAUG G GAGGUUGG	2489	CCAACCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUGCUGU	5889
2854	CAGCAUGG G AGGUUGGU	2490	ACCAACCU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAUGCUG	5890
2856	GCAUGGGA G GUUGGUCU	2491	AGACCANC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UCCCAUGC	5891
2860	GGGAGGUU G GUCUUCCA	2492	UGGAAGAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACCUCCC	5892
2880	CUCGRAAA G GCAUGGGG	2493	CCCCAUGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUUUCGAG	5893
2885	AAAGGCAU G GGGACAAA	2494	UUUGUCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGCCUUU	5894

2886	AAGGCAUG G GGACAAAU	2495	AUTUGUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAUGCCUU	5895
2887	AGGCAUGG G GACAAAUC	2496	GAUTUGUE GGAGGAAACUEE EU UCAAGGACAUCGUECGGG CEAUGCEU	5896
2888	GGCAUGGG G ACAAAUCU	2497	AGAUTUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCCAUGCC	5897
2915	AAUCCCCU G GGAUUCUU	2498	AAGAAUCC GEAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGGGGAUU	5898
2916	AUCCCCUG G GAUUCUUC	2499	GAAGAAUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAGGGGAU	5899
2917	uccccugg g Aurcuncc	2500	GGAAGAAU GGAGGAAACUCC CU UCAAGGACAUCGUCOGGG OCAGGGGA	2900
2939	CAUCAGUU G GACCCUGC	2501	GCAGGGUC GGAGGAAACUCC CU UCAAGGACAUCGUCOGGG AACUGAUG	1065
2940	AUCAGUUG G ACCCUGCA	2502	UGCAGGGU GGAGGNAACUCC CU UCAAGGACAUCGUCCGGG CAACUGAU	5902
2973	UAAAUCCA G AUUGGGAC	2503	GUCCCAAU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGAUUUA	5903
2977	UCCAGAUU G GGACCUCA	2504	UGAGGUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AAUCUGGA	5904
2978	CCAGAUUG G GACCUCAA	2505	UNGAGGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAAUCUGG	5905
2979	CAGAUUGG G ACCUCAAC	2506	GUUGAGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAAUCUG	2906
2996	CCGCACAA G GACAACUG	2507	CAGUUGUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGUGCGG	5907
2997	CGCACAAG G ACAACUGG	2508	CCAGUUGU GGAGGNANCUCC CU UCAAGGACAUCGUCCGGG CUUGUGCG	5908
3004	GGACAACU G GCCGGACG	2509	CGUCCGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AGUUGUCC	5909
3008	AACUGGCC G GACGCCAA	2510	UNGECEUC GENEGARACUCC CU UCAAGGACAUCGUCCGGG GGCCAGUU	5910
3009	ACUGGCCG G ACGCCAAC	2511	GUUGGCGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CGGCCAGU	5911
3020	GCCAACAA G GUGGGAGU	2512	ACUCCCAC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUGUUGGC	5912
3023	AACAAGGU G GGAGUGGG	2513	CCCACUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCUUGUU	5913
3024	ACAAGGUG G GAGUGGGA	2514	UCCCACUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACCUUGU	5914
3025	CAAGGUGG G AGUGGGAG	2515	CUCCCACU GGAGGNANCUCC CU UCAAGGACAUCGUCGGG CCACCUUG	5915
3029	GUGGGAGU G GGAGCAUU	2516	AAUGCUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACUCCCAC	5916
3030	UGGGAGUG G GAGCAUUC	2517	GAAUGCUC GGAGGNAACUCC CU UCAAGGACAUCGUCCGGG CACUCCCA	5917
3031	GGGAGUGG G AGCAUUCG	2518	CGAAUGCU GGAGGNANCUCC CU UCAAGGACAUCGUCCGGG CCACUCCC	5918
3039	GAGCAUUC G GGCCAGGG	2519	CCCUGGCC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG GAAUGCUC	5919
3040	AGCAUUCG G GCCAGGGU	2520	ACCCUGGC GGAGGNAACUCC CU UCAAGGACAUCGUCCGGG CGAAUGCU	5920
3045	UCGGGCCA G GGUUCACC	2521	GGUGAACC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGGCCCGA	5921
3046	CGGGCGVG G GANCYCCC	2522	OCCUPANC GENERANACIOC OU UCANGGACAUCGUCGGGG CUGGCCCCG	5922
3063	COCCCAN G GGGGACUG	2523	CAGUCCCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AUGGGGAG	5923
3064	noncepne e eeeronen	2524	VODDON'S DEPONDED IN DOME OF THE PROPERTY OF T	5924
3065	CCCCAUGG G GGACUGUU	2525	AACAGUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCAUGGGG	5925
3066	cccanggg g gacugnug	2526	CAACAGUC GGAGGAAACUCC CU UCAAGGACAUCGUCGGG CCCAUGGG	5926
3067	ccyndede a vendande	2527	CCAACAGU GGAGGNAACUCC CU UCAAGGACAUCGUCCGGG CCCCAUGG	5927
3074	GGACUGUU G GGGUGGAG	2528	CUCCACCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG AACAGUCC	5928

5929	5930	5931	5932	5933	5934	5935	2936	5937	. 5938	5939	5940	5941	5942
GCUCCACC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CAACAGUC	GGCUCCAC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CCAACAGU	GAGGGCUC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG ACCCCAAC	UGAGGGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CACCCCAA	AGUAGGCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAGCGUG	GAGUAGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CUGAGCGU	CUGACUGE GGAGGAMACUCE CU UCAAGGACAUCGUCEGGG GAUUGGUG	CUBCCUUC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UGACUGCC	GCUGCCUU GGAGGAACUCC CU UCAAGGACAUCGUCCGGG CUGACUGC	UAGGCUGC GGAGGAACUCC CU UCAAGGACAUCGUCCGGG UUCCUGAC	GAGUGUCC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UUAGAGGU	UGAGUGUE GGAGGAAACUCE CU UCAAGGACAUCGUCCGGG CUUAGAGG	AUGAGUGU GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG CCUUAGAG	UGCAUGGC GGAGGAAACUCC CU UCAAGGACAUCGUCCGGG UGAGGAUG
2529	2530	2531	2532	2533	2534	2535	2536	2537	2538	2539	2540	2541	2542
GACUGUUG G GGUGGAGC	ACUGUUGG G GUGGAGCC	GUUGGGGU G GAGCCCUC	UUGGGGUG G AGCCCUCA	CACGCUCA G GGCCUACU	ACGCUCAG G GCCUACUC	CACCAAUC G GCAGUCAG	GGCAGUCA G GAAGGCAG	GCAGUCAG G AAGGCAGC	GUCAGGAA G GCAGCCUA	ACCUCURA G GGACACUC	CCUCUAAG G GACACUCA	CUCUAAGG G ACACUCAU	CAUCCUCA G GCCAUGCA
3075	3076	3079	3080	3095	3096	3145	3153	3154	3157	3187	3188	3189	3203

Input Sequence = AF100308. Cut Site = YG/M or UG/U.
Stem Longlin = 8. Cove Sequence = GASGANACUC CU UDAAGGACAUCGUCCOOG
Stem Longlin = 8. Cove Sequence = GASGANACUC CU UDAAGGACAUCGUCCOOG

Table 43: Human HBV Ribozyme and Target Sequence

+	+	+	-	+	+	CACAAA B 6298	+	+	+	+-++	++++	 - - - - 	+					 											
put (append)	GACUECE CUGAUGAGGCCGUUAGGCCGAA AUUUUGG B	GACUGGA CUGAUGAGGCCGUUAGGCCGAA AUUUGGG B	GEUGAGU CUGAUGAGGCCGUUAGGCCCGAA ACUGGAG B	GGAUGCA CUGAUGAGGCCGUUAGGCCGAA AGGAAGA B	UGAGGGA CUGAUGAGGCCGUUAGGCCGAA ACAUAGA B	CAGAGGA CUGAUGAGGCCGUUAGGCCGAA ACACAAA B	COGOGIJA CUGAUGAGGCCGUUAGGCCGAA AGAGAGG B		UNAACCU CUGAUGAGGCCGUUAGGCCGAA ACCUCCU B	UUAACCU CUGAUGAGGCCGUUAGGCCGAA ACCUCCU B UGAACAG CUGAUGAGGCCGUUAGGCCGAA AGGACAU B	UDAACCI CUGAUGAGGCCGUUAGGGCGGAA ACCUCCU B UGAACAG CUGAUGAGGCCGUUAGGCCGAA AGAACAU B GGUACCG CUGAUGAGGCCGUUAGGCCGAA AGAAGAA B	UNANCEL CUGALIGAGECCGUIAGECCGAA ACCIDCOL B DEAACAG CIGAGIAGAGGCCGUIAGAGCAA AGGARAU B GUIACCC CUGAUIAGGGCCGUIAGAGCCGAA AGAAGAA B UGGAAAG CUGAIIGAGGCCGUIAAGGCCGAA GGUIGGAG B	TURACCO CIGANICAGECCOUNAGECCEAN ACCUCOU B TIGANCAC CIGANICAGECCEUNAGECCEAN AGGACAU B GEUNACCE CUGANICAGECCEUNAGECCEAN AGGACAU B GEUNACCE CUGANICAGECCEUNAGECCEAN AGGACAN B TUGGANAGE CUGANICAGECCEAN AGGACA B TUGGUGAG CUGANICAGECCEAN GACUGGA B TUGGUGAG CUGANICAGECCCEAN GACUGGA B	UUMACCU CUGAUGAGGCCGUINGGCCGAA ACCUCCU B GGIACCE CUGAUGAGGCCGUINGGCCGAA AGAGAAN B CGIACCE CUGAUGAGGCCGUINAGGCCGAA GAAGAAN B UGGAAAG CUGAUGAGGCCGUINAGGCCGAA GAGGAAC B UGGAAAG CUGAUGAGGCCGUINAGGCCAA GAGGAAC B CGGAAG CUGAUGAGGCCGUINGGCCGAA GAGGAC B	UJAKCEJ CU GALUGAGGCGGUJAGGCGGAA ACQUCU B 10 GARCAG CUGAUGAGGCCGUJAGGCCGAA ACAAGAA B 10 GARCAG CUGAUGAGGCCGUJAGGCCGAA ACAAGAA B 10 GARCAG CUGAUGAGGCCGUJAGGCCGAA ACAAGAA B 10 GARCAG CUGAUGAGGCCGUJAGGCCGAA ACAAGAA B 10 GARCAG CUGAUGAGGCCGUJAGGCCGAA ACAUGGAB 10 GARCAG CUGAUGAGGCCGUJAGGCCGAA ACAUGGAB 10 GGCAJUJU CUGAUGAGGCCGUJAGGCCGAA ACAUGGAB 10 GGCAJUJU CUGAUGAGGCCGUJAGGCCGAA ACAUGGAB 10 GGCAJUJU CUGAUGAGGCCGUJAGGCCGAA ACAUGGAB 10 GGCAJUJU CUGAUGAGGCCGAA ACAAGAA ACAAGAA B 10 GGCAJUJU CUGAUGAGGCCGAA ACAAGAA ACAAGAA B 10 GGCAJUJU CUGAUGAGGCCGAA ACAAGAA ACAAGAAA ACAAAAA ACAAAAA ACAAAAA ACAAAAAA ACAAAAA ACAAAAAA	UNACCU CUANUGAGGCCUUNAGCCCAA ACUUCU B IGAACA CUANUGAGCCCUUNAGCCCAA ACUUCU B GGANCC CUANUGAGCCCUUNAGCCCAA ACUUCAA CGANCCC CUANUGAGCCCUUNAGCCCAA ACUUCAA IUGAACA CUANUGAGCCCUUNAGCCCAA ACUUCAA IUGAACA CUANUGAGCCCUUNAGCCCCAA ACAUGAA IUGAACAA CUICANGAGCCCUUNAGCCCCAA ACAUGAA CGCCACA CUICANGAGCCCUUNAGCCCCAA ACAUGAA IGAACAA IUGAACAACAA ACAACAA CGCCACA CUICANGAGCCCAUNAGCCCCAA ACAACAA GACAA IUGAACAACAAA IUGAACAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	UNACCU CIGANGAGGCCGUIAGGCCGAA ACCUCCU B UGAACCU CIGANGAGGCCGUIAGGCCGAA ACCUCCU B CGUIACCC CIGANGAGGCCGUIAGGCCGAA ACCUCCAA CGUIACCC CIGANGAGGCCGUIAGGCCGAA GGUIGGAB UGGAAAG CUANUAGGCCCGUIAGGCCGAA GGUIGGAB UGGAAA CIGANGAGCCCUINAGGCCGAA GGUIGGAB GGCAUIU CIGANGAGCCCUINAGGCCGAA GGUIGGAB GAGAAU CIGANGAGCCCUINAGGCCCAA GGUIGGAB CACAA UGANGAGCCCUINAGGCCCAA GGUIGGU B CACAA UGANGAGCCCUINAGGCCCAA GGUIGGU B CACAA UGANGGCCCUINAGGCCCAA GGUIAGGCAA GAGAA UGANGGCCCUINAGGCCCAA GGUIAGGU B CACAA UGANGGCCCUINAGGCCCAA GGUIAGGI B CACAA UGANGGCCAUCACCCCCAA GGUIAGGI B	UNACCU CUANURACECTRU MAGECTEM ACUPCUI I UGANCE CURANING COCIOUNA GEOCOGNA RECARANI UGANCE CURANING COCIOUNA GEOCOGNA RECARANI UGGANCE 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₽	18391 HBV-430 CHz-6 allyl stab1	a _{s9s} a _{s9} a cUGAuGaggccguuaggccGaa laggca B	0350
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5978 18397	7 HBV-683 CHz-6 allyl stab1	g _S g _S c _S a _S cu cUGAuGaggccguuaggccGaa nuaaac b	6320
5979 1840	18402 HBV-1150 CHz-6 allyl stab1	gscsasascd cDGAuGaggccguuaggcccaa iguaaa b	0353
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5995	18340 HBV-271 Rz-7 allyl stab1	a _s a _s a _s uga cUGAuGaggccguuaggccGaa Agaaguc B	6340
9669	18341 HBV-273 Rz-7 allyl stab1	g _s a _s a _s auu cUGAuGaggccguuaggccGaa Agagaag B	6346
UCUCAAU U UUCUAGG 5997 183	18342 HBV-277 Rz-7 allyl stab1	cscsusagaa cUGAuGaggccguuaggccGaa Auugaga B	9547
CUCAAUU U UCUAGGG 5998 183	18343 HBV-278 Rz-7 allyl stab1	c _s c _s c _s u _s aga cUGAuGaggccguuaggccGaa Aauugag B	0340
UCAAUUU U CUAGGGG 5999 183	18344 HBV-279 Rz-7 allyl stab1	cscscsuag cuckucaggccgunaggccsaa Aaauuga B	0259
CAAAAUU C GCAGUCC 6000 183	18347 HBV-314 Rz-7 allyl stab1	9 _S 9 _S 9 _S c _S ugc cUGAuGaggccguuaggcccaa Aauuuug B	0000
GAUGUGU C UGCGGCG 6001 183	18348 HBV-385 Rz-7 allyl stab1	c _S g _C s _C gca cUGAuGaggccguuaggccGaa Acacauc b	0353
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6353	6354	6355	6356	6357	6358	6329	6360	6361	6362	6363	6364	6365	6366	6367	6368	0200	6370	200	6371	6372	5562	93/4	6375	6376	120	6378	6379	9380	6381	6382	6383
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HBV-402 Rz-7 allyl stab1	18353 HBV-423 Rz-7 allyl stab1	19354 HRV-420 R2-7 allvi stab1	10004 PDV-429 PZ-1019 chop4	HDV-079 RZ-1 dilyi sub 1	1835/ HBV-580 RZ-7 allyl stabi	18358 HBV-681 KZ-7 alilyi stabi	18359 HBV-684 Rz-7 allyl stab 1	18360 HBV-692 Rz-7 allyl stab1	18361 HBV-693 Rz-7 allyl stab1	18363 HBV-1534 Rz-7 allyl stab1	18364 HBV-1536 Rz-7 allyl stab1	18365 HBV-1538 Rz-7 allyl stab1	18369 HBV-1787 Rz-7 allyl stab1	18370 HBV-1793 Rz-7 allyl stab1	18372 HBV-1874 Rz-7 allyl stab1	18373 HBV-1887 Rz-7 allyl stab1	HBV-2383 Rz-7 allyl stab1	18377 HBV-2828 Rz-7 allyl stab1	18378 HBV-2829 Rz-7 allyl stab1	18380 HBV-2831 Rz-7 allyl stab1	HBV-255 CHz-7 allyl stab1	18382 HBV-267 CHz-7 allyl stab1	18383 HBV-270 CHz-7 allyl stab1	18384 HBV-272 CHz-7 allyl stab1	18385 HBV-274 CHz-7 allyl stab1	18386 HBV-386 CHz-7 allyl stab1	18387 HRV-419 CH7-7 allvl stab1	18388 HRV-422 CHz-7 allvl stab1	40500 UDV 427 CH2-7 allyl stab1	18309 FIBV 428 CHz.7 alki stab1	18392 HBV-430 CHz-7 allyl stab1
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35 CF	18408 HBV-15	6041 18408 HBV-1535 CHz-7 allyl stab1
37 CF	18409 HBV-1537 CHz-7 allyl stab1	6042 18409 HBV-15
91 C	18413 HBV-1791 CHz-7 allyl stab1	6043 18413 HBV-17
31 0		6044 18415 HBV-18
32 CI	18416 HBV-1832 CHz-7 allyl stab1	6045 18416 HBV-18
72 CI	18417 HBV-1872 CHz-7 allyl stab1	6046 18417 HBV-18
3 C	18418 HBV-18	6047 18418 HBV-1873 CHz-7 allyl stab1
75 CI	18419 HBV-1875 CHz-7 allyl stab1	6048 18419 HBV-18
76 C	18421 HBV-18	6049 18421 HBV-1876 CHz-7 allyl stab1
80 C	18423 HBV-1880 CHz-7 allyl stab1	6050 18423 HBV-18
382 C	18424 HBV-2382 CHz-7 allyl stab1	6051 18424 HBV-23
384 C	18425 HBV-2384 CHz-7 allyl stab1	6052 18425 HBV-2
2385 C	18426 HBV-2385 CHz-7 allyl stab1	6053 18426 HBV-
2422 C	18427 HBV-2422 CHz-7 allyl stab1	6054 18427 HBV-
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268 Rz	19182 HBV-268 Rz-6 amino stab1	6058 19182 HBV-:
280 Rz	19190 HBV-280 Rz-6 amino stab1	6059 19190 HBV-
313 Rz	19191 HBV-313 Rz-6 amino stab1	+
195 Rz	19195 HBV-395 Rz-6 amino stab1	6061 19195 HBV-3
402 Rz	19196 HBV-402 Rz-6 amino stab1	6062 19196 HBV-
607 Rz	19200 HBV-607 Rz-6 amino stab1	6063 19200 HBV-
697 Rz	19207 HBV-697 Rz-6 amino stab1	6064 19207 HBV-

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19211 HBV-1539 Rz-6 amino stab1	19212 HBV-1599 Rz-6 amino stab1	19213 HBV-1607 Rz-6 amino stab1	10216 HRV-1833 R2-6 amino stab1	125.10 LIDY 2303 R2-6 amino clah1	DA-2303 NE-3 amino elabo	19221 TDV-2429 NZ-0 SIIIII SIGN	19224 HBV-2831 RZ-0 amino stabil	19236 HBV-450 CH2-6 amino sabi	19241 HBV-676 CHz-b amino stabi	19242 HBV-683 CHZ-6 amilio stabi	19247 HBV-1150 CHZ-6 amino stabi	19248 HBV-1200 CHZ-6 amino stati	19249 HBV-1201 CHZ-5 amino statut	19250 HBV-1444 CHz-6 amino stab1	19251 HBV-1451 CHz-6 amino stab1	19252 HBV-1533 CHz-6 amino stab1	19255 HBV-1600 CHz-6 amino stab1	19256 HBV-1698 CHz-6 amino stab1	19257 HBV-1784 CHz-6 amino stab1	19259 HBV-1829 CHz-6 amino stab1	19265 HBV-1876 CHz-6 amino stab1	19267 HBV-1880 CHz-6 amino stab1	19178 HBV-218 Rz-7 amino stab1	19181 HBV-257 Rz-7 amino stab1	HBV-268 Kz-/ amino stabi	19184 HBV-269 Rz-7 amino stab1	19185 HBV-271 Rz-7 amino stab1	19186 HBV-273 Rz-7 amino stab1	19187 HBV-277 Rz-7 amino stab1	19188 HBV-278 Rz-7 amino stab1	
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6477	9478	6419	6480	6481	6482	6483	6484	6485	6486	6487	6488	6489	6490	6491	6400	7640	0493	940	0460	6496	6497	6498	6488	6500	6501	6502	6503	6504	6505	6506	6507	
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6239	6540	6541	6542	6543	6544	6545	6546	6547	6548	6249	6550	6551	6552	6553	GEEA	BEEF	9556	2000	200	9229	8560	0000	000	6563	2000	6565	9999	0000	020	9	6000
gsasgsasagg GccgaaagGCCaGugaGGuCu acagacg B	g.g.u.g.aag GccgaaagGCGaGugaGGuCu gaagugc B	a una deccassage George George B	a-II-a-G-ood GoogaagGCGaGugaGGuCu auuuggu B	B See See See See See See See See See Se	Paragraph Conseand Coad and Co	9898898 Construe Cons	Lgagugggag Congrand Calcina Grand Calcina actago B	Csuspengaa occigaaagooogaagaagaagaagaagaagaagaagaagaaga	uscscsasora Grogosady Cosaccas Sassas us	asagguscca occidadagoccascugacoccas asaggus	gsgsasigng congagagoocoagas	Sasys Sustained Control of Suspension of Suspension B	asascsgscog congagagoccacongacocaca agreement	asasasag decigasageceaequasecae agasas	n sagge condendado con a sagge a condendado con a condendado condendado con a condendado co	g _{Scsasus} ag GccgaaagGCGacugaeCucu agcagg b	a _{sascs} g _{sg} g GccgaaagGCGaGugaGGuCuu aacada b	asgsasgs GccgaaagGCCacugaccucu aaacgg c	asgsusasaa GccgaaagGCGaGngaGGnCn ngagcc B	u _S a _S g _S u _S aaa GccgaaagGCGaGugaGGuCu ugagcca B	a _S u _S g _S g _S ca GccgaaagGCGaGugaGGuCu uaguaa B	asasusged Geogaaage CGaGugaeGoron nagnaaa b	c _s a _s a _s a _s ugg GccgaaagGCGaGugaGGuCu acuagua B	g _S a _S a _S csa GcogaaagGCCadcugaGcucu ugaaca b	usascsgaaa Gccgaaagcccaacugacacuga a	c _S u _S a _S c _S gaa GccgaaagGCGaGugaGGuCu cacugaa B	gsgsasag GccgaaagGCGaGugaGGuCu ccuacg B	a _S a _S a _S ga GcogaaagGCGaGugaGGuCu ccacaa B	asgsususgg GccgaaagGCGaGugaGGucu gagaaa b	asasgsusugg GccgaaagGCGaGugaGGucu gagaaag B	c _S a _S g _S c _S aaa GccgaaagGCGaGugaGGuCu acuuggc B
20119 HRV-1559 Zin.Rz-7 amino stab2	20120 July 1500 7in Bz-7 amino stab2	TBV-1390 ZIII.K-1 SIIIII SACE	20121 HBV-1053 ZHIRZ-O dimino stabo	20122 HBV-2311 ZIII.RZ-1 diliilio sees	20123 HBV-2420 Zin.Hz-1 amino statuz	20124 HBV-65 Zm.Rz-/ amino stabz	HBV-192 Zin.Rz-6 amino statiz	20126 HBV-198 Zin.Rz-6 amino stab2	20127 HBV-258 Zin.Rz-7 amino stab2	HBV-261 Zin.Rz-7 amino stab2	HBV-315 Zin.Rz-6 amino stab2	20130 HBV-381 Zin.Rz-6 amino stab2			HBV-417 Zin.Rz-6 amino stab2	20134 HBV-420 Zin.Rz-6 amino stab2	20135 HBV-468 Zin.Rz-6 amino stab2	HBV-476 Zin.Rz-6 amino stab2	20137 HBV-677 Zin.Rz-6 amino stab2	20138 HBV-677 Zin.Rz-7 amino stab2	20139 HBV-685 Zin.Rz-6 amino stab2	20140 HBV-685 Zin.Rz-7 amino stab2	20141 HBV-687 Zin.Rz-7 amino stab2	20142 HBV-699 Zin.Rz-6 amino stab2	20143 HBV-702 Zin.Rz-6 amino stab2	20144 HBV-702 Zin.Rz-7 amino stab2	20145 HBV-711 Zin.Rz-6 amino stab2	HBV-1006 Zin.Rz-6 amino stab2	20147 HBV-1103 Zin.Rz-6 amino stab2	20148 HBV-1103 Zin.Rz-7 amino stab2	20149 HBV-1184 Zin.Rz-7 amino stab2
20119	2000	20120	12102	22102	20123	20124	20125	20126	20127	20128	20129	20130	20131	20132	20133	20134	20135	20136	20137	20138	20139	20140	20141	20142	20143		20145	20146		20148	20149
6180	+	-	-+	-	\rightarrow	-	-	9619	6197	6198	6199	6200	6201	6202	6203	6204	6205	6206	6207	6208	6209	6210	6211	6212	6213	6214	6215	6216	6217	6218	6219
	+	5	+	-	-	0	ACCCCU 6 CUCGUG	⊢	UAGACUC G UGGUGGA	ACUCGUG G UGGACUU	AAAUUC G CAGUCC	CUGGAU GUGUCUG	nenench e ceecenn	UCUGCG G CGUUUU	CAUCCU G CUGCUA	CCUGCU G CUAUGC	UAUGUU G CCCGUU	CCGUUU G UCCUCU	COCIOS GUILIACU	LIGGCIICA G UUUACUA	UNACUA G UGCCAU	HILIACHA G UGCCAUU	UACUAGO G CCAUUUG	UGUUCA G UGGUUC	UCAGUG G UUCGUA	UUCAGUG G UUCGUAG	CGUAGG G CUUUCC	UUGUGG G UCUUUU	UNICIDE G CCAACU	CHILICITO G CCAACUU	-
	1229	1590	1835	2311	2420	65	192	198	258	261	315	381	387	390	417	420	468	476	277	677	685	SBR BR	687	669	202	702	1	1006	1103	1403	1184

	cceuce e cecuea	6220	20150	20150 HBV-1440 Zin.Rz-6 amino stab2	u _s c _s a _s g _s cg GccgaaagGCGaGugaGGuCu cgacgg B	6570
۲	GUCGGC G CUGAAU	6221	20151	20151 HBV-1442 Zin.Rz-6 amino stab2	a _{SuSuSuS} esag GccgaaagGCGaGugagGuCu gccgac B	6571
O	COUCGGC G CUGAAUC	6222	20152	20152 HBV-1442 Zin.Rz-7 amino stab2	g _s a _s u _s u _s cag GccgaaagGCGaGugaGGuCu gccgacg B	6572
1	cuccoc a ucuana	6223	20153	20153 HBV-1553 Zin.Rz-6 amino stab2	c _{Sascs} asga GccgaaagGCGaGugaGGuCu ggggag B	6573
1	cceucu e ueccuu	6224	20154	20154 HBV-1557 Zin.Rz-6 amino stab2	a _s a _{sgsgs} ca GccgaaagGCGaGugaGGuCu agacgg B	6574
1	encuen e connon	6225	20155	20155 HBV-1559 Zin.Rz-6 amino stab2	a _S g _S a _S a _S gg GccgaaagGCGaGugaGGuCu acagac B	9259
1	cceugu e cacuuc	6226	20156	20156 HBV-1583 Zin.Rz-6 amino stab2	gsasasus GccgaaagGCGaGugaGGuCu acacgg B	9259
1	CACUUC G CUUCAC	6227	20157	20157 HBV-1590 Zin.Rz-6 amino stab2	g _s u _s g _s a _s ag GccgaaagGCGaGugaGGuCu gaagug B	6577
	ACCACC G UGAACG	6228	20158	20158 HBV-1622 Zin.Rz-6 amino stab2	c _s g _S u _S u _S ca GccgaaagGCGaGugaGGuCu gguggu B	6578
1-	JGUUCAA G CCUCCAA	6229	20159	20159 HBV-1870 Zin.Rz-7 amino stab2	u _s u _{sgs} g _s agg GccgaaagGCGaGugaGGuCu uugaaca B	6259
10	CCAAGCU G UGCCUUG	6230	20160	20160 HBV-1881 Zin.Rz-7 amino stab2	c _s a _s a _s g _s gca GccgaaagGCGaGugaGGuCu agcuugg B	6580
	AGCUGU G CCUUGG	6231	20161	20161 HBV-1883 Zin.Rz-6 amino stab2	c _S c _S a _S a _S gg GccgaaagGCGaGugaGGuCu acagcu B	6581
	AAGCUGU G CCUUGGG	6232	20162	20162 HBV-1883 Zin.Rz-7 amino stab2	c _S c _S c _S a _S agg GccgaaagGCGaGugaGGuCu acagcuu B	6582
	CCAAAU G CCCCUA	6233	20163	20163 HBV-2311 Zin,Rz-6 amino stab2	u _s a _s g _s g _s gg GccgaaagGCGaGugaGGuCu anuugg B	6583
	ACUGUU G UUAGAC	6234	20164	20164 HBV-2347 Zin.Rz-6 amino stab2	g _{Suscs} usaa GccgaaagGCGaGugaGGuCu aacagu B	6584
	AGGCAG G UCCCCU	6235	20165	20165 HBV-2364 Zin.Rz-6 amino stab2	a _{sgsgsgs} ga GccgaaagGCGaGugaGGuCu cugccu B	6585
	GAGGCAG G UCCCCUA	6236	20166	20166 HBV-2364 Zin.Rz-7 amino stab2	u _s a _s g _s gga GccgaaagGCGaGugaGGuCu cugccuc B	9859
	ucccuc e ccucec	6237	20167	20167 HBV-2388 Zin.Rz-6 amino stab2	g _S c _S g _S agg GccgaaagGCGaGugaGGuCu gaggga B	6587
	CGCCUC G CAGACG	6238		20168 HBV-2393 Zin.Rz-6 amino stab2	c _s g _s u _s c _s ug GccgaaagGCGaGugaGGuCu gaggcg B	6588
	ceccec e ucecae	6239	20169	20169 HBV-2417 Zin.Rz-6 amino stab2	c _S u _S g _S c _S ga GccgaaagGCGaGugaGGuCu gcggcg B	6283
	CGCGUC G CAGAAG	6240	20170	20170 HBV-2420 Zin.Rz-6 amino stab2	c _{SuSuSuS} ug GccgaaagGCGaGugaGGuCu gacgcg B	6590
	CAUAAG G UGGGAA	6241	20171	20171 HBV-2474 Zin.Rz-6 amino stab2	u _S u _S c _S ca GccgaaagGCGaGugaGGuCu cuuaug B	6591
	GCUGGAU G UGUCUGC	6242	20172	20172 HBV-381 Amb.Rz-7 stab2	g _S c _S a _S g _S aca gga L ucCCUUCaagga L ucCGGG auccagc B	6592
	UAUGGGA G UGGGCCU	6243	20173	20173 HBV-648 Amb.Rz-7 stab2	aggagcsca gga L ucccuucaagga L uccGGG ucccaua B	6593
	UGCUCGU G UUACAGG	6244	20174	20174 HBV-198 Amb.Rz-7 stab2	c _S c _S u _S g _S uaa gga L uc CCUUC aagga L ucCGGG acgagca B	6594
	UAUCGCU G GAUGUGU	6245	20175	20175 HBV-377 Amb.Rz-7 stab2	ascsascsauc aga L ucCCUUCaagga L ucCGGG agcgaua B	9629
	AUCGCUG G AUGUGUC	6246	20176	20176 HBV-378 Amb.Rz-7 stab2	g _S a _S c _S a _S cau gga L uc CCUUC aagga L uc C GGG cagcgau B	9629
	UGGAUGU G UCUGCGG	6247	20177	20177 HBV-383 Amb.Rz-7 stab2	cscsgscsaga gga L ucccuucaagga L uccGGG acaucca B	6597
	GGAUGU G UCUGCG	6248	20178	20178 HBV-383 Amb.Rz-6 stab2	c _S g _S c _S a _S ga gga L uc CCUUC aagga L uc C GGG acaucc B	6598
	AUGGGA G UGGGCC	6249		20179 HBV-648 Amb.Rz-6 stab2	gsgscscs gga LucCCUUCaagga LucCGGG ucccau B	629
	UGGGAGU G GCCCUCA	6250	20180	20180 HBV-650 Amb.Rz-7 stab2	usgsasgsoc aga L ucccuucaagga L uccGGG acucca B	0099

20181 HBV-650 Amb.Rz-6 stab2
20182 HBV-694 Amb. RZ-7 stab2
20183 HBV-699 Amb.Rz-7 stab2
20184 HBV-701 Amb.Rz-7 stab2
20185 HBV-710 Amb.Rz-7 stab2
20186 HBV-1525 Amb.Rz-6 stab2
20187 HBV-1624 Amb.Rz-6 stab2
20188 HBV-2069 Amb.Rz-6 stab2
20189 HBV-2375 Amb.Rz-7 stab2
6260 20190 HBV-2476 Amb.Rz-7 stab2
6261 20191 HBV-65 Amb.Rz-7 stab2
6262 20192 HBV-67 Amb.Rz-6 stab2
6263 20193 HBV-198 Amb.Rz-6 stab2
6265 20195 HBV-263 Amb.Rz-7 stab2
-
6267 20197 HBV-378 Amb.Rz-6 stab2
6268 20198 HBV-476 Amb.Rz-6 stab2
6269 20199 HBV-651 Amb.Rz-7 stab2
6270 20200 HBV-677 Amb.Rz-7 stab2
6271 20201 HBV-685 Amb.Rz-7 stab2
6272 20202 HBV-702 Amb.Rz-7 stab2
20203 HBV-709 Amb.Rz-7 stab2
6274 20204 HBV-710 Amb.Rz-6 stab2
_
6276 20206 HBV-1557 Amb.Rz-6 stab2
6277 20207 HBV-1881 Amb.Rz-7 stab2
6278 20208 HBV-2347 Amb.Rz-6 stab2
6279 20209 HBV-2375 Amb.Rz-6 stab2
6280 20210 HBV-2378 Amb.Rz-6 stab2
6281 20211 HBV-2423 Amb.Rz-7 stab2

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	POLICIES & ALICHOA	6282	20212	CCACAA G ALICLICA 6282 20212 HBV-2426 Amb.Rz-6 stab2	u _{sgsags} au gga L ucccUVCaagga L ucCGGGG uucugc B	2699
- 12	CCCACA CALICICAA	6283	20213	20213 HBV-2426 Amb.Rz-7 stab2	u.u.g.a.gau gga L ucccuucaagga L uccGGG uucugcg B	6633
		6284	_	20214 HBV-2476 Amb.Rz-6 stab2	g _{Susus} us og gga L ucCCUUCaagga L ucCGGG accuua B	6634
	DAAGGUG G GAAACUU	6285	20215	20215 HBV-2477 Amb.Rz-7 stab2	asasgsusuuc gga L ucccuuCaagga L ucCGGG caccuua B	6635
	AAGGUG G GAAACU	6286		20216 HBV-2477 Amb.Rz-6 stab2	asgsusus aga L ucCCUUCaagga L ucCGGG caccuu B	9836
	Τ,	6287	20697	6287 20697 HBV-1607 Rz-7 allyl stab1 (7/4)	uscsesauge cUGAuGaggeegunaggeeGaa Aegugea B	6637
	9911991111999119	6288		20698 HBV-1887 Rz-6 allyl stab1 (6/4)	c _s c _s a _s c _s cc cUGAuGaggccguuaggccGaa Aggcac B	6638
	GCACGU C GCAUGG	6289		20699 HBV-1607 Rz-6 allyl stab1 (6/3)	c _s c _s a _s u _s gc cUGAuGaggcguuagccGaa Acgugc B	6639
	LIGCACGLI C. GCALIGGA	6290	20700	6290 20700 HBV-1607 Rz-7 allyl stab1 (7/3)	uscses asuge cUGAuGaggegunageeGaa Aegugea B	6640
	GIRCOU U GGGUGG	6291	20701	6291 20701 HBV-1887 Rz-6 allyl stab1 (6/3)	c _s c _s a _s c _s cc cUGAuGaggcgunagccGaa Aggcac B	6641
	١.,	6292	20702	6292 20702 HBV-1887 Rz-7 allvl stab1 (7/3)	gcccaaccc cUGAuGaggcguuagccGaa Aggcaca B	6642

UPPER CASE = RIBO lover case = 2*-O-methyl se = phosphorothioate linkage B = inverted deoxyabasic residue U = 2*-deoxy2*-canity Uridine U = 2*-deoxy2*-amino Uridine C = 2*-deoxy2*-amino Cytidine C = 2*-deoxy2*-amino Cytidine

Table 44: Group Designation and Dosage levels for HBV transgenic mouse study

Group	Compound	Dose	Number of Mice	Duration of Treatment
1	RPI.18341 (site 273)	100 mg/kg/day*	10F	14 days
2	RPI.18371 (site 1833)	100 mg/kg/day*	10F	14 days
3	RPI.18418 (site 1873)	100 mg/kg/day*	10F	14 days
4	RPI.18372 (site 1874)	100 mg/kg/day*	10F	14 days
5	Saline control	100 mg/kg/day*	10F	14 days
6	Untreated		10F	0 days

^{*}administered via sc infusion using Alzet mini-osmotic pumps

Table 45

TABLE 45. NUCLEOSIDES USED FOR CHEMICAL SYNTHESIS OF MODIFIED NUCLEOTIDE TRIPHOSPHATES

	NUCLEOSIDES	Abbreviation	CHEMICAL STRUCTURE
1	2'-O-methyl-2,6- diaminopurine riboside	2'-O-Me-DAP	HO OCH ,
2	2'-deoxy-2'amino-2,6- diaminopurine riboside	2'-NH2-DAP	NH ₂ NH ₂ N NH ₂ N NH ₂ N NH ₂ N NH ₂
3	2'-(N-alanyl)amino-2'- deoxy-uridine	ala-2′- NH₂ U	HO HN H-CH ₃
4	2'-(N- phenylalaryl)amino-2'- deoxy-uridine	phe-2′- NH₂-U	HO HN H-CH ₂ Ph
- 5	2'-(N-β-alanyl) amino- 2'-deoxy uridine	2'-β-Ala-NH ₂ -U	HO HN NH ₂

Table 45

6	2'-Deoxy-2'-(lysiyl)	2'-L-lys-NH2-U	0
	amino uridine		N.H
			HO ONO
	1		$ \qquad \qquad $
			HÓ HN NH₂
			NH ₂
7	2'-C-allyl uridine	2'-C-allyl-U	9
			HO, NO
8			но 🥠
8	2'-O-amino-uridine	2'-O-NH ₂ -U	L.H
	}		[N ·]
			HO
			HO O, NH₂
9	2'-O-methylthiomethyl adenosine	2'-O-MTM-A	NH ₂
	aderiosine		HO N
)
			но о
			s
10	2'-O-methylthiomethyl cytidine	2'-O-MTM-C	NH ₂
	Cytiaine		r
			HO
			> -
			но і
			s

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Table 45

		Table 4	15
11	2 ² -O-methylthiomethyl guanosine	2'-O-MTM-G	HO NH NH2
12	2-O-methylthiomethyl- uridine	2'-O-MTM-U	HO O
13	2-(N-histidyl) amino uridine	2'-his-NH ₂ -U	HO NH ₂
14	2'-Deoxy-2'-amino-5- methyl cytidine	5-Me-2'-NH⊬C	HO NH ₂

Table 45

15	2'-(Λ-β-carboxamidine- β-alanyi)amino-2'- deoxy-uridine	β-ala-CA-NH2-U	HO HO C C C NH2
16	2'4(N-β-alanyl) guanosine	β-Ala-NH2-G	HO NH ₂
17	2'-O-Amino-Uridine	2'-O-NH2-U	HO NH ₂
18	2'-(N-lysyl)amino -2'- deoxy-cytidine	2'- NH₂-lys-C ·	10 100

Table 45

	19	T		
	-	2°-Deoxy -2°-(L- histidine) amino Cyt'dine	2'- NHz-his-C	HO - NH -
	20	5-Imidazoleacetic acid 2'-deoxy uridine	5-IAA-U	HO NH HI
	21	5-[3-(N-4- imidazoleacetyl)amino propynyl]-2'-O-methyl uridine	5-IAA- propynylamino- 2'-OMe U	HO DCH ₃
	22	5-(3-aminopropynyl)- 2'-O-methyl uridine	5-aminopropynyl- 2'-OMe U	HO OCH ₃
Ţ	23	5-(3-aminopropyl)-2'- O-methyl uridine	5-aminopropyl- 2'-OMe U	HO OCH3
	24	5-[3-(N-4- imidazoleacetyl)amino propyl]-2'-O-methyl Uridine	5-IAA- propylamino-2'- OMe U	HQ (CH ₃)-NHCOC-I

Table 45

25	5-(3-aminopropyl)-2'- deoxy-2-fluoro uridine	5-aminopropyl- 2'-F dU	HO CCH2)3NH2
26	2'-Deoxy-2'-(β-alanyl- L-histidyl)amino Uridine	2'-amino-β-ALA- HIS dU	DH CHAPTER THE CHA
	!	*	HN NH ₂ NH
27	2'-deoxy-2'-β- alaninamido-uridine	2'-β-ALA dU	HO HN NH2
28	3-(2'-deoxy-2'-fluoro-β- D- ribofuranosyl)piperazin o[2,3-D]pyrimidine-2- one	2'-F piperazino- pyrimidinone	HO S
29	5-[3-(N-4- imidazoleacetyl)amino propyll-2'-deoxy-2'- fluoro Uridine	5-IAA- propylamino-2'-F dU	HO (CH ₂),NHCCCH ₂

Table 45

			Table 2	+5
***	30	5-[3-(N-4- imidazoleacetyl)amino propynyl]-2'-deoxy-2'- fluoro uridine	5-IAA- propynylamino- 2'-F dU	HO F
	31	5-E-{2-carboxyvinyl-2'- deoxy-2'-fluoro uridine	5-carboxyvinyl- 2'-F dU	но о н
,	32	5-[3-(N-4- aspartyl)aminopropyny I-2'-fluoro uridine	5-ASP- aminopropyl-2'-F- dU	NHGOCHN9-2CH2COOH
	3 3	5-(3-aminopropyl)-2'- deoxy-2-fluoro cyticine	5-aminopropyl- 2'-F dC	HO NH2
	34	5-[3-(N-4- succynyl)aminopropyl- 2'-deoxy-2-fluoro cytidine	5-succynylamino- propyl-2'-F dC	#H ₂ NHCO(CH ₃) ₂ COOH

605 Table 46

Table 46: PHOSPHORYLATION OF URIDINE IN THE PRESENCE OF DMAP

0 equiv	. DMAP	0.2 equi	v. DMAP	0.5 equi	v. DMAP	1.0 equi	v. DMAP
Time	Product	Time	Product	Time	Product	Time	Product
(min)	%	(min)	%	(min)	%	(min)	%
0	1	0	0	0	0	0	0
40	7	10	8	20	27	30	74
80	10	50	24	60	46	70	77
120	12	90	33	100	57	110	84
160	14	130	39	140	63	150	83
200	17	170	43	180	63	190	84
240	19	210	47	220	64	230	77
320	20	250	48	260	68	270	79
1130	48	290	49	300	64	310	77
1200	46	1140	68	1150	76	1160	72
		1210	69	1220	76	1230	74

Table 47: Detailed Description of the NTP Incorporation Reaction Conditions

Condition	TRIS-HCL	MgCl ₂	E į	Spermidine	Triton	METHANOL	LiCi	PEG	Temp(°C)
, Z	(miwi)	(MILL)	(MIM)	(mim)	V-100 (%)	(%)		8	30
_	40 (pH 8.0)	₹	2	ဂ	0.0	2	_		2
5	40 (pH 8.0)	20	9	2	0.01	9	-	4	52
က	40 (pH 8.1)	12	ß	-	0.002			4	25
4	40 (pH 8.1)	12	2	-	0.002	9		4	25
2	40 (pH 8.1)	12	2	-	0.002		-	4	25
9	40 (pH 8.1)	12	2	-	0.002	10	-	4	25
AND THE RESERVE	THE RESERVE OF THE PARTY OF THE						の対象を		
7	40 (pH 8.0)	20	10	5	0.01	10	-		37
œ	40 (pH 8.0)	20	9	2	0.01	9	-	4	37
6	40 (pH 8.1)	12	2	-	0.002		1	4	37
9	40 (pH 8.1)	12	2	-	0.002	9	,	4	37
1	40 (pH 8.1)	12	2	-	0.002		-	4	37
12	40 (pH 8.1)	12	ß	-	0.002	9	_	4	37

Table 48: INCORPORATION OF MODIFIED NUCLEOTIDE TRIPHOSPHATES

Modification	COND#	COND#	COND#	COND#	COND#	COND#	COND#	COND#	COND#	COND#	COND#	COND#
	-	~	٣	4	S	9	7	80	6	9	=	12
2'-NH ₂ -ATP	F	2	9	5	2	4	-	2	9	11	9	6
2'- NH ₂ -CTP	1	37	45	94	25	70	56	54	292	264	109	244
2'- NH ₂ -GTP	4	7	9	14	5	17	က	16	10	21	6	16
2'- NH ₂ -UTP	14	45	4	100	85	82	48	88	20	418	429	440
2'-dATP	6	6	19	23	6	24	9	3	84	2	28	51
2'-dCTP	-	10	43	46	35	47	27	127	204	212	230	235
2'-dGTP	9	10	6	15	6	12	8	34	38	122	31	46
2'-dTTP	6	6	14	18	13	18	8	15	116	114	29	130
2'-O-Me-ATP	0	0	0	0	_	0	-	1	2	2	2	2
2'-O-Me-CTP	no data c	no data compared to ribo; incorporates at low level	to ribo; i	ncorpora	tes at low	level						
2'-O-Me-GTP	4	6	4	4	4	4	2	4	4	2	4	5
2'-O-Me-UTP	22	52	39	38	41	48	55	71	93	103	81	77
2'-O-Me-DAP	4	4	3	4	4	9	4	3	4	5	9	2
2'- NH ₂ -DAP	0	0	Ī	-	_		-	0	°	0	_	°
ala-2'-NH ₂ -UTP	2	2	2	2	en	4	14	18	15	20	13	14
phe-2'-NH ₂ -UTP	8	12	7	7	8	8	4	10	9	9	10	9
2'-ß NH ₂ -ala-UTP	92	48	25	17	21	21	220	223	265	300	275	248
2'-F-C5-carboxyvinyl UTP									100	0		
2'-F-C5-aspartyl-									100	0		

Table 4

aminopropył UTP							
2'-F-C5-propylamine CTP					100		
2'-O-Me CTP					0		
2'-O-Me UTP					25		
2'-O-Me 5-3-aminopropyl UTP					4		
2'-O-Me 5-3-aminopropyl					10		

Table 49: INCORPORATION OF MODIFIED NUCLEOTIDE TRIPHOSPHATES USING WILD TYPE BACTERIOPHAGE T7 POLYMERASE

Modification	label	% ribo control
2'-NH2-GTP	ATP	4%
2'-dGTP	ATP	3%
2'-O-Me-GTP	ATP	3%
2'-F-GTP	ATP	4%
2'-O-MTM-GTP	ATP	3%
2'-NH2-UTP	ATP	39%
2'-dTTP	ATP	5%
2'-O-Me-UTP	ATP	3%
ala-2'-NH2-UTP	ATP	●%
phe-2'-NH ₂ - UTP	ATP	1%
2'-β-ala-NH2-UTP	ATP	3%
2'-C-allyl-UTP	ATP	●%
2'-O-NH2-UTP	ATP	1%
2'-O-MTM-UTP	ATP	64%
2'-NH2-ATP	GTP	1%
2'-O-MTM-ATP	GTP	1%
2'-NH2-CTP	GTP	59%
2'-dCTP	GTP	40%
2'-F-CTP	GTP	100%
2'-F-UTP	GTP	100%
2'-F-TTP	GTP	0%
2'-F-C5-carboxyvinyl UTP	GTP	100%
2'-F-C5-aspartyl-aminopropyl UTP	GTP	100%
2'-F-C5-propylamine CTP	GTP	100%
2'-O-Me CTP	GTP	0%
2'-O-Me UTP	GTP	0%
2'-O-Me 5-3-aminopropyl UTP	GTP	0%
2'-O-Me 5-3-aminopropyl UTP	GTP	0%

Table 50 a: Incorporation of 2'-his-UTP and Modified CTP's

modification	2'-his-UTP	rUTP
CTP	16.1	100
2'-amino-CTP	9.5*	232.7
2'-deoxy-CTP	9.6*	130.1
2'-OMe-CTP	1.9	6.2
2'-MTM-CTP	5.9	5.1
control	1.2	

Table 50 b: Incorporation of 2'-his-UTP, 2-amino CTP, and Modified ATP's

modification	2'-his-UTP and 2'-amino-CTP	rUTP and rCTP
ATP	15.7	100
2'-amino-ATP	2.4	28.9
2'-deoxy-ATP	2.3	146.3
2'-OMe-ATP	2.7	15
2'-F-ATP	4	222.6
2'-MTM-ATP	4.7	15.3
2'-OMe-DAP	1.9	5.7
2'-amino-DAP	8.9*	9.6

Numbers shown are a percentage of incorporation compared to the all-RNA control

^{* -}Bold number indicates best observed rate of modified nucleotide triphosphate incorporation

Table 51: INCORPORATION OF 2'-his-UTP, 2'-NH₂-CTP, 2'-NH₂-DAP, and rGTP USING VARIOUS REACTION CONDITIONS

Conditions	compared to all rNTP
7	8.7*
8	7*
9	2.3
10	2.7
11	1.6
12	2.5

Numbers shown are a percentage of incorporation compared to the all-RNA control

^{*} Two highest levels of incorporation contained both methanol and LiCI

Table 52: Selection of Oligonucleotides with Ribozyme Activity

pool	Generation	time	substrate remaining(%)	time	Substrate remaining (%)
N60	0	4 hr	100.00	24 hr	100.98
N60	14	4 hr	99.67	24 hr	97.51
N60	15	4 hr	98.76	24 hr	96.76
N60	16	4 hr	97.09	24 hr	96.60
N60	11	4 hr	79.50	24 hr	64.01
N40	0	4 hr	99.89	24 hr	96.76
N40	10	4 hr	99.74	24 hr	99.42
N40	11	4 hr	97.18	24 hr	90.38
N40	12	4 hr	61.64	24 hr	44.54
N40	13	4 hr	54.28	24 hr	36.46
N20	0	4 hr	99.18	24 hr	100.00
N20	11	4 hr	100.00	24 hr	100.00
N20	12	4 hr	99.51	24 hr	100.00
N20	13	4 hr	90.63	24 hr	84.89
N20	11	4 hr	91.16	24 hr	85.92
N60B	0	4 hr	100.00	24 hr	100.00
N60B	1	4 hr	100.00	24 hr	100.00
N60B	2	4 hr	100.00	24 hr	100.00
N60B	3	4 hr	100.00	24 hr	100.00
N60B	4	4 hr	99.24	24 hr	100.00
N60B	5	4 hr	97.81	24 hr	96.65
N60B	6	4 hr	89.95	24 hr	77.14

Table 53: Kinetic Activity of Combinatorial Libraries

Pool	Generation	k _{obs} (min ⁻¹)
N60	14	0.0372
	18	0.0953
	19	0.0827
N40	12	0.0474
	13	0.037
	14	0.065
	15	0.0254
N20	19	0.0359
	14	0.0597
	15	0.0549
	16	0.0477
N60B	6	0.0209
	7	0.0715
	8	0.0379

Table 54: Kinetic Activity of Clones within N60 and N40 Combinatorial Libraries

clone	library	activity(min ⁻¹)	k _{rel}
G18	N60	0.00226	1.00
0-2	N60	0.0389	17.21
0-3	N60	0.000609	0.27
0-5	N60	0.000673	0.30
0-7	N60	0.00104	0.46
0-3	N60	0.000739	0.33
0-11	N60	0.0106	4.69
0-12	N60	0.00224	0.33
0-13	N60	0.0255	11.28
0-14	N60	0.000878	0.38
0-15	N60	0.0000686	0.03
0-21	N60	0.0106	4.82
0-22	N60	0.000835	0.37
0-24	N60	0.000854	0.29
0-24	N40	0.000741	0.33
0-35	N40	0.00658	2.91
3-1	N40	0.0264	11.68
3-3	N40	0.000451	0.29
3-7	N40	0.000854	0.38
3-15	N40	0.000832	0.37

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Table 55: Effect of Magnesium Concentration of the Cleavage Rate of N20

[Mg ⁺⁺]	k _{obs} (min ⁻¹)
25	0.0259
20	0.0223
15	0.0182
10	0.0208
5	0.0121
2	0.00319
2	0.00226

Table 56

Enzymatic Nucleic Acid Motifs Targeting HCV

Rz Seq ID	39	40	41	42	43	44	45	46	47	48	4.9	20	51	52	53	54	55	26	57	28	29	09	61	62	63	64	9	99	29	89	69	7.0	7	
	cccau B	gugaa B	auggc B	caugg B	acgac B	agacc B	agunc B	a nanaa	aauuc B	agucg B	cgguc B	aggca B	agucu B	aacac B	caaca B	gaccc B	cuuuc B	acaag B	cuauc B	acccu B	cccca B		cggga B	acuan B	gcaga B	aagaa B	g n6666	auuga B	aganc B	caaau B	ccaaa B	acgcc B	99999 B	
Sequence	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCGGG		Ggaggaaacucc cu uchhGGACAUCGUCGGG	Ggaggaaacucc cu UCAAGGACAUCGUCCGGG	cccaaaucuc GgaggaaacucC CU UCAAGGACAUCGUCGGG aggca	CU UCAAGGACAUCGUCGGG agueu	Ggaggaaacucc CU UCAAGGACAUCGUCCGGG aacac	Ggaggaaacucc CU UCAAGGACAUCGUCGGG caaca	Ggaggaaacucc CU UCAAGGACAUCGUCGGG	Ggaggaaacucc CU UCAAGGACAUCGUCGGG cuuuc B	caggoaguac Ggaggaaacucc CU UCAAGGACAUCGUCGGG acaag	ucgcaagcac GgaggaaacucC CU UCAAGGACAUCGUCCGGG cuauc	Ggaggaaacucc CV UCAAGGACAUCGUCGGG acccu	GgaggaaacucC CU UCAAGGACAUCGUCGGG cccca	auggeueuee Ggaggaaaeuee eu UCAAGGACAUCGUCGGG gggag	uauggcucuc Ggaggaaacucc cu uchAGGACAUCGUCCGGG cggga	UCAAGGACAUCGUCCGGG acuau	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCGGGG	UCAAGGACAUCGUCCGGG	UCAAGGACAUCGUCCGGG	
Se	Ggaggaaacucc CU	Ggaggaaacucc CU		Ggaggaaacucc CU	Ggaggaaacucc CU	Ggaggaaacucc CU	Ggaggaacucc				GgaggaaacucC CU	Ggaggaaacucc CU	GgaggaaacucC			GgaggaaacucC CU	Ggaggaaacucc CO	Ggaggaaacucc CO	Ggaggaaacucc CO	GgaggaaacucC CU	GgaggaaacucC CT	Ggaggaaacucc CU	GgaggaaacucC CU	uuccgcagac GgaggaaacucC CU	GaagaaacucC CO	GgaggaaacucC CU	GgaggaaacucC CU	Gaagaaacncc co	Ggaggaaacucc CU	GgaggaaacucC CT		GgaggaaacucC CU	Ggaggaaacucc CO	
	ggaguguege	acgcuuucug	anacuaacgc	cauacuaacg	cnagaagana	accggnuccg	guguacucac	cuggcaauuc	66ncon6cn66	agaaaggacc	aagaaaggac	cccaaaucuc	acueggenag	unucgcgacc	cuuucgegae	aggccuucg	uaccacaagg	caggcaguac	ucgcaagcac	cacucgcaag	uggagugueg	auggeueuce	uauggcucuc	uuccgcagac	ucaccaguuc	cgggunauc	aggcauugag	aancnccagg	ggggcacgcc	9999954595	cgggggcacg	cangeggggg	agcagucuug	
Alías	HCV.R1A-6 Amb.Rz-10/5	HCV.R1A-56 Amb.Rz-10/5	HCV.R1A-75 Amb.Rz-10/5	HCV.R1A-76 Amb.Rz-10/5	HCV.R1A-95 Amb.Rz-10/5	HCV.R1A-138 Amb.Rz-10/5	HCV.R1A-146 Amb.Rz-10/5	HCV.R1A-158 Amb.Rz-10/5	HCV.R1A-164 Amb.Rz-10/5	HCV.R1A-176 Amb.Rz-10/5	HCV.R1A-177 Amb.Rz-10/5	HCV.R1A-209 Amb.Rz-10/5	HCV.R1A-237 Amb.Rz-10/5	HCV.R1A-254 Amb.Rz-10/5	HCV.R1A-255 Amb.Rz-10/5	HCV.R1A-259 Amb.Rz-10/5	HCV.R1A-266 Amb.Rz-10/5	HCV.R1A-273 Amb.Rz-10/5	HCV.R1A-288 Amb.Rz-10/5	HCV.R1A-291 Amb.R2-10/5	HCV.R1A-7 Amb.Rz-10/5	HCV.R1A-119 Amb.Rz-10/5	HCV.R1A-120 Amb.Rz-10/5	HCV.R1A-133 Amb.Rz-10/5	HCV.R1A-140 Amb.Rz-10/5	HCV.R1A-188 Amb.Rz-10/5	HCV.R1A-198 Amb.Rz-10/5	HCV.R1A-205 Amb.Rz-10/5	HCV.R1A-217 Amb.Rz-10/5	HCV.R1A-218 Amb.Rz-10/5	HCV.R1A-219 Amb.Rz-10/5	HCV.R1A-223 Amb.Rz-10/5	HCV.R1A-229 Amb.Rz-10/5	
Seq ID	н	2	9	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	
	SUCC	3000	30,80	JAUG	CCAG	39GU	CAC	CAG	CGAC	JUCT	JCOD	3666	3AGU	SAAA	AAAG	3ccn	BGUA	COUG	3CGA	AGUG	JCCA	SCAU	CAUA	3GAA	3UGA	5000	CCU	SAUU	သင္သင	၁၁၁၁	2000	CAAG	JGCU	ı

Table 56

295	295 UGCUUGCGAGUGCCCC	35	HCV.R1A-295 Amb.Rz-10/5	gggcacucg Gga	ggggcacucg GgaggaaacucC CU UCAAGGACAUCGUCCGGG aagca B	73
301	301 CGAGUGCCCCGGGAGG	36	HCV.R1A-301 Amb.Rz-10/5	concoceded Gaa	g Sonoe 9990000000000000000000000000000000000	74
306	GCCCCGGGAGGUCUCG	3.7	HCV.R1A-306 Amb.Rz-10/5	cgagaccucc Ggag	cgagaccucc GgaggaaacucC CU UCAAGGACAUCGUCGGG ggggc B	7.5
307	CCCCGGGAGGUCUCGU	38	HCV.R1A-307 Amb.Rz-10/5	_	acgagaccuc GgaggaaacucC CU UCAAGGACAUCGUCGGG cgggg B	9/
No				Ggaaaggugugcaa	GgaaaggugugcaaccggagucaucauaauggcuucCCUUCaaggaCaUCgCCg	
Ribo				ggacggcB		
Ribo				GGAAAGGUGUGCAA	SGAAAGGUGUGCAACCGGAGUCAUCAUAAUGGCUCCCUUCAAGGACAUCGUCCGGG	
				ACGGCB		

lower case = 2.-O-methyl
U, C = 2'-deoxy-2'-amino U, E 2'-deoxy-2'-amino C
U, C = 2'-deoxy-2'-amino D
B = inverted deoxyabasic

618

Table 57. Additional Class II enzymatic nucleic acid Motifs

Class II Motif ID	Sequence	Seq ID No.	Kinetic Rate
A2	GGGAGGAGGAGUGCCUGGUCAGUCACACCGAGACUGGCAGACGCUGAAACC GCCGCGCUCGCUCCCAGUCC	77	UNK
A12	GGGAGGAGGAAGUGCCUGGUAGUAAUAUAUAAUCGUUACUACGAGUGCAAGGUC GCCGCGCUCGCUCCCAGUCC	78	UNK
A11	GGGAGGAGGAAGUGCCUGGUAGUUGCCCGAACUGUGACUACGAGUGAGGUC GCCGCGCUCGCUCCCAGUCC	79	UNK
B14	GGGAGGAGGAGGCCUGGCGAUCAGAUGAGAUGAUGGCAGACGCAGAGACC GCCGCGCUCGCUCCCAGUCC	80	UNK
B10	GGGAGGAGGAAGUGCCUGGCGACUGAUACGAAAAGUCGCAGUUUCGAAACC GCCGCGCUCGCUCCCAGUCC	81	UNK
B21	GGGAGGAGGAAGUGCCUGGCGACUGAUACGAAAAGUCGCAGGUUUCGAAACC GCCGCGCUCCCCAGUCC	82	UNK
В7	GGGAGGAGGAAGUGCCUUGGCUCAGCAUAAGUGAGCAGAUUGCGACACC GCCGCGCUCGCUCCCAGUCC	83	UNK
C8	GGGAGGAGGAAGUGCCUUGGUCAUUAGGAUGACAAACGUAUACUGAACACU GCCGCGCUCGCUCCCAGUCC	84	0.01 MIN ⁻¹

Table 58 Tab

Ribozyme Alias
erbB2-180 Zin.Rz-6 amino stabl
erbB2-184 Zin.Rz-6 amino stabl
erbB2-276 Zin.Rz-7
erbB2-314 Zin.Rz-6 amino stabl
erbB2-314 Zin.Rz-7
erbB2-379 Zin.Rz-6 amino stabl
erbB2-433 Zin.Rz-7 amino stabl
erbB2-594 Zin.Rz-6 amino stabl
erbB2-594 Zin.Rz-7 amino stabl
erbB2-597 Zin.Rz-6 amino scabl
erbB2-597 Zin.Rz-7
crbB2-659 Zin.Rz-6 amino stabl
erbB2-659 Zin.Rz-7 amino stabl
erbB2-878 Zin.Rz-6 amino stabl
erbB2-878 Zin.Rz-7 amino stabl
erbB2-881 Zin.Rz-6 amino stabl
erbB2-881 Zin.Rz-7 amino stabl
erbB2-888 Zin.Rz-7 amino stabl
erbB2-929 Zin.Rz-6 amino stabl
erbB2-929 Zin.Rz-7 amino stabl
erbB2-934 Zin.Rz-6
erbB2-934 Zin.Rz-7 amino stabl
erbB2-938 Zin.Rz-6 amino stabl
erbB2-938 Zin.Rz-7
erbB2-969 Zin.Rz-6 amino stabl
erbB2-969 Zin.Rz-7 amino stabl
erbB2-972 Zin.Rz-6 amino stabl
erbB2-972 Zin.Rz-7 amino stabl
erbB2-972 Zin.Rz-6 amino stabl

223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253
gecage of accelerated of accelerated agence B	მ გეგი მ მინმიგიმიშებიმის გამის გამის გამის გ	მ დეგინი ინიციანიცის ინიცი მის შემცის გემცის მ	gesaggand decactAnuuGuddcagGGaGucaaGGuCu agcuca B	g ₈ c ₈ a ₈ g ₈ ng gccgaaaggCgagugagucca agcuca B	g დათანდ იტიცნდნინდნტნმდფანაან ნი ⁸ ნ ⁸ დ ⁸ ა ⁸ ნ	ც ითიდად იტიტულიდიტტენდოდიტიატ ნდ [®] ი [®] დ [®] ი	a gounese ugugeaugagggeaugaag gengesses	a canad noncasedocasedocasedocasedocasedocasedocasedocasedocase	gacacadus GeegaaagGGgaducaaddugu canagea B	g ეღმდე იერტელიენტეტიდიმეტე მი ^რ ი ^რ ე ^რ ე ^რ ე	g ecapa nonconsaconosego de ecesas a se es	nage cassage GccgaaagGCGaaGucaaGGucu ucccaaa B	g ნნაათია ი <u>პოტეროიიტოტპტენდადნაატ</u> ნად [©] ი [©] ი	a egugu u <u>o</u> usosassogogassegoos se _a u ₈ e _a e	g ოომონო იპოცელოფილეფენდიონიაც ნო ⁸ ო ⁸ ა ⁸ ა	მ გაგე _{ნი} ცი იტიმინის განის გამინის საგეგი გაგეგი მ	8 case on outpeaced on the second of the sec	a segue de cosana godes de caso de a segue de a segue de caso	g Secooba nongerongegobbereboog eco ⁸ c ⁸ S ⁸ e ⁸ o	g აგაონნო ი <mark>ე</mark> ოტებიათიტაცეენდოონაატ ნონ [®] ი [®] ი [®] ი	მ ნონნნო იტიცედაციანტებად გამის იმმის გ	g წმონწმო იტიტიდიდიდიდიდი დიდ ⁸ ე ⁸ დ ⁸ ნ ⁸ ი	a pagas a Googaaagoogaaacaagaaa acagaaaa a	g იგმმია ი <u>ეიცეადიიციეემგადამიე</u> დე დე გემი	a ganana uQuebeangagQgamagcana acacus B	g 66.138 15.18 gcc3gaagGGgaGrcaaGG:Or acacu36 B	a cacas undubascacedededededededededededededededededede	c _a u _g c _a c _a ugg GccgaaagG <u>c</u> GaGucaaGDu <u>c</u> u cccgaag B	n ⁸ 8 ⁸ 8 ⁸ 8 ⁸ 0 OccaaaagGGaaccaaGuGa aguaga B	g nebande nongoverongegogereeboog engeneen g
erbB2-972 Zin.Rz-6 amino stabl	erbB2-972 Zin.Rg-6 amino stabl	erbB2-972 Zin.Rz-6 amino stabl	erbB2-972 Zin.Rz-6 amino stabl	erbB2-972 Zin.Rz-6 amino stabl	erb82-972 Zin.Rz-6 amino stabl	erbB2-1199 Zin.Rz-6 amino stabl	erbB2-1199 Zin.Rz-7 amino stabl	erbB2-1205 Zin.Rz-6 amino stabl	erbB2-1205 Zin.Rz-7 amino stabl	erbB2-1211 Zin.Rz-6 amino stabl	erbB2-1292 Zin.Rz-6 amino stabl	erbB2-1292 Zin.Rz-7 amino stabl	erbB2-1313 Zin.Rz-7 amino stabl	erbB2-1397 Zin.Rz-6 amino stabl	erbB2-1414 Zin.Rz-6 amino stabl	erbB2-1414 Zin.Rz-7 amino stabl	erbB2-1536 Zin.Rz-6 amino stabl	erbB2-1541 Zin.Rz-6 amino stabl	erbB2-1562 Zin.Rz-7 amino stabl	erbB2-1626 Zin.Rz-7 amino stabl	erbB2-1755 Zin.Rz-6 amino stabl	erbB2-1755 Zin.Rz-7 amino stabl	erbB2-1757 Zin.Rz-6 amino stabl	erbB2-1757 Zin.Rz-7 amino stabl	erbB2-1759 Zin.Rz-6 amino stabl	erbB2-1759 Zin.Rz-7 amino stabl	erbB2-1784 Zin.Rz-6 amino stabl	erbB2-1784 Zin.Rz-7 amino stabl	erbB2-2063 Zin.Rz-6 amino stabl	erbB2-2063 Zin.Rz-7 amino stabl
						113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137
						GAGUGU G CURUGG	coadudu e cuandeu	actuatia a ucuosa	DOCUANG G DCDGGGC	GUCUGG G CAUGGA	DECOGA G CCUOCC	UNIGORA G CCUGGCA	CCGGAGA G CUUUGAU	UCACAG G UUACCU	AUCUCA G CAUGGC	CAUCUCA G CAUGGCC	GCUGGG G CUGCGC	GGCDGC G CUCACU	CUGOGCA G UGGACUG	довасся в специис	CACCCA G UGUGUC	covecea e nenanca	CCCAGU G UGUCAA	ACCCAGU G UGUCAAC	CAGUGU G UCAACU	covenen e novvene	UDOGGG G CCAGGA	CUDOGGG G CCAGGAG	UCARCU G CACCCA	AUCAACU G CACCCAC
972	972	9.12	972	972	972	1199	1199	1205	1205	1211	1292	1292	1313	1397	1414	1414	1536	1541	1562	1626	1755	1755	1757	1757	1759	1759	1784	1784	2063	2063
19295	19293	19292	19296	19727	19728	18659	18658	18724	18669	18725	18726	18698	18727	18699	18728	18670	18671	18687	18829	18830	19700	18672	18688	18660	18689	19690	18701	18673	16981	19981

254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284
nacaga ago de	g ნიეიეი იპიტედიეიდეპენიდინებე ნნ ⁸ ი ⁸ ე ⁸ ნ ⁸ ნ	nauge of cub accessed of consequences agosauc B	g დეთიენნ იეიცედითიედეენდიდნებე ნდე ⁸ ი ⁸ ნ ⁸ ი ⁸ ნ	g noonno nongoveongegogosvetooog sosnansos	c _g a _g a _g g ca GccgaaggGGagucaaggGU cuucac B	g ეედერი რემიტილიომეტენოდონებე დენ ⁸ დ ⁸ დ ⁸ ე ⁸ ე	a cacas a goodsaaagggaaagggaa accaca	aguage age georgasago Coagucaso Cucu accuuca B	g ensano occesses do consesso conses B	a nananne nancosesacioses ecocas ecuana annonco	c _B a _B c _B c _B ag GccgaaagGCGaGncaaGGnCn cancac B	c _g	g ენიონო იეიველიეიცეეცნოონეეც 55°8°8°3°8°8	ც მიანდა იეიცედდიიცოცენტდოდნააც დამი ⁸ ი ⁸ ნში ⁸ ნ	c _{BaBuga} ag dccgaangoogoacaagout uguga	g eonānān nōnesaggōgasaggos pas ^a n ^a s ^a s	g 6nonee nonceachesocobeeecoo 65°nance	g conwon nangemenagogeweesoo Busassa	c _a a _g g _g g _g uag GccgaaagO <u>O</u> OaducaaOOu <u>O</u> u ucauccc B	9 ₈ u _B u _B g ₉ ga GccgaaagGCgaaGucaaGGuCu ucuugac B	g cacasagagagagagagagagagagagagagagagagaga	Cacaaagacag GoogaaagGGGaGucaaGGuCu cgagcoa B	g ng cg cg dccgeaagGGGaGucaaGGuGu agccga B	n ⁸ 8 ⁸ n ⁸ c ⁸ ca8 Gcc8aaagCG8aGucaaGGnGn agcc8a8 B	a sugue of cogasacoocosocosocosocosocosocosocosocosoco	c _s a _{us} g _s gua GccgaaagCDCaGucaaGCuCu ucugucu B	c _a c _a a _a u _g cug GccgaaagGCGaaGucaaGGugc augguac B	a _g c _g c _g ugugugugugugugugugugugugugugugugugugu	აგი _გ ი _გ ისსე მიიცაგიტმტმომსიაგიტი იიიაგი გ	Cgugaca Googaaagoogaagoogaagooga ancacno B
erbB2-2075 Zin.Rz-6 amino scabl	erbB2-2116 Zin.Rz-6 amino stabl	erbB2-2247 Zin.Rz-7 amino stabl	erbB2-2271 Zin.Rz-7 amino stabl	erbS2-2341 Zin.Rz-6 amino stabl	erbB2-2347 Zin.Rz-6 amino stabl	erbB2-2347 Zin.Rz-7 amino stabl	erbB2-2349 Zin.Rz-6 amino stabl	erbB2-2349 Zin.Rz-7 amino stabl	erbB2-2384 Zin.Rz-7 amino stabl	erbB2-2410 2in.R2-7 amino stabi	erbB2-2497 Zin.Rz-6 amino stabl	erbB2-2501 Zin.Rz-6 amino stabl	erbB2-2540 Zin.R2-6 amino stabl	erbB2-2563 Zin.Rz-6 amino stabl	erbB2-2571 Zin.R2-6 amino stabl	erbB2-2571 Zin.Rz-7 amino stabl	erbB2-2662 Zin.Rz-6 amino stabl	erbB2-2675 Zin.Rz-6 amino stabl	erbB2-2675 Zin.Rz-7 amino stabl	exbB2-2738 Zin.Rz-7 amino stabl	erbB2-2773 Zin.Rz-6 amino stabl	erbB2-2778 Zin.Rz-7 amino stabl	erbB2-2781 Zin.Rz-6 amino stabl	erbB2-2781 Zin.Rz-7 amino stabl	erbB2-2802 Zin.Rz-6 amino stabl	erbB2-2802 Zin.Rz-7 amino stabl	erbB2-2809 Zin.Rz-7 amino stabl	erbB2-2819 Zin.Rz-6 amino stabl	erbB2-2819 Zin.Rz-7 amino stabl	erbB2-2887 Zin.Rz-7 amino stabl
138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	191	162	163	164	165	166	167	168
ACTUCEU G UGUSGA	CAGAGA G CCAGCC	выстости с смовыма	USGAGCE G CUGACAC	ADDANG G UDANGG	GUGANG G UGCUUG	оспачно в поспас	gaaggu g cousga	UGANGGU G CUUDDAU	UNCANGE & CAUCUGE	GGAGAAU G UGAAAAU	GUGAUG G CUGGUG	noscne a nansee	ocaucu a ccuaac	CAGCUG G UGACAC	GACACA G CUUAUG	UGACACA G CUUAUGC	CAGAUU G CCAAGG	GGAUGA G CUACCU	godauca e cuaccue	GUCANGA G UCCCAAC	agactia a cucago	DOCCHOS & CHECKISE	UCOGCU G CUGGAC	CUCOCOU G CUGGACA	CACAGA G UACCAU	AGACAGA G UACCAUG	GUACCAU G CAGAUGG	AUGGGG G CAAGGU	GAUGGGG G CAGGGUG	GAGUGAU G UGUGGAG
2075	2116	2247	2271	2341	2347	2347	2349	2349	2384	2410	2497	2501	2540	2563	2571	2571	2992	2675	2675	2738	2773	2778	2781	2781	2802	2802	2809	2819	2819	2887
18692	18729	18832	18833	18702	18730	18674	18713	18693	18731	18714	18732	18703	18715	18733	18734	18675	18716	18704	18676	18735	18705	18836	18694	18662	18737	18736	18717	18738	18706	18695

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285	286	287	288	289	290	291	292	293	294	295	296	297	298	599	300	301	302	303	304	305	306	307	308	309
cacacacacacacacacacacacacacacacacacaca	uacaca Geogramagogogacheanoguou agueaca B	c _g u _g c _g c _g ca GccgaaagGGGaGucaaGGuGu acaguc B	მ დეგიზი მის მის მის მის მის მის მის მის მის მი	c _g a _g u _g c _g ag GccgaaagGCGaGucaaGGuCu ucccac B	uscasa GeogramagGGaducaaGGugu ucceaca B	g anana ng	Sagaus ago GccgaaagGCGaducaaGCuCu cccaaaa B	useguasegocesaseconocasecon ancann B	aguagu acceasageCoacacacou accasus B	aguacacaa OccgaaagGCGaGacaaGGuCu anuuga B	d seguan Conganagooogaagoon annagac B	g 66000n nongeronsesonsessons as accept a	a scan uQuobecadoogeaagooaa Googaa B	a garago CocgaaagGCGaducaaGCOGu cocuuc B	ი ⁸ ი ⁸ მ ⁸ მ ტიიმათამტეტიციითატი ითმიიი გ	ც ააიინდა იეიტედდაიტატეტმდდანაავი მდგ ⁸ გ ⁸ ი ⁸ დ	a _B S _B S _B Ca GccgasagQQGacacGoogQGnQCacaa	c _B a _B g _B c _B uca GccgaaagGCgaGucaaGuCuCu caucaaa B	g ng ago occgaaagocgaacaaocaaocoo	ი ⁸ მ ⁸ ი ⁸ ის მიიმდომმტტეფლის იმიომომ ც	g caa a cccsaaagoocaacaacaacaacaa a cannus B	g 88a88e nOncomeonoecoogseae8ooo 86aaaa8aaa	g e88aga noncoesagooogosesagooo saasagaaga g	8 ng cg gagggaaageCcaecaacooco a cuucco B
erbB2-2908 Zin.Rz-6 amino stabl	erbB2-2908 Zin.Rz-7 amino stabl	erbB2-2910 Zin.Rz-6 amino stabl	exbB2-2910 Zin.Rz-7 amino stabl	erbB2-2916 Zin.Rz-6 amino stabl	erbB2-2916 Zin.Rz-7 amino stabl	erbB2-2932 Zin.Rz-6 amino stabl	erbB2-2932 Zin.Rz-7 amino stabl	erbB2-3025 Zin.Rz-6 amino stabl	erbB2-3025 Zin Rz-7 amino stabl	erbB2-3047 Zin.Rz-6 amino stabl	erbB2-3047 Zin.Rz-7 amino stabl	erbB2-3087 Zin.Rz-6 amino stabl	erbB2-3087 Zin.Rz-7 amino stabl	erbB2-3415 Zin.Rz-6 amino stabl	erbB2-3419 Zin.Rz-6 amino stabl	erbB2-3419 Zin.Rz-7 amino stabl	erbB2-3437 Zin.Rz-6 amino stabl	erbB2-3437 Zin.Rz-7 amino stabl	erbB2-3504 Zin.Rz-6 amino stabl	erbB2-3504 Zin.Rz-7 amino stabl	erbB2-3724 Zin.Rz-7 amino stabl	erbB2-3808 Zin.Rz-6 amino stabl	erbB2-3808 Zin.Rz-7 amino stabl	erbB2-3996 Zin.R2-6 amino stabi
169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193
GUSACU G UGUGGG	UGUGACU G UGUGGGA	GACUGU G UGGGAG	ucacucu e uccasoc	GUGGGA G CUCAUG	DOUGGGA G CUCAUGA	UNIGOS O CCANAC	UNUUGGG G CCAAACC	AUUGAU G UCUACA	CAUUGAU G UCUACAU	UCAAAU G UUSGAU	GUCKAAU G UUSGAUG	ccosen e meene	UCCOGGA G UUGGUGU	GAAGGG G CUGGCU	GGGCUG G CUCCGA	GOOGUIG G CUCCGAU	UNGAUG G DGACCU	UUUCAUG G UGACCUG	ucuaca e cesuac	CUCUACA G COGUACA	CAAAGAC G UUUUUGC	concon e connos	nocacoa e contrae	dogwa a ccuarc
2908	2908	2910	2910	2916	2916	2932	2932	3025	3025	3047	3047	3087	3087	3415	3419	3419	3437	3437	3504	3504	3724	3808	3808	3996
18663	18826	18664	18650	13677	18652	18707	18678	18719	18718	18720	18696	18739	18708	18740	18741	18837	18709	13679	18823	18710	18721	18834	18827	18824

UPPER CASE = RIBO
Lower case = 2'-0-methyl

<u>C</u> = 2'-deoxy-2'-amino Cytidine
s = phosphorothioate
B = inverted deoxyabasic

Table 59

Table 59: Human HER2 Class II (zinzyme) Ribozyme and Target Sequece

Pos	Substrate	Seq ID	Ribozyme	Rz Seq ID
46	GGGCAGCC G CGCGCCCC	310	GGGGCGCG GCCGAAAGGCGAGUCAAGGUCU GGCUGCCC	895
48	GCAGCCGC G CGCCCCUU	311	AAGGGGCG GCCGAAAGGCGAGUCAAGGUCU GCGGCUGC	896
50	AGCCGCGC G CCCCUUCC	312	GGAAGGG GCCGAAAGGCGAGUCAAGGUCU GCGCGGCU	897
75	CCUUUACU G CGCCGCGC	313	GCGCGGCG GCCGAAAGGCGAGUCAAGGUCU AGUAAAGG	898
77	UUUACUGC G CCGCGCGC	314	GCGCGCGG GCCGAAAGGCGAGUCAAGGUCU GCAGUAAA	899
80	ACUGCGCC G CGCGCCCG	315	CGGGCGCG GCCGAAAGGCGAGUCAAGGUCU GGCGCAGU	900
82	UGCGCCGC G CGCCCGGC	316	GCCGGGCG GCCGAAAGGCGAGUCAAGGUCU GCGGCGCA	901
84	CGCCGCGC G CCCGGCCC	317	GGGCCGGG GCCGAAAGGCGAGUCAAGGUCU GCGCGGCG	902
102	CACCCCUC G CAGCACCC	318	GGGUGCUG GCCGAAAGGCGAGUCAAGGUCU GAGGGGUG	903
112	AGCACCCC G CGCCCCGC	319	GCGGGGCG GCCGAAAGGCGAGUCAAGGUCU GGGGUGCU	904
114	CACCCCGC G CCCCGCGC	320	GCGCGGGG GCCGAAAGGCGAGUCAAGGUCU GCGGGGUG	905
119	CGCGCCCC G CGCCCUCC	321	GGAGGGCG GCCGAAAGGCGAGUCAAGGUCU GGGGCGCG	906
121	CGCCCCGC G CCCUCCCA	322	UGGGAGGG GCCGAAAGGCGAGUCAAGGUCU GCGGGGCG	907
163	CCGGAGCC G CAGUGAGC	323	GCUCACUG GCCGAAAGGCGAGUCAAGGUCU GGCUCCGG	908
194	GGCCUUGU G CCGCUGGG	324	CCCAGCGG GCCGAAAGGCGAGUCAAGGUCU ACAAGGCC	909
197	CUUGUGCC G CUGGGGGC	325	GCCCCCAG GCCGAAAGGCGAGUCAAGGUCU GGCACAAG	910
214	UCCUCCUC G CCCUCUUG	326	CAAGAGG GCCGAAAGGCGAGUCAAGGUCU GAGGAGGA	911
222	GCCCUCUU G CCCCCCGG	327	CCGGGGG GCCGAAAGGCGAGUCAAGGUCU AAGAGGGC	912
235	CCGGAGCC G CGAGCACC	328	GGUGCUCG GCCGAAAGGCGAGUCAAGGUCU GGCUCCGG	913
251	CCAAGUGU G CACCGGCA	329	UGCCGGUG GCCGAAAGGCGAGUCAAGGUCU ACACUUGG	914
273	AUGAAGCU G CGGCUCCC	330	GGGAGCCG GCCGAAAGGCGAGUCAAGGUCU AGCUUCAU	915
283	GGCUCCCU G CCAGUCCC	331	GGGACUGG GCCGAAAGGCGAGUCAAGGUCU AGGGAGCC	916
309	CUGGACAU G CUCCGCCA	332	UGGCGGAG GCCGAAAGGCGAGUCAAGGUCU AUGUCCAG	917
314	CAUGCUCC G CCACCUCU	333	AGAGGUGG GCCGAAAGGCGAGUCAAGGUCU GGAGCAUG	918
332	CCAGGGCU G CCAGGUGG	334	CCACCUGG GCCGAAAGGCGAGUCAAGGUCU AGCCCUGG	919
342	CAGGUGGU G CAGGGAAA	335	UUUCCCUG GCCGAAAGGCGAGUCAAGGUCU ACCACCUG	920
369	ACCUACCU G CCCACCAA	336	UUGGUGGG GCCGAAAGGCGAGUCAAGGUCU AGGUAGGU	921
379	CCACCAÁU G CCAGCCUG	337	CAGGCUGG GCCGAAAGGCGAGUCAAGGUCU AUUGGUGG	922
396	UCCUUCCU G CAGGAUAU	338	AUAUCCUG GCCGAAAGGCGAGUCAAGGUCU AGGAAGGA	923
414	CAGGAGGU G CAGGGCUA	339	UAGCCCUG GCCGAAAGGCGAGUCAAGGUCU ACCUCCUG	924
426	GGCUACGU G CUCAUCGC	340	GCGAUGAG GCCGAAAGGCGAGUCAAGGUCU ACGUAGCC	925
433	UGCUCAUC G CUCACAAC	341	GUUGUGAG GCCGAAAGGCGAGUCAAGGUCU GAUGAGCA	926
462	GUCCCACU G CAGAGGCU	342	AGCCUCUG GCCGAAAGGCGAGUCAAGGUCU AGUGGGAC	927
471	CAGAGGCU G CGGAUUGU	343	ACAAUCCG GCCGAAAGGCGAGUCAAGGUCU AGCCUCUG	928
480	CGGAUUGU G CGAGGCAC	344	GUGCCUCG GCCGAAAGGCGAGUCAAGGUCU ACAAUCCG	929
511	ACAACUAU G CCCUGGCC	345	GGCCAGGG GCCGAAAGGCGAGUCAAGGUCU AUAGUUGU	930
522	CUGGCCGU G CUAGACAA	346	UUGUCUAG GCCGAAAGGCGAGUCAAGGUCU ACGGCCAG	931
540	GGAGACCC G CUGAACAA	347	UUGUUCAG GCCGAAAGGCGAGUCAAGGUCU GGGUCUCC	932
585	GGAGGCCU G CGGGAGCU	348	AGCUCCCG GCCGAAAGGCGAGUCAAGGUCU AGGCCUCC	933
594	CGGGAGCU G CAGCUUCG	349	CGAAGCUG GCCGAAAGGCGAGUCAAGGUCU AGCUCCCG	934
659	CCAGCUCU G CUACCAGG	350	CCUGGUAG GCCGAAAGGCGAGUCAAGGUCU AGAGCUGG	935
737	CACCAACC G CUCUCGGG	351	CCCGAGAG GCCGAAAGGCGAGUCAAGGUCU GGUUGGUG	936
749	UCGGGCCU G CCACCCCU	352	AGGGGUGG GCCGAAAGGCGAGUCAAGGUCU AGGCCCGA	937

Table 59

782	GGGCUCCC G CUGCUGGG	353	CCCAGCAG GCCGAAAGGCGAGUCAAGGUCU GGGAGCCC	938
785	CUCCCGCU G CUGGGGAG	354	CUCCCCAG GCCGAAAGGCGAGUCAAGGUCU AGCGGGAG	939
822	AGCCUGAC G CGCACUGU	355	ACAGUGCG GCCGAAAGGCGAGUCAAGGUCU GUCAGGCU	940
824	CCUGACGC G CACUGUCU	356	AGACAGUG GCCGAAAGGCGAGUCAAGGUCU GCGUCAGG	941
835	CUGUCUGU G CCGGUGGC	357	GCCACCGG GCCGAAAGGCGAGUCAAGGUCU ACAGACAG	942
847	GUGGCUGU G CCCGCUGC	358	GCAGCGGG GCCGAAAGGCGAGUCAAGGUCU ACAGCCAC	943
851	CUGUGCCC G CUGCAAGG	359	CCUUGCAG GCCGAAAGGCGAGUCAAGGUCU GGGCACAG	944
854	UGCCCGCU G CAAGGGGC	360	GCCCCUUG GCCGAAAGGCGAGUCAAGGUCU AGCGGGCA	945
867	GGGCCACU G CCCACUGA	361	UCAGUGGG GCCGAAAGGCGAGUCAAGGUCU AGUGGCCC	946
878	CACUGACU G CUGCCAUG	362	CAUGGCAG GCCGAAAGGCGAGUCAAGGUCU AGUCAGUG	947
881	UGACUGCU G CCAUGAGC	363	GCUCAUGG GCCGAAAGGCGAGUCAAGGUCU AGCAGUCA	948
895	AGCAGUGU G CUGCCGGC	364	GCCGGCAG GCCGAAAGGCGAGUCAAGGUCU ACACUGCU	949
898	AGUGUGCU G CCGGCUGC	365	GCAGCCGG GCCGAAAGGCGAGUCAAGGUCU AGCACACU	950
905	UGCCGGCU G CACGGGCC	366	GGCCCGUG GCCGAAAGGCGAGUCAAGGUCU AGCCGGCA	951
929	CUCUGAÇU G CCUGGCCU	367	AGGCCAGG GCCGAAAGGCGAGUCAAGGUCU AGUCAGAG	952
938	CCUGGCCU G CCUCCACU	368	AGUGGAGG GCCGAAAGGCGAGUCAAGGUCU AGGCCAGG	953
972	UGUGAGCU G CACUGCCC	369	GGGCAGUG GCCGAAAGGCGAGUCAAGGUCU AGCUCACA	954
977	GCUGCACU G CCCAGCCC	370	GGGCUGGG GCCGAAAGGCGAGUCAAGGUCU AGUGCAGC	955
1020	GAGLICCALI G CCCAALICC	371	GGAUUGGG GCCGAAAGGCGAGUCAAGGUCU AUGGACUC	956
1051	CAUUCGGC G CCAGCUGU	372	ACAGCUGG GCCGAAAGGCGAGUCAAGGUCU GCCGAAUG	957
1066	GUGUGACU G CCUGUCCC	373	GGGACAGG GCCGAAAGGCGAGUCAAGGUCU AGUCACAC	958
1106	GGGAUCCU G CACCCUCG	374	CGAGGGIG GCCGAAAGGCGAGIICAAGGUCU AGGAUCCC	959
1118	CCUCGUCU G CCCCCUGC	375	GCAGGGG GCCGAAAGGCGAGUCAAGGUCU AGACGAGG	960
1125	UGCCCCCU G CACAACCA	376	UGGUUGUG GCCGAAAGGCGAGUCAAGGUCU AGGGGGCA	961
1175	HIGAGAAGU G CAGCAAGC	377	GCUUGCUG GCCGAAAGGCGAGUCAAGGUCU ACUUCUCA	962
1189	AGCCCUGU G CCCGAGUG	378	CACUCGGG GCCGAAAGGCGAGUCAAGGUCU ACAGGGCU	963
1199	CCGAGUGU G CUAUGGUC	379	GACCAUAG GCCGAAAGGCGAGUCAAGGUCU ACACUCGG	964
1224	GAGCACUU G CGAGAGGU	380	ACCUCUCG GCCGAAAGGCGAGUCAAGGUCU AAGUGCUC	965
1249	UUACCAGU G CCAAUAUC	381	GAUAUUGG GCCGAAAGGCGAGUCAAGGUCU ACUGGUAA	966
1267	AGGAGUUU G CUGGCUGC	382	GCAGCCAG GCCGAAAGGCGAGUCAAGGUCU AAACUCCU	967
1274	UGCUGGCU G CAAGAAGA	383	UCUUCUUG GCCGAAAGGCGAGUCAAGGUCU AGCCAGCA	968
1305	GCAUUUCU G CCGGAGAG	384	CUCUCCGG GCCGAAAGGCGAGUCAAGGUCU AGAAAUGC	969
1342	CCAACACU G CCCCGCUC	385	GAGOGGG GCCGAAAGGCGAGUCAAGGUCU AGUGUUGG	970
1347	ACUGCCCC G CUCCAGCC	386	GGCUGGAG GCCGAAAGGCGAGUCAAGGUCU GGGGCAGU	971
1431	GACAGCCU G CCUGACCU	387	AGGUCAGG GCCGAAAGGCGAGUCAAGGUCU AGGCUGUC	972
1458	CAGAACCU G CAAGUAAU	388	AUUACUUG GCCGAAAGGCGAGUCAAGGUCU AGGUUCUG	973
1482	CGAAUUCU G CACAAUGG	389	CCAUUGUG GCCGAAAGGCGAGUCAAGGUCU AGAAUUCG	974
1492	ACAAUGGC G CCUACUCG	390	CGAGUAGG GCCGAAAGGCGAGUCAAGGUCU GCCAUUGU	975
1500	GCCUACUC G CUGACCCU	390	AGGGUCAG GCCGAAAGGCGAGUCAAGGUCU GAGUAGGC	975
1500	CUGACCCU G CAAGGGCU	391	AGCCCUUG GCCGAAAGGCGAGUCAAGGUCU AGGGUCAG	976
	CUGACCCU G CAAGGGCU	392	AGUGAGCG GCCGAAAGGCGAGUCAAGGUCU AGCCCCAG	977
1539				
1541	GGGGCUGC G CUCACUGA	394	UCAGUGAG GCCGAAAGGCGAGUCAAGGUCU GCAGCCCC	979
1598	CCACCUCU G CUUCGUGC	395	GCACGAAG GCCGAAAGGCGAGUCAAGGUCU AGAGGUGG	980
1605	UGCUUCGU G CACACGGU	396	ACCGUGUG GCCGAAAGGCGAGUCAAGGUCU ACGAAGCA	981
1614	CACACGGU G CCCUGGGA	397	UCCCAGGG GCCGAAAGGCGAGUCAAGGUCU ACCGUGUG	982
1641	CGGAACCC G CACCAAGC	398	GCUUGGUG GCCGAAAGGCGAGUCAAGGUCU GGGUUCCG	983
1653	CAAGCUCU G CUCCACAC	399	GUGUGGAG GCCGAAAGGCGAGUCAAGGUCU AGAGCUUG	984

Table 59

1663	UCCACACU G CCAACCGG	400	CCGGUUGG GCCGAAAGGCGAGUCAAGGUCU AGUGUGGA	985
1706	CCUGGCCU G CCACCAGC	401	GCUGGUGG GCCGAAAGGCGAGUCAAGGUCU AGGCCAGG	986
1718	CCAGCUGU G CGCCCGAG	402	CUCGGGCG GCCGAAAGGCGAGUCAAGGUCU ACAGCUGG	987
1720	AGCUGUGC G CCCGAGGG	403	CCCUCGGG GCCGAAAGGCGAGUCAAGGUCU GCACAGCU	988
1733	AGGGCACU G CUGGGGUC	404	GACCCCAG GCCGAAAGGCGAGUCAAGGUCU AGUGCCCU	989
1766	UGUCAACU G CAGCCAGU	405	ACUGGCUG GCCGAAAGGCGAGUCAAGGUCU AGUUGACA	990
1793	CCAGGAGU G CGUGGAGG	406	CCUCCACG GCCGAAAGGCGAGUCAAGGUCU ACUCCUGG	991
1805	GGAGGAAU G CCGAGUAC	407	GUACUCGG GCCGAAAGGCGAGUCAAGGUCU AUUCCUCC	992
1815	CGAGUACU G CAGGGGCU	408	AGCCCCUG GCCGAAAGGCGAGUCAAGGUCU AGUACUCG	993
1843	AUGUGAAU G CCAGGCAC	409	GUGCCUGG GCCGAAAGGCGAGUCAAGGUCU AUUCACAU	994
1857	CACUGUUU G CCGUGCCA	410	UGGCACGG GCCGAAAGGCGAGUCAAGGUCU AAACAGUG	995
1862	UUUGCCGU G CCACCCUG	411	CAGGGUGG GCCGAAAGGCGAGUCAAGGUCU ACGGCAAA	996
1936	LIGGCCLIGIT & CCCACUALI	412	AUAGUGGG GCCGAAAGGCGAGUCAAGGUCU ACAGGCCA	997
1961	UCCCUUCU G CGUGGCCC	413	GGGCCACG GCCGAAAGGCGAGUCAAGGUCU AGAAGGGA	998
1970	CGUGGCCC G CUGCCCCA	414	UGGGGCAG GCCGAAAGGCGAGUCAAGGUCU GGGCCACG	999
1973	GGCCCGCU G CCCCAGCG	415	CGCUGGGG GCCGAAAGGCGAGUCAAGGUCU AGCGGGCC	1000
2007	HCCHACAU G CCCAUCUG	416	CAGAUGGG GCCGAAAGGCGAGUCAAGGUCU AUGUAGGA	1001
2038	AGGAGGC G CAUGCCAG	417	CUGGCAUG GCCGAAAGGCGAGUCAAGGUCU GCCCUCCU	1002
2042	GGGCGCAU G CCAGCCUU	418	AAGGCUGG GCCGAAAGGCGAGUCAAGGUCU AUGCGCCC	1003
2051	CCAGCCUU G CCCCAUCA	419	UGAUGGGG GCCGAAAGGCGAGUCAAGGUCU AAGGCUGG	1004
2063	CAUCAACU G CACCCACU	420	AGUGGGUG GCCGAAAGGCGAGUCAAGGUCU AGUUGAUG	1005
2099	CAAGGGCU G CCCCGCCG	421	CGGCGGGG GCCGAAAGGCGAGUCAAGGUCU AGCCCUUG	1006
2104	GCUGCCCC G CCGAGCAG	422	CUGCUCGG GCCGAAAGGCGAGUCAAGGUCU GGGGCAGC	1007
2143	UCAUCICU G CGGUGGUU	423	AACCACCG GCCGAAAGGCGAGUCAAGGUCU AGAGAUGA	1008
2143	GGCAUUCU G CUGGUCGU	424	ACGACCAG GCCGAAAGGCGAGUCAAGGUCU AGAAUGCC	1009
2235	UACACGAU G CGGAGACU	425	AGUCUCCG GCCGAAAGGCGAGUCAAGGUCU AUCGUGUA	1010
2244	CGGAGACU G CUGCAGGA	426	UCCUGCAG GCCGAAAGGCGAGUCAAGGUCU AGUCUCCG	1011
2247	AGACUGCU G CAGGAAAC	427	GUUUCCUG GCCGAAAGGCGAGUCAAGGUCU AGCAGUCU	1012
2271	GUGGAGCC G CUGACACC	428	GGUGUCAG GCCGAAAGGCGAGUCAAGGUCU GGCUCCAC	1013
2292	GGAGCGAU G CCCAACCA	429	UGGUUGGG GCCGAAAGGCGAGUCAAGGUCU AUCGCUCC	1014
2304	AACCAGGC G CAGALIGCG	430	CGCAUCUG GCCGAAAGGCGAGUCAAGGUCU GCCUGGUU	1015
2310	GCGCAGAU G CGGAUCCU	431	AGGAUCCG GCCGAAAGGCGAGUCAAGGUCU AUCUGCGC	1016
2349	GUGAAGGU G CUUGGAUC	432	GALICCAAG GCCGAAAGGCGAGLICAAGGLICU ACCULICAC	1017
2362	GAUCUGGC G CUUUUGGC	433	GCCAAAAG GCCGAAAGGCGAGUCAAGGUCU GCCAGAUC	1018
2525	UGUCUCCC G CCUUCUGG	434	CCAGAAGG GCCGAAAGGCGAGUCAAGGUCU GGGAGACA	1019
2540	GGGCAUCU G CCUGACAU	435	AUGUCAGG GCCGAAAGGCGAGUCAAGGUCU AGAUGCCC	1020
2556	UCCACGGU G CAGCUGGU	436	ACCAGCIIG GCCGAAAGGCGAGIICAAGGIICU ACCGUGGA	1021
2577	CAGCUUAU G CCCUAUGG	437	CCAUAGGG GCCGAAAGGCGAGUCAAGGUCU AUAAGCUG	1022
2588	CHAUGGOU G CCUCUUAG	438	CUAAGAGG GCCGAAAGGCGAGUCAAGGUCU AGCCAUAG	1023
2615	GGAAAACC G CGGACGCC	439	GCCGUCCG GCCGAAAGGCGAGUCAAGGUCU GGUUUUCC	1024
2621	CCGCGGAC G CCUGGGCU	440	AGCCCAGG GCCGAAAGGCGAGUCAAGGUCU GUCCGCGG	1025
2621	CAGGACCII G CUGAACIIG	441	CAGUICAG GCCGAAAGGCGAGUCAAGGUCU GUCCGCGG	1025
	UGGUGUAU G CUGAACUG	441	CABUICEG GCCGAAGGCGAGUCAAGGUCU AUGCCCGG	1026
2655	UGCAGAUU G CAGAUUGC	443	CCCCITIGG GCCGAAAGGCGAGUCAAGGUCU AUCUGCA	1027
2662				
2691	GAGGAUGU G CGGCUCGU	444	ACGAGCOS GCCGAAAGGCGAGUCAAGGUCU ACAUCCUC GUUCCGAG GCCGAAAGGCGAGUCAAGGUCU GGCCAAGU	1029
2716	ACUUGGCC G CUCGGAAC			
2727	CGGAACGU G CUGGUCAA	446	UUGACCAG GCCGAAAGGCGAGUCAAGGUCU ACGUUCCG	1031

Table 59

			14510 55	
2781	GCUCGGCU G CUGGACAU	447	AUGUCCAG GCCGAAAGGCGAGUCAAGGUCU AGCCGAGC	1032
2809	AGUACCAU G CAGAUGGG	448	CCCAUCUG GCCGAAAGGCGAGUCAAGGUCU AUGGUACU	1033
2826	GGCAAGGU G CCCAUCAA	449	UUGAUGGG GCCGAAAGGCGAGUCAAGGUCU ACCUUGCC	1034
2844	UGGAUGGC G CUGGAGUC	450	GACUCCAG GCCGAAAGGCGAGUCAAGGUCU GCCAUCCA	1035
2861	CAUUCUCC G CCGGCGGU	451	ACCGCCGG GCCGAAAGGCGAGUCAAGGUCU GGAGAAUG	1036
2976	CCUGACCU G CUGGAAAA	452	UUUUCCAG GCCGAAAGGCGAGUCAAGGUCU AGGUCAGG	1037
2997	GAGCGGCU G CCCCAGCC	453	GGCUGGGG GCCGAAAGGCGAGUCAAGGUCU AGCCGCUC	1038
3014	CCCCAUCU G CACCAUUG	454	CAAUGGUG GCCGAAAGGCGAGUCAAGGUCU AGAUGGGG	1039
3107	AUUCUCCC G CAUGGCCA	455	UGGCCAUG GCCGAAAGGCGAGUCAAGGUCU GGGAGAAU	1040
3128	CCCCCAGC G CUUUGUGG	456	CCACAAAG GCCGAAAGGCGAGUCAAGGUCU GCUGGGGG	1041
3191	CUUCUACC G CUCACUGC	457	GCAGUGAG GCCGAAAGGCGAGUCAAGGUCU GGUAGAAG	1042
3198	CGCUCACU G CUGGAGGA	458	UCCUCCAG GCCGAAAGGCGAGUCAAGGUCU AGUGAGCG	1043
3232	UGGUGGAU G CUGAGGAG	459	CUCCUCAG GCCGAAAGGCGAGUCAAGGUCU AUCCACCA	1044
3280	CAGACCCU G CCCCGGGC	460	GCCCGGGG GCCGAAAGGCGAGUCAAGGUCU AGGGUCUG	1045
3289	CCCCGGGC G CUGGGGGC	461	GCCCCCAG GCCGAAAGGCGAGUCAAGGUCU GCCCGGGG	1046
3317	CAGGCACC G CAGCUCAU	462	AUGAGCUG GCCGAAAGGCGAGUCAAGGUCU GGUGCCUG	1047
3468	AAGGGCU G CAAAGCCU	463	AGGCUUUG GCCGAAAGGCGAGUCAAGGUCU AGCCCCUU	1048
3534	GUACCCCU G CCCUCUGA	464	UCAGAGGG GCCGAAAGGCGAGUCAAGGUCU AGGGGUAC	1049
3559	GCUACGUU G CCCCCCUG	465	CAGGGGG GCCGAAAGGCGAGUCAAGGUCU AACGUAGC	1050
3572	CCUGACCU G CAGCCCCC	466	GGGGGCUG GCCGAAAGGCGAGUCAAGGUCU AGGUCAGG	1051
3627	CCCCCUUC G CCCCGAGA	467	UCUCGGGG GCCGAAAGGCGAGUCAAGGUCU GAAGGGGG	1052
3645	GGCCCUCU G CCUGCUGC	468	GCAGCAGG GCCGAAAGGCGAGUCAAGGUCU AGAGGGCC	1053
3649	CUCUGCCU G CUGCCCGA	469	UCGGGCAG GCCGAAAGGCGAGUCAAGGUCU AGGCAGAG	1054
3652	UGCCUGCU G CCCGACCU	470	AGGUCGGG GCCGAAAGGCGAGUCAAGGUCU AGCAGGCA	1055
3661	CCCGACCU G CUGGUGCC	471	GGCACCAG GCCGAAAGGCGAGUCAAGGUCU AGGUCGGG	1056
3667	CUGCUGGU G CCACUCUG	472	CAGAGUGG GCCGAAAGGCGAGUCAAGGUCU ACCAGCAG	1057
3730	ACGUUUUU G CCUUUGGG	473	CCCAAAGG GCCGAAAGGCGAGUCAAGGUCU AAAAACGU	1058
3742	UUGGGGGU G CCGUGGAG	474	CUCCACGG GCCGAAAGGCGAGUCAAGGUCU ACCCCCAA	1059
3784	GAGGAGCU G CCCCUCAG	475	CUGAGGGG GCCGAAAGGCGAGUCAAGGUCU AGCUCCUC	1060
3808	CUCCUCCU G CCUUCAGC	476	GCUGAAGG GCCGAAAGGCCGAGUCAAGGUCU AGGAGGAG	1061
3933	CUGGACGU G CCAGUGUG	477	CACACUGG GCCGAAAGGCGAGUCAAGGUCU ACGUCCAG	1062
3960	CCAAGUCC G CAGAAGCC	478	GGCUUCUG GCCGAAAGGCGAGUCAAGGUCU GGACUUGG	1063
4007	UGACUUCU G CUGGCAUC	479	GAUGCCAG GCCGAAAGCCGAGUCAAGGUCU AGAAGUCA	1064
4056	GGGAACCU G CCAUGCCA	480	UGGCAUGG GCCGAAAGGCGAGUCAAGGUCU AGGUUCCC	1065
4061	CCUGCCAU G CCAGGAAC	481	GUUCCUGG GCCGAAAGGCGAGUCAAGGUCU AUGGCAGG	1066
4094	UCCUUCCU G CUUGAGUU	482	AACUCAAG GCCGAAAGGCGAGUCAAGGUCU AGGAAGGA	1067
4179	GAGGCCCU G CCCAAUGA	483	UCAUUGGG GCCGAAAGGCGAGUCAAGGUCU AGGGCCUC	1068
4208	CAGUGGAU G CCACAGCC	484	GGCUGUGG GCCGAAAGGCGAGUCAAGGUCU AUCCACUG	1069
4351	CUAGUACU G CCCCCCAU	485	AUGGGGG GCCGAAAGGCGAGUCAAGGUCU AGUACUAG	1070
4406	UACAGAGU G CUUUUCUG	486	CAGAAAAG GCCGAAAGGCGAGUCAAGGUCU ACUCUGUA	1071
192	GCGGCCUU G UGCCGCUG	487	CAGCGGCA GCCGAAAGGCGAGUCAAGGUCU AAGGCCGC	1072
249	ACCCAAGU G UGCACCGG	488	CCGGUGCA GCCGAAAGGCGAGUCAAGGUCU ACUUGGGU	1073
387	GCCAGCCU G UCCUUCCU	489	AGGAAGGA GCCGAAAGGCGAGUCAAGGUCU AGGCUGGC	1074
478	UGCGGAUU G UGCGAGGC	490	GCCUCGCA GCCGAAAGGCGAGUCAAGGUCU AAUCCGCA	1075
559	CCACCCCU G UCACAGGG	491	CCCUGUGA GCCGAAAGGCGAGUCAAGGUCU AGGGGUGG	1076
678	ACGAUUUU G UGGAAGGA	492	UCCUUCCA GCCGAAAGGCGAGUCAAGGUCU AAAAUCGU	1077
758	CCACCCCU G UUCUCCGA	493	UCGGAGAA GCCGAAAGGCGAGUCAAGGUCU AGGGGUGG	1078

Table 59

768	UCUCCGAU G UGUAAGGG	494	CCCUUACA GCCGAAAGGCGAGUCAAGGUCU AUCGGAGA	1079
770	UCCGAUGU G UAAGGGCU	495	AGCCCUUA GCCGAAAGGCGAGUCAAGGUCU ACAUCGGA	1080
809	UGAGGAUU G UCAGAGCC	496	GGCUCUGA GCCGAAAGGCGAGUCAAGGUCU AAUCCUCA	1081
829	CGCGCACU G UCUGUGCC	497	GGCACAGA GCCGAAAGGCGAGUCAAGGUCU AGUGCGCG	1082
833	CACUGUCU G UGCCGGUG	498	CACCGGCA GCCGAAAGGCGAGUCAAGGUCU AGACAGUG	1083
845	CGGUGGCU G UGCCCGCU	499	AGCGGGCA GCCGAAAGGCGAGUCAAGGUCU AGCCACCG	1084
893	UGAGCAGU G UGCUGCCG	500	CGGCAGCA GCCGAAAGGCGAGUCAAGGUCU ACUGCUCA	1085
965	UGGCAUCU G UGAGCUGC	501	GCAGCUCA GCCGAAAGGCGAGUCAAGGUCU AGAUGCCA	1086
1058	CGCCAGCU G UGUGACUG	502	CAGUCACA GCCGAAAGGCGAGUCAAGGUCU AGCUGGCG	1087
1060	CCAGCUGU G UGACUGCC	503	GGCAGUCA GCCGAAAGGCGAGUCAAGGUCU ACAGCUGG	1088
1070	GACUGCCU G UCCCUACA	504	UGUAGGGA GCCGAAAGGCGAGUCAAGGUCU AGGCAGUC	1089
1166	ACAGCGGU G UGAGAAGU	505	ACUUCUCA GCCGAAAGGCGAGUCAAGGUCU ACCGCUGU	1090
1187	CAAGCCCU G UGCCCGAG	506	CUCGGGCA GCCGAAAGGCGAGUCAAGGUCU AGGGCUUG	1091
1197	GCCCGAGU G UGCUAUGG	507	CCAUAGCA GCCGAAAGGCGAGUCAAGGUCU ACUCGGGC	1092
1371	CUCCAAGU G UUUGAGAC	508	GUCUCAAA GCCGAAAGGCGAGUCAAGGUCU ACUUGGAG	1093
1685	GGACGAGU G UGUGGGCG	509	CGCCCACA GCCGAAAGGCGAGUCAAGGUCU ACUCGUCC	1094
1687	ACGAGUGU G UGGGCGAG	510		1095
1716	CACCAGCU G UGCGCCCG	511	CGGGCGCA GCCGAAAGGCGAGUCAAGGUCU AGCUGGUG	1096
1757	CACCCAGU G UGUCAACU	512		1097
1759	CCCAGUGU G UCAACUGC	513	GCAGUUGA GCCGAAAGGCGAGUCAAGGUCU ACACUGGG	1098
1837	GGGAGUAU G UGAAUGCC	514		1099
1853	CAGGCACU G UUUGCCGU	515		1100
1874	CCCUGAGU G UCAGCCCC	516		1101
1901	AGUGACCU G UUUUGGAC	517		1102
1925	UGACCAGU G UGUGGCCU	51.8		1103
1927	ACCAGUGU G UGGCCUGU	519		1104
1934	UGUGGCCU G UGCCCACU	520		1105
1984	CCAGCGGU G UGAAACCU	521		1106
2075	CCACUCCU G UGUGGACC	522		1107
2077	ACUCCUGU G UGGACCUG	523		1108
2410	GGGAGAAU G UGAAAAUU	524		1109
2436	AUCAAAGU G UUGAGGGA	525		1110
2503	neecneen e neecncc	526		1111
2518	CCCCAUAU G UCUCCCGC	527		1112
2602	UAGACCAU G UCCGGGAA	528		1113
2651	GAACUGGU G UAUGCAGA	529		1114
2689	UGGAGGAU G UGCGGCUC	530		1115
2749	CCAACCAU G UCAAAAUU	531		1116
2887	AGAGUGAU G UGUCGAGU	532		1117
2889	AGUGAUGU G UGGAGUUA	533		1118
2902	GUUAUGGU G UGACUGUG	534		1119
2908	GUGUGACU G UGUGGGAG	535		1120
2910	GUGACUGU G UGGGAGCU	536		1121
3025	CCAUUGAU G UCUACAUG	537		1122
3047	GGUCAAAU G UUGGAUGA	538		1123
3068	CUCUGAAU G UCGGCCAA	539		1124
3093	GAGUUGGU G UCUGAAUU	540	AAUUCAGA GCCGAAAGGCGAGUCAAGGUCU ACCAACUC	1125

Table 59

1313 AGOSCOUT & URSUEAUC 541 GAUSACCA GCCGAAAGGCGRUCARGUUC ARAGGGCU 1126 3427 GUUCCGAN & DAULUGAN 543 AUCARAIN GCCGAAAGGCGRUCARGUUC ARAGGAC 1128 3427 GUUCCGAN & DAULUGAN 543 AUCARAIN GCCGAAAGGCGRUCARGUUC ARAGGAC 1128 3427 GUUCCGAN & DAULUGAN 544 CUUGUUCA GCCGAAAGGCGRUCARGUUC ARUCAGAC 1128 3427 AGCCRAD & UUCGGCC 545 GGGCCGAA GCCGAAAGGCGRUCARGUUC ARUCAGAC 1130 3428 GUUCCARU & UUCGCCC 545 GGGCCGAA GCCGAAAGGCGRUCARGUUC ARUCAGAC 1130 3439 GUUCCARU & GUUCCAC 547 GGGCCGAA GCCGAAAGGCGRUCARGUUC ARUCAGAC 1131 3470 GCCCUARU & GUUCCAC 547 GGGCCGAA GCCGAAAGGCGRUCARGUUC ARUCAGAC 1131 3470 GCCCUARU & GUUCCAC 547 GGGCCGAA GCCGAAAGGCGRUCARGUUC ARUCAGAC 1131 3470 CCURRAUU & GUUCCAC 547 GUUCCAC 648 CUUGAGA GCCGAAAGGCGRUCARGUUC ARUCAGAC 1133 3470 CCUCRAU & GUUCAGA 548 CCUURAGA GCCGAAAGGCGRUCARGUUC ARUCAGAC 1133 3470 AGCCAGAC GUUCAGA 549 CCUURAGA GCCGAAAGGCGRUCARGUUC ARUCACAC 1134 3470 AAGCAGAG GUUCAGAA 550 AGANUCCA GCCGAAAGGCGRUCARGUUC ARUCACAC 1136 3430 AAGCAGAG GUUCAGAA 551 UUCUURAGA GCCGAAAGGCGRUCARGUUC ARUCACAC 1136 3430 CARGGAC GUUCAGAC 553 AGANUCCA GCCGAAAGGCGRUCARGUUC ARUCACAC 1136 3430 CARGGAC GUUCAGAC 553 AGANUCCA GCCGAAAGGCGRUCARGUUC ARUCACAC 1136 3431 CARGGAC GUUCAGAC 554 CUUCUURAGA GCCGAAAGGCGRUCARGUUC ARUCACAC 1136 3441 GUUUUUUU GUUCAGA 554 GUUCAGA GCCGAAAGGCGRUCARGUUC ARUCACAC 1136 3441 GUUUUUU GUUCAGA 554 GUUCAGA GCCGAAAGGCGAGAGCARGUCARGUUC ARUCACAC 1136 3441 GUUUUUU				,	
3422 GUCCGAN G UNUUUUUU	3133	AGCGCUUU G UGGUCAUC	541	GAUGACCA GCCGAAAGGCGAGUCAAGGUCU AAAGCGCU	1126
3592 CUGANINU G UGAACCAG 544 CUGGUUCA CCCGAAAGGCGAGUCAAGGUCI AUATUCAG 1129 3697 AGCCRAD G UUCAGCCC 454 GGGCCGAA GCCGAAAGGCGAGUCAAGGUCI AUATUCAG 1130 3974 GCCCUGAU G UGAACCAG 546 CUGGUUCA CCCGACAAGGCGAGUCAAGGUCI AUCUGACC 1131 3974 GCCCUGAU G UGACCAG 547 UGAGGACA GCCGAAAGGCGAGUCAAGGUCI AUCUGACC 1131 3976 CUCUAGUG G UGACCAG 547 UGAGGACA GCCGAAAGGCGAGUCAAGGUCI AUCAGGGC 1131 3976 CUCUAGUG G UCCUGAG 548 CCCUGAGA GCCGAAAGGCGAGUCAAGGUCI AUCAGGGC 1131 4072 AGGAACCU G UCCUGAG 548 CCCUGAGA GCCGAAAGGCGAGUCAAGGUCI AUCAGGC 1131 4145 GACUCUTU G UGAGTUCT 559 AGANUCCA GCCGAAAGGCGAGUCAAGGUCI AGGUCI ACCUCCU 1134 4150 AAGCCAG G UCCUAAGA 551 UUCUAGA GCCGAAAGGCGAGUCAAGGUCI AUGUCAC 1135 4130 AAGCCAG G UCCCUGAA 552 UUCUAGA GCCGAAAGGCGAGUCAAGGUCI AUGUCCU 1136 4131 CAGAGAGU G UCCCUGAA 552 UUCUAGA GCCGAAAGGCGAGUCAAGGUCI AUGUCCU 1136 4138 CCAAGGUG G UCCCUGAA 552 UUCUAGA GCCGAAAGGCGAGUCAAGGUCI AUGUCCU 1136 4138 CCAAGGUG G UCCCUGAA 552 UUCUAGA GCCGAAAGGCGAGUCAAGGUCI AUGUCCU 1136 4139 CAGAGAGU G UCCCUGAA 553 ACUACUAG GCCGAAAGGCGAGUCAAGGUCI AUGUCCU 1137 4140 GCUUUCU G UUUUGUUU 555 AAACCAAA GCCGAAAGGCGAGUCAAGGUCI AAAGCCAG 1139 4141 GCUUUCUU G UUUUGUUU 555 AAACCAAA GCCGAAAGGCGAGUCAAGGUCI AAAAGCAG 1141 4149 UUUGUUUU G UUUUGUUU 556 AAACCAAA GCCGAAAGGCGAGUCAAGGUCI AAAAGCAA 1141 4149 UUUGUUUU G UUUGUUU 557 AAACCAAA GCCGAAAGGCGAGUCAAGGUCI AAAAAAAG 1141 4149 UUUGUUUU G UUUGUUU 556 AAACCAAA GCCGAAAGGCGAGUCAAGGUCI AAAAAAAA 1141 4149 UUUGUUUU G UUUGUUU 556 AAACCAAA GCCGAAAGGCGAGUCAAAGGUCI AAAAAAAA 1141 4149 UUUGUUUU G UUUGUUU 556 AAACCAAA GCCGAAAGGCGAGUCAAAGGUCI AAAAAAAA 1141 4150 AAACCCAG G CACCCGG 556 CAGAGGGG GCCGAAAGGCGAGUCAAAGGUCI AAAAAAAA 1141 416 GGCCCCGG G CACCCGG G 556 CAGAGGGG GCCGAAAGGCGAGUCAAGGUCU AAAGGCAA 1146 417 GCCCCACCG G CACCCCGG 556 GGCCGGG GCCGAAAGGCGAGUCAAGGUCU ACGGCCA 1146 418 CAGGCCCG G CC	3269	CUUCUUCU G UCCAGACC	542	GGUCUGGA GCCGAAAGGCGAGUCAAGGUCU AGAAGAAG	1127
AGCCAGAN UUUCGCCC	3427	GCUCCGAU G UAUUUGAU	543	AUCAAAUA GCCGAAAGGCGAGUCAAGGUCU AUCGGAGC	1128
	3592	CUGAAUAU G UGAACCAG	544	CUGGUUCA GCCGAAAGGCGAGUCAAGGUCU AUAUUCAG	1129
1971 COCCUEND 6 UNICITICA 547	3607	AGCCAGAU G UUCGGCCC	545	GGGCCGAA GCCGAAAGGCGAGUCAAGGUCU AUCUGGCU	1130
1975 CURANDED 6 UCCUEAGE 546 CUUJAGGA GCCGAAAAGCCGAUUCAAGGUU ACAUCAGC 1133 1134 1132 1134	3939	GUGCCAGU G UGAACCAG	546	CUGGUUCA GCCGAAAGGCGAGUCAAGGUCU ACUGGCAC	1131
AGRANCO	3974	GCCCUGAU G UGUCCUCA	547	UGAGGACA GCCGAAAGGCGAGUCAAGGUCU AUCAGGGC	1132
1450	3976	CCUGAUGU G UCCUCAGG	548	CCUGAGGA GCCGAAAGGCGAGUCAAGGUCU ACAUCAGG	1133
ARROGARDI G UCUNARDA 551	4072	AGGAACCU G UCCUAAGG	549	CCUUAGGA GCCGAAAGGCGAGUCAAGGUCU AGGUUCCU	1134
CALAGAGU 6 UCCCUCADA 552 UUCCAGOAD GCCGAAAAGCGGGUUCAAGGUU ABUCUCUC 1137	4162	GAGUCUUU G UGGAUUCU	550	AGAAUCCA GCCGAAAGGCGAGUCAAGGUCU AAAGACUC	1135
GEALDGGG	4300	AAGGGAGU G UCUAAGAA	551	UUCUUAGA GCCGAAAGGCGAGUCAAGGUCU ACUCCCUU	1136
1397 CAGGECTUT 6 UNACAGEAGU 554	4332	CAGAGACU G UCCCUGAA	552	UUCAGGGA GCCGAAAGGCGAGUCAAGGUCU AGUCUCUG	1137
4414 CCUUTUCUU G UTUURGUUU 555 AAACUARA GCCGARAGGGGUUCARGGUU AGARARGC 1140 4434 CUUTUUUU G UTUURGUUU 555 AAACUARA GCCGARAGGGGGUUCARGGUU AGARARGC 1141 4439 UTUUGUUU G UTUUGUUU 556 AAACUARA GCCGARAGGGGGUUCARGGUU ARAACARA 1142 9 AAGGGGAG G URAACCUG 558 CAGGGUUR GCCGARAGGGGGUUCARGGUU ARAACARA 1142 18 URAACCUG G CCCUTURG 558 CAGGGUUR GCCGARAGGGGGUUCARGGUU CHCCCGUU 143 18 URAACCUG G CCCUTURG 559 CAGGGGGGGGGGGGGGGGGGGGGGGGGCARGGUUCARGGUU CHCCCGUU 143 27 CCCUTUU G UGGGGGC 560 GGCCCGA GCCGARAGGGGGGUUCARGGUU CARAGGGG 1145 13 UGGUCGGG G CCCCGGGGG 561 GGCCCGA GCCGARAGGGGGGUUCARGGUU CARAGGGG 1146 14 GGCCCCGG G CCCUTURG 562 GGCGGCGG GCCGARAGGGGGUUCARGGUU CARAGGGG 1147 14 GGCCCCGG G CCCCUTURG 564 GGCGGCGG GCCGARAGGGGGUUCARGGUU CCCCGUU 1147 15 CCCCGGG G CCCUTURG 564 GGCGGCGG GCCGARAGGGGGUUCARGGUUU CCCCGGG 1147 16 CGCGGCGG G CCCCCCC 565 GGUUGAGG GCCGARAGGGGGUUCARGGUUU CCCCGGGG 1148 16 CCCCCCCG G CCCCCCC 565 GGUUGAGG GCCGARAGGGGGUUCARGGUUU CCCCGGG 1150 17 CCCCCGCG G CCCCCCC 567 GGCGGCGG GCCGARAGGGGGUUCARGGUUU CCGGGGGG 1150 16 CCCUCCCG G CCCCCCC 567 GGCGCGGG GCCGARAGGGGGUUCARGGUUU CCGGGGGG 1151 16 CCCUCCCG G CCCCCCC 567 GGCCCGGG GCCGARAGGGGGUUCARGGUUU UCGGGGGG 1151 16 CCCUCCCG G CCCCCCC 567 GGCCCGGG GCCGARAGGGGGUUCARGGUUU UCGGGGGG 1151 16 CCCUCCCG G CCCCACCC 567 GGCCCGG GCCGARAGGGGGUUCARGGUUU UCGGGCGC 1151 16 CCCUCCCG G CCCCACCC 567 GGCCCGG GCCGARAGGGGGUUCARGGUUU UCGGGCGC 1151 16 CCCUCCCG G CCCCACCC 567 GGCCCGG GCCGARAGGGGGGUUCARGGUUU UCGGGCGC 1151 16 CCCUCCCG G CCCCACCC 567 GGCCCCGG GCCGARAGGGGGGUUCARGGUUU UCGGGCCC 1151 16 CCCUCCGG G CCCCARGG C 569 GGCCCGG GCCGARAGGGGGGUUCARGGUUU UCGGGCCC 1151 16 GGCCGGG G CCCCACGG GCCGARGGGGGGGGGGGGGG	4380	GCAAUGGU G UCAGUAUC	553	GAUACUGA GCCGAAAGGCGAGUCAAGGUCU ACCAUUGC	1138
4439 UUUUUUUU 556 AAACAAA CCCGAAAGGCGGGUCAAGGUCA AAAAAAA 1141 4439 UUUUUUUU UUUUUUUU 556 AAACAAAA CCCGAAAGGCGGGUCAAGGUCA AAAACAAA 1141 4439 WUUUUUUU UUUUUUUU 557 UAAAAAAA CCCGAAAGGCGGGUCAAGGUCA AAAACAAA 1141 18 WAACCCUG G CCCCUTURG 558 CAGGUUA CCCGAAGGCGAGUCAAGGUCU (CCCCCUU 1143 18 WAACCCUG G CCCCUTURG 559 CAAAGGAG GCCGAAAGGCGAGUCAAGGUCU (CCCCCUU 1143 18 WAACCCUG G CCCCCUTURG 559 CAAAGGAG GCCGAAAGGCGAGUCAAGGUCU (CCGACCCA 1146 14 GCCCCGGG G CAGCCGG 560 GCCCCGAG GCCCAAAGGCGAGUCAAGGUCU (CCGACCCA 1146 14 GCCCCGGG G CAGCCGG 561 GCCCGGGG GCCCAAAGGCGAGUCAAGGUCU (CCGACCCA 1146 14 GCCCGGGG G CAGCCGG 562 GCCCGGGG GCCCAAAAGGCGAGUCAAGGUCU (CCGACCCA 1146 14 GCCCGGGG G CACCCCGG 563 GCGGGGGG GCCGAAAGGCGAGUCAAGGUCU (CCGACCCA 1146 15 CCCCCCCG G CACCCCCG 565 GGGGGGG GCCGAAAGGCGAGUCAAGGUCU (CCGGCGG C 1146 16 GCCCCCCCC G CCCCCCC 565 GGGGGGG GCCGAAAGGCGAGUCAAGGUCU (CCGGCGG C 1150 16 CCCCCCCCC G CCCCCCC 566 GGGGGGG GCCGAAAGGCCGAGUCAAGGUCU (CCGGGGGG C 1150 16 CCCCCCCC G CCCCCCC 566 GGGGGGG GCCGAAAGGCCGAGUCAAGGUCU (CCGGGGGG C 1150 16 CCCCCCCC G CCCCCCC 566 GGGGGGG GCCGAAAGGCCGAGUCAAGGUCU (CCGGGGG C 1151 16 CCCCCCCC G CCCCCCC 567 GGCGCGGG GCCGAAAGGCCGAGUCAAGGUCU (CCGGGGGG C 1151 16 CCGCCCCC G CCCCCCC 567 GCGCCCGG GCCGAAAGGCCGAGUCAAGGUCU (CCGGGGGG C 1151 16 CCGCCCCC G CCCCCCC 567 GCGCCCGG GCCCAAAGGCCGAGUCAAGGUCU (CCGGCGG C 1151 16 GGCCCCGG G CCCCCAAGGC 568 GCGCCCGG GCCCAAAGGCCGAGUCAAGGUCU (CCGCGCG C 1151 16 GGCCCCGG G CCCCCAAGGC C 568 GCCCCCGG GCCCAAAGGCCGAGUCAAGGUCU (CCCAAAGGCCGAGUCAAGGCCGCGCCCCAAGGCCGAGUCAAGGCCGAGUCAAGGCCGCGCCCAAGGCCGAGUCAAGGCCGCGCCCAAGGCCGAGUCAAGGCCGCGCCCCAAGGCCCGAGUCAAGGCCGCGCCCCAAGGCCCGAGUCAAGGCCGCCCCCAAGGCCCGAGUCAAGGCCGCCCCCCAAGGCCCGAGUCAAGGCCGCGCCCCAAGGCCCGAGUCAAGGCCGCGCCCCCCAAGGCCCGAGUCAAGGCCGAGUCAAGGCCGCCCCCCAAGGCCCGAGCCCAAGGCCCGCCC	4397	CAGGCUUU G UACAGAGU	554	ACUCUGUA GCCGAAAGGCGAGUCAAGGUCU AAAGCCUG	1139
1449 100000000 100000000 1557 100000000 100000000000000000000000	4414	GCUUUUCU G UUUAGUUU	555	AAACUAAA GCCGAAAGGCGAGUCAAGGUCU AGAAAAGC	1140
NACOSSIGN & UNACCCUS 558 CAGGUIUM, GCCGAAAGGGGGUCAAGGGUC CTCCCCUU 1143	4434	COMMOND & MANAGAMA	556	AAACAAAA GCCGAAAGGCGAGUCAAGGUCU AAAAAAAG	1141
19	4439	UUUGUUUU G UUUUUUUA	557	UAAAAAA GCCGAAAGGCGAGUCAAGGUCU AAAACAAA	1142
27	9	AAGGGGAG G UAACCCUG	558	CAGGGUUA GCCGAAAGGCGAGUCAAGGUCU CUCCCCUU	1143
33	18	UAACCCUG G CCCCUUUG	559	CAAAGGGG GCCGAAAGGCGAGUCAAGGUCU CAGGGUUA	1144
43	27	CCCCUUUG G UCGGGGCC	560	GGCCCCGA GCCGAAAGGCGAGUCAAGGUCU CAAAGGGG	1145
148 CCCGGGGG G CCCCUTURAC 563 GCGGGGGG GCCGAAAGGGGGGUCAAGGGUT UGCCCGGG 1146 55 CCCACGGG G CCCCUTURAC 564 GGGAAGGG GCCGAAAGGCGGAGUCAAGGUT UGCCCGGG 1149 56 GCGCCCG G CCCCCACC 565 GGGGGGG GCCGAAAGGCGAGUCAAGGUTU UGCCGGGG 1150 105 CCCUCCGA G CACCCCGG 566 GGGGGGGG GCCGAAAGGCGAGUCAAGGUTU UGCGGGGG 1150 105 CCCUCCCA G CCGGUCC 566 GGGGGGG GCCGAAAGGCGAGUCAAGGUTU UGCGAGGG 1151 105 CCCUCCCA G CCGGUCC 566 GGGGGGG GCCGAAAGGCGAGUCAAGGUTU UGCGAGGG 1151 105 CCCUCCCA G CCGGUCC 567 GGCGCCGG GCCGAAAGGCGAGUCAAGGUTU UGCGAGGG 1152 105 CCACCGG G UCCACCCG 568 GGGCGGGA GCCGAAAGGCGAGUCAAGGUTU UGCGAGGG 1153 105 CCACCGGG G UCCACCCG 568 GGGCCGGG GCCGAAAGGCGAGUCAAGGUTU UGCGACGG 1153 106 CGGCGCGA G CCGGAGCC 569 GCGCCGGG GCCGAAAGGCGAGUCAAGGUTU UGCGGCCC 1154 107 GCCAGGGG G CCCGAAGG GCCGAAAGGCGAGUCAAGGUTU UGCGGCCC 1155 166 GGGCCGGA G CCGGAGCC 571 GCCUCCGG GCCGAAAGGCGAGUCAAGGUTU UGCGCCCC 1156 166 GGGCCGGA G CCGGAGGC 573 GGUGCCG GCCGAAAGGCGAGUCAAGGUTU UGCGCCCC 1157 166 GGGCCCGA G UGAGGAC 573 GGUGCCG GCCGAAAGGCGAGUCAAGGUTU UGCGCCCC 1158 167 GCCAGGAG G CCCCAAAGGCGAGUCAAGGCAGUCAAGGUTU UGCGCCCC 1158 168 ACCAUGGA G CUUGCGG 575 GCGCCCAG GCCCAAAGGCGAGUCAAGGUTU UCCAUGGU 1159 189 UGAGGCC G CUUGCGG 575 GCGCCCAG GCCCAAAGGCAGUCAAGGUTU UCCAUGGU 1150 189 UGAGGGC G CUUCUCC 576 AGGCGCAG GCCCAAAGGCAGUCAAGGUTU UCCAUGGU 1160 189 UGAGGCG G CUUCUCC 577 GCACAAGG GCCCAAAAGGCAGUCAACGAGUTU CCCCACCU 1162 180 ACCAUCCG G CCUUCUCC 578 AGGAGGAG GCCCAAAAGGCAGUCAACGAGUTU CCCCACCU 1162 180 ACCCCCAG G CCUUCUCC 578 AGGAGGAG GCCCAAAAGGCAGUCAACGAGUTU CCCCACCU 1162 180 ACCCCCAG G CCUUCUCC 578 AGGAGGAG GCCCAAAAGGCAGUCAACGAGGUTU CCCCACCU 1163 180 ACCCCCAG G CCUUCUCC 578 AGGAGGAG GCCCAAAAGGCAGUCAACGAGGUTU CCCCACCC 1163 180 ACCCCCAA G UGUCCCCC 581 GGGCCAAGGCCAAAGGCAGUCAACGAGGUTU CCCCACCC 1163 180 ACCCCCAAG G CC	33	UGGUCGGG G CCCCGGGC	561	GCCCGGGG GCCGAAAGGCGAGUCAAGGUCU CCCGACCA	1146
65 CCCACGGG G CCCUCIUNC 564 GUNARIGG CCCCANAGGCCGGGUCAAGGUC CCCCGGGC 1149	40	GGCCCCGG G CAGCCGCG	562	CGCGGCUG GCCGAAAGGCGAGUCAAGGUCU CCGGGGCC	1147
89	43	CCCGGGCA G CCGCGCGC	563	GCGCGCGG GCCGAAAGGCGAGUCAAGGUCU UGCCCGGG	1148
105	65	CCCACGGG G CCCUUUAC	564	GUAAAGGG GCCGAAAGGCGAGUCAAGGUCU CCCGUGGG	1149
130 CCCUCCCA G CCGCUCC 567 GCACCGG GCCANAGGCGAGUCAAGGCGAGUCAAGGCU UGGGAGGC 1152 135 CCACCGGG G UCCAGCG 568 GGGCGGGA GCCCAAGGC 1153 146 CGGGGGG G CCANAGGC 569 GGCCUCCGG GCCCGAAAGGCCAGUCAAGGCGUU UGGGGCG 1154 146 CAGCCGGA G CCANAGGG 570 CCCCAUGG 570 LCCCAUGGG 1154 146 GCAGCGAG G CCGAAAGC 571 CCCCAUGGG 570 LCCCAUGGG 1154 146 GCAGCGAG G CCGAAAGC 571 CCCCAUGGG GCCGAAAGGCGAUCAAGGUCU UCCGAUGGC 1157 166 GGGCCGAG G CCGAAAGGCGAGUCAAGGCGAGUCAAGGCCGAAGUCAAGGCCGAAGUCAAGGCCGAAGUCAAGGCCGAAGUCAAGGCCGAAGUCAAGGCCGAAGUCAAGGCCGAAGUCAAGGCCGAAGUCAAGGCCGAAGUCAAGGCCGAACGCAAGGCAAGUCAAGGCCGAACGCAAGGCAAGGCAAGUCAAGGCCGAACGCAAGGCAA	89	CGCGCCCG G CCCCCACC	565	GGUGGGG GCCGAAAGGCGAGUCAAGGUCU CGGGCGCG	1150
135 CCAGCOGG & UCCAGCOG 568 CGGCUGGA & CCCGAAAGGCGAGUCAAGGUCU CCGGCUGG 1153 140 CGGGUCCA & CCCGAGCC 569 GCCUCCGG GCCGAAAGGCGAGUCAAGGUCU UGGCCGC 1154 146 CAGCOGG & CCAUGGG 579 CCCCCAUGG GCCCAAAGGCGAGUCAAGGUCU UGGCCGC 1155 154 GCCAUGGG G CCGGAGCC 571 GCCCCUGGG GCCGAAAGGCGAGUCAAGGUCU CCCAUGGC 1156 160 GGGCCGGA G CCCCAUGG 572 CACUGGG GCCCAAAGGCGAGUCAAGGUCU UCCAUGGC 1157 166 GGGCCGGA G CCCAUGGG 574 CCCUGGG GCCCAAAGGCGAGUCAAGGUCU UCACUGGC 1157 170 CGCAGGAG C CCCAUGGG 574 CCUUGGGG GCCAAAGGCGAGUCAAGGUCU UCACUGGU 1159 184 UGGAGCUG A CCCCAUGG 575 CCAGCAGGG GCCAAAGGCGAGUCAAGGUCU UCACUGGU 1161 186 ACCACUGG G CCUUGUGC 576 CAAGAGGG GCCCAAAGGCGAGUCAAGGUCU UCACUGGU 1162 187 AGCCAGG G CCUCCUCU 578 AGCACAGG GCCCAAAAGGCGAGUCAAGGUCU UCCCAGCG 1162 240 CCCUCGGG G CUUCUCCU 578 AGCACAGG GCCCAAAAGGCGAGUCAAGGUCU UCCCAGCG 1162 232 CCCCCAGG G CCCCAGGC 579	105	CCCUCGCA G CACCCCGC	566	GCGGGGUG GCCGAAAGGCGAGUCAAGGUCU UGCGAGGG	1151
140 CGGGBICCA G CCGGRGCC 569 GGCCCGGG CCCANAGGGCGAGUCAAGGCCTUUCAGGUCU USGACCCG 1154 146 CAGCCGAG A CCANAGGG 570 CCCCANAGGGCGAGUCAAGGCCAGUCAAGGCCAGUCACCAGGCC 1155 154 GCCADUGGG 570 CCCCANAGGGCAGUCAAGGCCAGUCACCAGGCC 1156 154 GCCADUGGG 573 CCCCUGGGCGGCAAAGGCGAGUCAAGGUCU UCCGGCCC 1157 166 GGGCCCCAG G UGAGCCC 573 CACUGGGG GCCCAAAAGGCGAGUCAAGGUCU UCCGCGCC 1157 176 CGCAGAGGA G CACCAUGG 574 CCAUGGGG GCCCAAAAGGCGAGUCAAGGUCU UCCAGGCCU 1159 180 ACACAUGG G CCGCAGGGC 575 GCCCCAAGGCCGAGUCAAGGCCAGUCAAGGCCUU UCCAUGCU 1160 181 UGGGACCG G CCUUGUCC 577 GCCCCAAAGGCCAGUCAAGGCCUUCAAGGCCUUCAAGGCCUUCAAGGCCUUCAAGGCCU 1161 187 AGCUGGGG G CUUCUCC 577 GCACAAGG GCCCAAAAGGCCAGUCAAGGCCU UCCAGCC 1162 240 GCCCOAG G CCCCCCAG 579 GCCCCAAGGCAGCAAGGCCAGUCAAGGCCUUCCAAGGCCUUCCAGCC 1163 232 ACCCCCAG G CACCAAG 580 CUUCGGGG GCCCAAAAGGCCAGUCAAGGCCUUCCAAGGCCUUCCAGCC 1165 247 GCACCCCAA G UCCCCC	130	CCCUCCCA G CCGGGUCC	567	GGACCCGG GCCGAAAGGCGAGUCAAGGUCU UGGGAGGG	1152
146 CAGCOGGA & CAULGGG 570 CCCCUIGG & CCCLANAGGGGARUUCAAGGUUU UCCGGCOG 1155 154 GCCAUGGG & CCGGAACC 571 GCCUCCG GCCGAAAGGCGAGUUCAAGGUUU UCCGAUGGC 1156 160 GGGCCGGA & CCGGAAGG 573 GGUUCCG GCCGAAAGGCGAGUCAAGGUUU UCCGCGCC 1157 166 GAGCCCCA & UGAGCAC 573 GGUUCCG GCCGAAAGGCGAGUCAAGGUUU UCCGCCC 1158 170 CCCAGAGA & CACCUGG 573 GGUUCCGA GCCGAAAGGCGAGUCAAGGUUU UCCGCCC 1158 180 ACCAUGGA & CUUGCGGC 575 GCCGCCAG & GCCCAAAGGCGAGUCAAGGUUU UCCAUGGU 1160 181 UGAGCACC & CUUGCGC 575 GCCGCCAG & GCCCAAAGGCGAGUCAAGGUUU CACCUCCA 1161 187 AGCCGCAG & GCCCCAAAGGCGAGUCAAAGGUUC CACCUCCA 577 GCACAAGG & GCCCAAAAGGCAGUUCAAGGUUC CACCUCCA 1162 204 CCCCCCGGA & CCCCCAAG 579 GCACCAAG & GCCCCAAAGGCAGUCCAAAGGCAGUCCAAGGUCCU UCCCGGGG 1163 219 AGCCCCAA & GUUCCACC 581 GUUCGGGG GCCGAAAGGCGAGUCAAAGGCAGUUCU UCCCGGGG 1165 247 GCACCCAA & GUUCCACC 581 GUUCCAGAAAGGCAGAGUCAAAGGCAGUUCU UCCAGGGUCU UCCA	135		568	CGGCUGGA GCCGAAAGGCGAGUCAAGGUCU CCGGCUGG	1153
154 GCCAUGGG G CCGGAGCC 571 GCCUCCG GCCGAAAGGCGAGUCAAGGUCAAGGUC 1156 160 GGGCCGGA G CCGCAUGG 572 CACUCCGG GCCGAAAGGCGAGUCAAGGUCU UCCGGCCC 1157 166 GAGCCGCA G UGAGCAC 573 CGUUCCGG GCCCAAAGGCGAGUCAAGGUCU UCCGGCCC 1158 170 GCCAGAGA G CACCAUGG 574 CCAUGGGG GCCCAAAGGCGAGUCAAGGUCU UCACUGGG 1159 184 HOGGAGCUG G CCCUUGG 576 CAAGGCCG GCCCAAAGGCGAGUCAAGGUCU UCACUGGG 1161 187 AGCUGGGG G CCUUGG 577 GCACAAGG GCCCAAAGGCGAGUCAAAGGUCU UCCCCAGCG 1162 189 AGCUGGGG G CUUCCCU 578 CAAGAGCG GCCCAAAGGCGAGUCAAAGGUCU UCCCAGCG 1162 140 GCCCCAGA G CGCCCAAAG 577 GCACAAGG GCCCAAAGGCGAGUCAAAGGUCU UCCCAGCG 1162 212 CCCCCCAGA G CGCCCAAAGGCAGCAAGGAGCAAGGAGCAGUCAAAGGCAGUUCUCCCCAGCG 578 GCUCCCAGCG GCCCAAAAGGCAGAGCAAGGCAGUCAAAGGCCGUUCCCAAGGCCGAGCCAAAGGCAGAGCAAGGCAGCCAAAGGCAGGAGCAAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCAGGCAGCCAAAGGCCAGGCAGCCAAAAGGCAGGCAGCCAAAGGCCAGGCAGCCAAAGGCCAGGCAGCCAAAGGCCAGGCCAAAGGCCAGGCCAAAGGCCAGGCCAAAGGCCAGGCCAAAAGGCCAGGCCAAAGGCCAAGGCCAAAGGCCAAGGCCAGGCCAAAGGCCAGCCACAAGGCCAGCCCAAAAGGCCAAGGCCAGCCCA	140	CGGGUCCA G CCGGAGCC	569	GGCUCCGG GCCGAAAGGCGAGUCAAGGUCU UGGACCCG	1154
166 GGECCOGA G. COCCIGAGIO 572 CACUGOGIG GCCCANAGGICGAGUVANGGUCU UCCCGCCC 1157 166 GAGCCOGA G. UGAGCACC 573 GGUGUCIA GCCCANAGGICGAGUVANGGUCU UCCCGCCC 1158 170 COCAGUGIA G. CUUGUGGIC 575 GCCGANAGGICAGUCANGGUCU UCCAUGGU 1159 180 ACCAUGGIA G. CUUGUGGIC 575 GCCGCANAGGICAGUCANGGUCU UCCAUGGU 1160 184 UGGAGCU G. CUUGUGG 575 GCCGCCAG GCCCANAGGICAGUCANGGUCU UCCAUGGU 1161 187 AGCUGGGIG G. CUUGUGG 577 GCACAGGI GCCCANAGGICAGUCANGGUCU COCCAGCU 1162 249 CACCCOGGIG G. CUUCUCCC 578 GCACAGGI G. CCCAAAAGGIGGUCU COCCAGGU 1163 232 CCCCCGGIA G. CCCCCAGA 580 CUUGGGIG G. CCCCAGAGGUCUCANGGUCU UCCGGGIG C. 1163 1164 239 AGCCCCCAG 581 GGUGCAGA GCCGAAAGGIGAUCANGGUCU UCCGGGIG C. 1165 1165 247 GCACCAGA G. UCCCCAG 581 GGUGCAGA GCCGAAAGGIGAUCANGGUCU UCCGGGIG C. 1167 276 GACCAGAGA G. CCCCAGAGGIG GCCGAAAGGIGAGUCANGGGGGUCU UCCAGGUCU UCCAGGUCU UCCAGGUCU G. 168 186 CUUGGGGIG GCCGAAAGGIGAGUCANGGGGUCU UCCAGGUCU G. 168 276 <td< td=""><td></td><td></td><td></td><td></td><td>1155</td></td<>					1155
166 GAGCOGCA G UGAGCACC 573 GGUGULCA GCCDANAGGCGAGUCNAGGUCU UGCGGCUC 1158 170 COCANDAG A CACCANGG 574 CCAUGGGG GCCCANAGGCGAGUCNAGGUCU UCACHGGG 1159 180 ACCANDGA G CHUGCGGC 575 GCGCCANAGGCGAGUCNAGGCGUCU UCACHGGU 1160 184 UGGAGCUG G GGCCUUG 576 CAAGGCG GCCGANAGGCGAGUCNAGGUCU UCACCUCA 1161 187 AGCUGGG G CCUUGUGC 577 GCACANAG GCCGANAGGCGAGUCNAGGUCU CCCCAGCG 1162 240 GCCUCOGG G CCUUGUGC 578 AGGAGAGG GCCGANAGGCGAGUCNAGGUCU CCCCAGCG 1163 232 CCCCCGGA G CCCCCAGA 579 GCUCACAGG GCCGANAGGCGAGUCNAGGUCU UCCCGGGG 1163 233 AGCCCGAG G CACCCAGA 580 CUUGCGGG GCCGANAGGCGAGUCNAGGUCU UCCGGGGU 1165 247 GCACCCAA G UGUGCAG 581 GGUGCACA GCCGANAGGCGAGUCNAGGUCU UCCGGGCU 1166 257 GACLAGAA 580 CUUGCGGAAAGGCGAGUCNAGGUCU UCCGGGCU 1167 276 AAGCUGAA CUCCGGGC 582 WICHUGGGG GCCGANAGGCGAGUCNAGGUCU UCCAGGUCU 1167 276 AAGCUGAA CCCCCAGACA <td< td=""><td></td><td></td><td></td><td></td><td>1156</td></td<>					1156
170 CCCAGGAR & CACCANGE 574 CCAUGAIG GCCGAAAGGCGAGUCAAGGCCTU UCACTIGCS 1159					
180 ACCADIGGA G CUIGGCGGC 575 GCCGCCAG GCCCDAAGGCCAUGUCAAGGUCU UCCAUGGU 1160 184 UGGAGCUG G GGCCUUG F76 CAAGGCCG GCCGAAAGGCAGUCAAGGUCU CARCUCCA 1161 187 AGCUGGG G GCUUGUCC 576 CAACAGA GCCCAAAGGCGAGUCAAGGUCU CARCUCCA 1162 204 CGCUGGG G CUUCUCCU 579 AGCADAGA GCCAAAGGCGAGUCAAGGUCU CCCCAGC 1163 212 CCCCCGGA G CCGGGAAGG 579 GCUCCCGG GCCGAAAAGGCGAGUCAAGGUCU UCCCGGGC 1164 232 AGCCCCGAA G CACCCAAG 580 CUUGGGG GCCGAAAAGGCAAGUCAAGGUCU UCCGGGCU 1162 247 GCACCAAA G UGUGACC 581 GUUCUGUG GCCGAAAAGGCAAGUCAAGGUCU UUCGGGCU 1166 257 GGACAUGAA CUUCGGCG 581 GUUCUGUG GCCGAAAGGCAAGUCAAGGUCU UUCAGGUC 1167 276 GACAUGAA CUUCCGCG 583 AGCCCCCAA GCCGAAAGGCAAGUCAAGGUCU UUCAGGUC 1168 276 AAGCUGGG G CUCCCUGC 584 GCACGAAAGGCAAGUCAAGGUCU UUCAGGUC 1169 287 CUCCUGG G CUCCCUGC 584 GCACGAAAAGGCAAGGCAAGUCAAAGGCAAGUCAAGGUCU UUCAGGCU 1179 287 CUCCUGCAA <td>1</td> <td></td> <td></td> <td></td> <td></td>	1				
184 UGGAGCUG G CGCCUUG 576 CAAGGCCG GCCGAAAGGCGAGUCAAGGUCU CAGCUCCA 1161 187 AGCUGGC G CCUURGUG GT77 GCACAAGG GCCGAAAGGCGAGUCAAGGUCU CGCCAGCU 1162 1162 240 GGUGGGG G CUCUCCU 578 AGAGGAG GCCGAAAGGCGAGUCAAGGUCU CCCAGGG 1163 1162 232 CCCCCGGA G CGCCAAAGGCGAGUCAAGGCGAGUCAAGGUCU UCCGGGGG 1163 1164 233 AGCCCGAG G CACCAAAG 580 CUUCGGGG GCCGAAAGGCGAGUCAAGGUCU UCCGGGGGC 1165 247 GCACCCAA G UGUGCACC 581 GGUGCGAC GCCGAAAGGCGAGUCAAGGUCU UCCGGGGCC 1165 257 GACACAAA 582 UGUUCGGG GCCGAAAGGCGAGUCAAGGUCU UCCGGGCC 1166 276 GACACAAA 582 UGUUCGGG GCCGAAAGGCGAGUCAAGGUCU UCCGGGCC 1167 276 GACACAAA 582 UGUCGGAAAGGCGAGUCAAGGUCU UCCGGGCC 1167 276 AAGCUGCG G CUCCCUC 584 GCACCAAG GCCGAAAGGCAGUCAAGGUCU UCCAGGUU 1169 287 ACCUCCAG G UCCCUCA 586 GCACAGAAGGCGAGUCAAGGCGCUCAAGGCCU UCCAGGUU 1170 287 CUCCCCAGA 585 UCUCCGGA GCCCAAAGGCCGAGUCAAGGCCUCCAAGGUCU UCCAGCUU 1170 287 CUCCCCAGA 585 UCUCCGGA GCCCAAAGGCCGAGUCAAGGCCUCCAAGGUCU UCCAGCUU 1170					
187					
204 CGCU000GG G CUCCUCCU 578 AGGADGAG GCCOAAAGGCGAGUCAAGGUCU CCCCAGCG 1163 212 CCCCCGGA G CGCGAGAG 579 GCUCCCGG GCCGAAAGGCGAGUCAAGGUCU UCCGGGGU 1164 213 AGCCCGCA G CACCAAG 580 CUUUGGGU GCCGAAAGGCGAGUCAAGGUCU UCCGGGCU 1165 247 GCACCAA G UGUGCACC 581 GGUGCACA G CCCAAAAGGCAAGGCCU UUCAGGUCU 1166 257 GUGCACCG G CACAGACA 582 UGUUGUG GCCGAAAAGGCAGUCAAGGUCU UUCAGGUC 1167 276 AAGCUGCG G CUCCCUGC 584 GCACGGAG GCCGAAAAGGCAGUCAAGGUCU UUCAGGU 1169 276 AAGCUGCG G CUCCCUGC 584 GCACGGAG GCCGAAAGGCAGUCAAGGUCU GCAGCUU 1169 287 CCCUGCCAG G UCCCUGC 584 GCACGGAG GCCGAAAGGCAGUCAAGGUCU GCAGCUU 1170 287 CCCUGCAG G UCCCUGA 585 UCUCCGGA GCCGAAAGGCCAGUCAAGGUCU GCAGCUU 1170 329 CUACCAGG G CUCCAGAG 585 UCUCCGGA GCCGAAAGGCCAGUCAAGGUCU GCAGCUU 1170					
233 CCCCCORGA 6 CCCGCCAGA 579 GCUCCCAG CCCCCAGA 1164 239 ALCCCCCAA 6 580 CUIUGGGIG CCCCAAAGCCAGAGUCAAAGGCCAGUCUCAGGCCU 1165 247 GCCCCCAA 0 UGUCCACC 581 GGUGCACA GCCCGAAAGGCCAGUCAAGGCUU UGUGCUC 1167 257 GUGCACCG CACAGACA 582 UGUUCUGG COCCAAAAGGCCAGUCAAAGGCCAGUCCAAAGGCCAGUCCAAAGGCCAGUCCAAAGGCCAGUCCAAAGGCCAGUCCAAAGGCCAGUCCAAAGGCCAGUCCACAAGGCCAGUCCAAAAGGCCAGUCCAAAAGCCAGCC					
239 AGCCCCGA G CACCCAAG 580 CUUUGGUG GCCGAAAGGGGAUCAAGGUCU UCGCGGCU 1165 247 GCACCCAA G UGUUGACC 581 GGUGCACA GCCGAAAGGGCAGUCAAGGUCU UUGGGUGC 1166 257 GUGCACCG GACAGAACA 582 USUUGUG GCCGAAAGGGCAGUCAAGGUCU UGGGAC 1167 270 GACAUGAA G CUGCGGCU 583 AGCCGCAG GCCGAAAGGGGAGUCAAGGUCU UUCAUGUC 1168 276 AAGCUGCG G CUCCCUGC 584 GCAGGAAAGGGCGAGUCAAGGUCU GCCAGCUU 1169 287 CCCUGGCA G UCCCCAGAA 585 USUCCGGAAAGGGCAAGGGCAGUCAAGGGUCU GCCAGGGGC 1170 329 CULACCAGG G CUGCCAGG 886 CCUGGCAG GCCGAAAGGGGAGUCAAGGUCU GCCCGGGC 1171					
247 GCACCONA G UGUGCACC 581 GGUGCACA GCCGAAAGGCGAGUCAAGGUCU UUU00GUGC 1166 257 GUGCACCG G CACAGACA 582 UGUCUGUG GCCGAAAGGCGAGUCAAGGUCU UCCGGGCCAC 1167 276 GACAGAAA GUCGCGGC 583 AGCCCCAG GCCGAAAGGCGAGUCAAGGUCU UCCAGGUC 1169 276 AAGCUGCG G CUCCCUGC 584 GCAGGAGG GCCGAAAGGCGAGUCAAGGUCU GCCAGCUU 1159 287 CCCUGCCA G UCCCGAGA 585 UCUCGGGA GCCGAAAGGCGAGUCAAGGUCU GCGAGCUU 1170 329 CULCCAGG G CTGCCAGG 586 CCTGGCAG GCCGAAAGGCCAAUCCAAGGUCU GCGAGCUU 1170					
257 GUGCACCG G CACAGACA 582 UGUCUGUG GCCGAAAGGCGAGUCAAGGUCU CGGUGCAC 1167 270 GACAUGAA G CUGCGGCU 583 AGCCGCAG GCCGAAAGGCGAGUCAAGGUCU UUCAUGUC 1168 276 AAGCUGCG G CUCCCUGC 584 GCAGGAG GCCGAAAGGCGAGUCAAGGUCU UUCAUGUC 1169 287 CCCTIGCCA G UCCCGAGA 585 UCTUGGGA GCCGAAAGGCGAGUCAAGGUCU UGCAGGG 1170 329 CUACCAGG G CUGCCAGG 586 CCTUGGCAG GCCGAAAGGCGAGUCAAGGUCU CCUGGUAG 1171					
270 GACAUGAA G CUGCGGCU 583 AGCCGCAG GCCGAAAGGCGAGUCAAGGUCU UUCAUGUC 1168 276 AAGCUGCG G CUCCCUGC 584 GCAGAGAG GCCGAAAGGGCGAGUCAAGGUCU GCCAGCUU 1169 287 CCCUGGCA G UCCCAGAG 585 UCUCGGCA GCCAAAAGGGCGAGUCU GCCAGGUCU GCCAGGGC 1170 329 CUACCAGG G CUGCCAGG 586 CCUGGCAG GCCGAAAGGCGAGUCAAGGUCU GCCGGCG 1171					
276 AAGCUSCO G CUCCCUSC 584 GCAGGAG G CCDAAAGGCGAGUCAAGGUC CCCAGUU 1169 287 CCCUGCCA G UCCCGAGA 585 UCUCCGGA GCCGAAAGGCAGUCAAGGUCAGGUC CCCGAGAGUCAAGGUC CCCGAGAGUCAGGUC CCCGGAGGUCAGGUC					
287 CCCUGCCA G UCCCGAGA 585 UCUCCOGA GCCGAAAGGCGAGUCAAGGUCU UGGCAGGG 1170 329 CUACCAGG G CUGCCAGG 586 CCUGGCAG GCCGAAAGGCGAGUCAAGGUCU CCUGGUAG 1171					
329 CUACCAGG G CUGCCAGG 586 CCUGGCAG GCCGAAAGGCGAGUCAAGGUCU CCUGGUAG 1171					
337 GCUGCCAG G UGGUGCAG 587 CUGCACCA GCCGAAAGGCGAGUCAAGGUCU CUGGCAGC 1172					
	337	GCUGCCAG G UGGUGCAG	587	CUGCACCA GCCGAAAGGCGAGUCAAGGUCU CUGGCAGC	1172

Table 59

340				
383	GCCAGGUG G UGCAGGGA	588	UCCCUGCA GCCGAAAGGCGAGUCAAGGUCU CACCUGGC	1173
	CAAUGCCA G CCUGUCCU	589	AGGACAGG GCCGAAAGGCGAGUCAAGGUCU UGGCAUUG	1174
412	UCCAGGAG G UGCAGGGC	590	GCCCUGCA GCCGAAAGGCGAGUCAAGGUCU CUCCUGGA	1175
419	GGUGCAGG G CUACGUGC	591	GCACGUAG GCCGAAAGGCGAGUCAAGGUCU CCUGCACC	1176
424	AGGGCUAC G UGCUCAUC	592	GAUGAGCA GCCGAAAGGCGAGUCAAGGUCU GUAGCCCU	1177
445	ACAACCAA G UGAGGCAG	593	CUGCCUCA GCCGAAAGGCGAGUCAAGGUCU UUGGUUGU	1178
450	CAAGUGAG G CAGGUCCC	594	GGGACCUG GCCGAAAGGCGAGUCAAGGUCU CUCACUUG	1179
454	UGAGGCAG G UCCCACUG	595	CAGUGGGA GCCGAAAGGCGAGUCAAGGUCU CUGCCUCA	1180
468	CUGCAGAG G CUGCGGAU	596	AUCCGCAG GCCGAAAGGCGAGUCAAGGUCU CUCUGCAG	1181
485	UGUGCGAG G CACCCAGC	597	GCUGGGUG GCCGAAAGGCGAGUCAAGGUCU CUCGCACA	1182
492	GGCACCCA G CUCUUUGA	598	UCAAAGAG GCCGAAAGGCGAGUCAAGGUCU UGGGUGCC	1183
517	AUGCCCUG G CCGUGCUA	599	UAGCACGG GCCGAAAGGCGAGUCAAGGUCU CAGGGCAU	1184
520	CCCUGGCC G UGCUAGAC	600	GUCUAGCA GCCGAAAGGCGAGUCAAGGUCU GGCCAGGG	1185
568	UCACAGGG G CCUCCCCA	601	UGGGGAGG GCCGAAAGGCGAGUCAAGGUCU CCCUGUGA	1186
581	CCCAGGAG G CCUGCGGG	602	CCCGCAGG GCCGAAAGGCGAGUCAAGGUCU CUCCUGGG	1187
591	CUGCGGGA G CUGCAGCU	603	AGCUGCAG GCCGAAAGGCGAGUCAAGGUCU UCCCGCAG	1188
597	GAGCUGCA G CUUCGAAG	604	CUUCGAAG GCCGAAAGGCGAGUCAAGGUCU UGCAGCUC	1189
605	GCUUCGAA G CCUCACAG	605	CUGUGAGG GCCGAAAGGCGAGUCAAGGUCU UUCGAAGC	1190
631	AAGGAGGG G UCUUGAUC	606	GAUCAAGA GCCGAAAGGCGAGUCAAGGUCU CCCUCCUU	1191
642	UUGAUCCA G CGGAACCC	607	GGGUUCCG GCCGAAAGGCGAGUCAAGGUCU UGGAUCAA	1192
654	AACCCCCA G CUCUGCUA	608	UAGCAGAG GCCGAAAGGCGAGUCAAGGUCU UGGGGGUU	1193
708	AACAACCA G CUGGCUCU	609	AGAGCCAG GCCGAAAGGCGAGUCAAGGUCU UGGUUGUU	1194
712	ACCAGCUG G CUCUCACA	610	UGUGAGAG GCCGAAAGGCGAGUCAAGGUCU CAGCUGGU	1195
745	GCUCUCGG G CCUGCCAC	611	GUGGCAGG GCCGAAAGGCGAGUCAAGGUCU CCGAGAGC	1196
776	GUGUAAGG G CUCCCGCU	612	AGCGGGAG GCCGAAAGGCGAGUCAAGGUCU CCUUACAC	1197
797	GGGAGAGA G UUCUGAGG	613	CCUCAGAA GCCGAAAGGCGAGUCAAGGUCU UCUCUCCC	1198
815	UUGUCAGA G CCUGACGC	514	GCGUCAGG GCCGAAAGGCGAGUCAAGGUCU UCUGACAA	1199
839	CUGUGCCG G UGGCUGUG	615	CACAGCCA GCCGAAAGGCGAGUCAAGGUCU CGGCACAG	1200
842	UGCCGGUG G CUGUGCCC	616	GGGCACAG GCCGAAAGGCGAGUCAAGGUCU CACCGGCA	1201
861	UGCAAGGG G CCACUGCC	617	GGCAGUGG GCCGAAAGGCGAGUCAAGGUCU CCCUUGCA	1202
888	UGCCAUGA G CAGUGUGC	618	GCACACUG GCCGAAAGGCGAGUCAAGGUCU UCAUGGCA	1203
891	CAUGAGCA G UGUGCUGC	619	GCAGCACA GCCGAAAGGCGAGUCAAGGUCU UGCUCAUG	1204
902	UGCUGCCG G CUGCACGG	620	CCGUGCAG GCCGAAAGGCGAGUCAACGUCU CGGCAGCA	1205
911	CUGCACGG G CCCCAAGC	621	GCUUGGGG GCCGAAAGGCGAGUCAAGGUCU CCGUGCAG	1206
918	GGCCCCAA G CACUCUGA	622	UCAGAGUG GCCGAAAGGCGAGUCAAGGUCU UUGGGGCC	1207
934	ACUGCCUG G CCUGCCUC	623	GAGGCAGG GCCGAAAGGCGAGUCAAGGUCU CAGGCAGU	1208
956	CAACCACA G UGGCAUCU	624	AGAUGCCA GCCGAAAGGCGAGUCAAGGUCU UGUGGUUG	1209
959	CCACAGUG G CAUCUGUG	625	CACAGAUG GCCGAAAGGCGAGUCAAGGUCU CACUGUGG	1210
969	AUCUGUGA G CUGCACUG	626	CAGUGCAG GCCGAAAGGCGAGUCAAGGUCU UCACAGAU	1211
982	ACUGCCCA G CCCUGGUC	627	GACCAGGG GCCGAAAGGCGAGUCAAGGUCU UGGGCAGU	1212
	CAGCCCUG G UCACCUAC	628	GUAGGUGA GCCGAAAGGCGAGUCAAGGUCU CAGGGCUG	1213
988	ACAGACAC G UUUGAGUC	629	GACUCAAA GCCGAAAGGCGAGUCAAGGUCU GUGUCUGU	1214
988 1008	ACAGACAC G GOOGAGOC			
	ACGUUUGA G UCCAUGCC	630	GGCAUGGA GCCGAAAGGCGAGUCAAGGUCU UCAAACGU	1215
1008		630 631	GGCAUGGA GCCGAAAGGCGAGUCAAGGUCU UCAAACGU UAUACCGG GCCGAAAGGCGAGUCAAGGUCU CCUCGGGA	1215 1216
1008	ACGUUUGA G UCCAUGCC			
1008 1014 1034	ACGUUUGA G UCCAUGCC UCCCGAGG G CCGGUAUA	631	UAUACCGG GCCGANAGGCGAGUCAAGGUCU CCUCGGGA	1216

Table 59

			Table 33	
1096	CUACGGAC G UGGGAUCC	635	GGAUCCCA GCCGAAAGGCGAGUCAAGGUCU GUCCGUAG	1220
1114	GCACCCUC G UCUGCCCC	636	GGGGCAGA GCCGAAAGGCGAGUCAAGGUCU GAGGGUGC	1221
1138	ACCAAGAG G UGACAGCA	637	UGCUGUCA GCCGAAAGGCGAGUCAAGGUCU CUCUUGGU	1222
1144	AGGUGACA G CAGAGGAU	638	AUCCUCUG GCCGAAAGGCGAGUCAAGGUCU UGUCACCU	1223
1161	GGAACACA G CGGUGUGA	639	UCACACCG GCCGAAAGGCGAGUCAAGGUCU UGUGUUCC	1224
1164	ACACAGCG G UGUGAGAA	640	UUCUCACA GCCGAAAGGCGAGUCAAGGUCU CGCUGUGU	1225
1173	UGUGAGAA G UGCAGCAA	641	UUGCUGCA GCCGAAAGGCGAGUCAAGGUCU UUCUCACA	1226
1178	GAAGUGCA G CAAGCCCU	642	AGGGCUUG GCCGAAAGGCGAGUCAAGGUCU UGCACUUC	1227
1182	UGCAGCAA G CCCUGUGC	643	GCACAGGG GCCGAAAGGCGAGUCAAGGUCU UUGCUGCA	1228
1195	GUGCCCGA G UGUGCUAU	644	AUAGCACA GCCGAAAGGCGAGUCAAGGUCU UCGGGCAC	1229
1205	GUGCUAUG G UCUGGGCA	645	UGCCCAGA GCCGAAAGGCGAGUCAAGGUCU CAUAGCAC	1230
1211	UGGUCUGG G CAUGGAGC	646	GCUCCAUG GCCGAAAGGCGAGUCAAGGUCU CCAGACCA	1231
1218	GGCAUGGA G CACUUGCG	647	CGCAAGUG GCCGAAAGGCGAGUCAAGGUCU UCCAUGCC	1232
1231	UGCGAGAG G UGAGGGCA	648	UGCCCUCA GCCGAAAGGCGAGUCAAGGUCU CUCUCGCA	1233
1237	AGGUGAGG G CAGUUACC	649	GGUAACUG GCCGAAAGGCGAGUCAAGGUCU CCUCACCU	1234
1240	UGAGGGCA G UUACCAGU	650	ACUGGUAA GCCGAAAGGCGAGUCAAGGUCU UGCCCUCA	1235
1247	AGUUACCA G UGCCAAUA	651	UAUUGGCA GCCGAAAGGCGAGUCAAGGUCU UGGUAACU	1236
1263	AUCCAGGA G UUUGCUGG	652	CCAGCAAA GCCGAAAGGCGAGUCAAGGUCU UCCUGGAU	1237
1271	GUUUGCUG G CUGCAAGA	653	UCUUGCAG GCCGAAAGGCGAGUCAAGGUCU CAGCAAAC	1238
1292	CUUUGGGA G CCUGGCAU	654	AUGCCAGG GCCGAAAGGCGAGUCAAGGUCU UCCCAAAG	1239
1297	GGAGCCUG G CAUUUCUG	655	CAGAAAUG GCCGAAAGGCGAGUCAAGGUCU CAGGCUCC	1240
1313	GCCGGAGA G CUUUGAUG	656	CAUCAAAG GCCGAAAGGCGAGUCAAGGUCU UCUCCGGC	1241
1330	GGGACCCA G CCUCCAAC	657	GUUGGAGG GCCGAAAGGCGAGUCAAGGUCU UGGGUCCC	1242
1353	CCGCUCCA G CCAGAGCA	658	UGCUCUGG GCCGAAAGGCGAGUCAAGGUCU UGGAGCGG	1243
1359	CAGCCAGA G CAGCUCCA	659	UGGAGCUG GCCGAAAGGCGAGUCAAGGUCU UCUGGCUG	1244
1362	CCAGAGCA G CUCCAAGU	660	ACUUGGAG GCCGAAAGGCGAGUCAAGGUCU UGCUCUGG	1245
1369	AGCUCCAA G UGUUUGAG	661	CUCAAACA GCCGAAAGGCGAGUCAAGGUCU UUGGAGCU	1246
1397	GAUCACAG G UUACCUAU	662	AUAGGUAA GCCGAAAGGCGAGUCAAGGUCU CUGUGAUC	1247
1414	ACAUCUCA G CAUGGCCG	663	CGGCCAUG GCCGAAAGGCGAGUCAAGGUCU UGAGAUGU	1248
1419	UCAGCAUG G CCGGACAG	664	CUGUCCGG GCCGAAAGGCGAGUCAAGGUCU CAUGCUGA	1249
1427	GCCGGACA G CCUGCCUG	665	CAGGCAGG GCCGAAAGGCGAGUCAAGGUCU UGUCCGGC	1250
1442	UGACCUCA G CGUCUUCC	666	GGAAGACG GCCGAAAGGCGAGUCAAGGUCU UGAGGUCA	1251
1444	ACCUCAGC G UCUUCCAG	667	CUGGAAGA GCCGAAAGGCGAGUCAAGGUCU GCUGAGGU	1252
1462	ACCUGCAA G UAAUCCGG	668	CCGGAUUA GCCGAAAGGCGAGUCAAGGUCU UUGCAGGU	1253
1490	GCACAAUG G CGCCUACU	669	AGUAGGCG GCCGAAAGGCGAGUCAAGGUCU CAUUGUGC	1254
1515	CUGCAAGG G CUGGGCAU	670	AUGCCCAG GCCGAAAGGCGAGUCAAGGUCU CCUUGCAG	1255
1520	AGGGCUGG G CAUCAGCU	671	AGCUGAUG GCCGAAAGGCGAGUCAAGGUCU CCAGCCCU	1256
1526	GGGCAUCA G CUGGCUGG	672	CCAGCCAG GCCGAAAGGCGAGUCAAGGUCU UGAUGCCC	1257
1530	AUCAGCUG G CUGGGGCU	673	AGCCCCAG GCCGAAAGGCGAGUCAAGGUCU CAGCUGAU	1258
1536	UGGCUGGG G CUGCGCUC	674	GAGCGCAG GCCGAAAGGCGAGUCAAGGUCU CCCAGCCA	1259
1559	GGAACUGG G CAGUGGAC	675	GUCCACUG GCCGAAAGGCGAGUCAAGGUCU CCAGUUCC	1260
1562	ACUGGGCA G UGGACUGG	676	CCAGUCCA GCCGAAAGGCGAGUCAAGGUCU UGCCCAGU	1261
1570	GUGGACUG G CCCUCAUC	677	GAUGAGGG GCCGAAAGGCGAGUCAAGGUCU CAGUCCAC	1262
1603	UCUGCUUC G UGCACACG	678	CGUGUGCA GCCGAAAGGCGAGUCAAGGUCU GAAGCAGA	1263
1612	UGCACACG G UGCCCUGG	679	CCAGGGCA GCCGAAAGGCGAGUCAAGGUCU CGUGUGCA	1264
1626	UGGGACCA G CUCUUUCG	680	CGAAAGAG GCCGAAAGGCGAGUCAAGGUCU UGGUCCCA	1265
1648	CGCACCAA G CUCUGCUC	681	GAGCAGAG GCCGAAAGGCGAGUCAAGGUCU UUGGUGCG	1266

Table 59

1671	GCCAACCG G CCAGAGGA	682	UCCUCUGG GCCGAAAGGCGAGUCAAGGUCU CGGUUGGC 1267
1683	GAGGACGA G UGUGUGGG	683	CCCACACA GCCGAAAGGCGAGUCAAGGUCU UCGUCCUC 1268
1691	GUGUGUGG G CGAGGGCC	684	GGCCCUCG GCCGAAAGGCGAGUCAAGGUCU CCACACAC 1269
1697	GGGCGAGG G CCUGGCCU	685	AGGCCAGG GCCGAAAGGCGAGUCAAGGUCU CCUCGCCC 1270
1702	AGGGCCUG G CCUGCCAC	686	GUGGCAGG GCCGAAAGGCGAGUCAAGGUCU CAGGCCCU 1271
1713	UGCCACCA G CUGUGCGC	687	GCGCACAG GCCGAAAGGCGAGUCAAGGUCU UGGUGGCA 1272
1728	GCCCGAGG G CACUGCUG	688	CAGCAGUG GCCGAAAGGCGAGUCAAGGUCU CCUCGGGC 1273
1739	CUGCUGGG G UCCAGGGC	689	GCCCUGGA GCCGAAAGGCGAGUCAAGGUCU CCCAGCAG 1274
1746	GGUCCAGG G CCCACCCA	690	UGGGUGGG GCCGAAAGGCGAGUCAAGGUCU CCUGGACC 1275
1755	CCCACCCA G UGUGUCAA	691	UUGACACA GCCGAAAGGCGAGUCAAGGUCU UGGGUGGG 1276
1769	CAACUGCA G CCAGUUCC	692	GGAACUGG GCCGAAAGGCGAGUCAAGGUCU UGCAGUUG 1277
1773	UGCAGCCA G UUCCUUCG	693	CGAAGGAA GCCGAAAGGCGAGUCAAGGUCU UGGCUGCA 1278
1784	CCUUCGGG G CCAGGAGU	694	ACUCCUGG GCCGAAAGGCGAGUCAAGGUCU CCCGAAGG 1279
1791	GGCCAGGA G UGCGUGGA	695	UCCACGCA GCCGAAAGGCGAGUCAAGGUCU UCCUGGCC 1280
1795	AGGAGUGC G UGGAGGAA	696	UUCCUCCA GCCGAAAGGCGAGUCAAGGUCU GCACUCCU 1281
1810	AAUGCCGA G UACUGCAG	697	CUGCAGUA GCCGAAAGGCGAGUCAAGGUCU UCGGCAUU 1282
1821	CUGCAGGG G CUCCCCAG	698	CUGGGGAG GCCGAAAGGCGAGUCAAGGUCU CCCUGCAG 1283
1833	CCCAGGGA G UAUGUGAA	699	UUCACAUA GCCGAAAGGCGAGUCAAGGUCU UCCCUGGG 1284
1848	AAUGCCAG G CACUGUUU	700	AAACAGUG GCCGAAAGGCGAGUCAAGGUCU CUGGCAUU 1285
1860	UGUUUGCC G UGCCACCC	701	GGGUGGCA GCCGAAAGGCGAGUCAAGGUCU GGCAAACA 1286
1872	CACCCUGA G UGUCAGCC	702	GGCUGACA GCCGAAAGGCGAGUCAAGGUCU UCAGGGUG 1287
1878	GAGUGUCA G CCCCAGAA	703	UUCUGGGG GCCGAAAGGCGAGUCAAGGUCU UGACACUC 1288
1889	CCAGAAUG G CUCAGUGA	704	UCACUGAG GCCGAAAGGCGAGUCAAGGUCU CAUUCUGG 1289
1894	AUGGCUCA G UGACCUGU	705	ACAGGUCA GCCGAAAGGCGAGUCAAGGUCU UGAGCCAU 1290
1915	GACCGGAG G CUGACCAG	706	CUGGUCAG GCCGAAAGGCGAGUCAAGGUCU CUCCGGUC 1291
1923	GCUGACCA G UGUGUGGC	707	GCCACACA GCCGAAAGGCGAGUCAAGGUCU UGGUCAGC 1292
1930	AGUGUGUG G CCUGUGCC	708	GGCACAGG GCCGAAAGGCGAGUCAAGGUCU CACACACU 1293
1963	CCUUCUGC G UGGCCCGC	709	GCGGGCCA GCCGAAAGGCGAGUCAAGGUCU GCAGAAGG 1294
1966	nonecene e cocecnec	710	GCAGCGGG GCCGAAAGGCGAGUCAAGGUCU CACGCAGA 1295
1979	CUGCCCCA G CGGUGUGA	711	UCACACCG GCCGAAAGGCGAGUCAAGGUCU UGGGGCAG 1296
1982	CCCCAGCG G UGUGAAAC	712	GUUUCACA GCCGAAAGGCGAGUCAAGGUCU CGCUGGGG 1297
2019	AUCUGGAA G UUUCCAGA	713	UCUGGAAA GCCGAAAGGCGAGUCAAGGUCU UUCCAGAU 1298
2036	UGAGGAGG G CGCAUGCC	714	GGCAUGCG GCCGAAAGGCGAGUCAAGGUCU CCUCCUCA 1299
2046	GCAUGCCA G CCUUGCCC	715	GGGCAAGG GCCGAAAGGCGAGUCAAGGUCU UGGCAUGC 1300
2096	UGACAAGG G CUGCCCCG	716	CGGGGCAG GCCGAAAGGCGAGUCAAGGUCU CCUUGUCA 1301
2109	CCCGCCGA G CAGAGAGC	717	GCUCUCUG GCCGAAAGGCGAGUCAAGGUCU UCGGCGGG 1302
2116	AGCAGAGA G CCAGCCCU	718	AGGGCUGG GCCGAAAGGCGAGUCAAGGUCU UCUCUGCU 1303
2120	GAGAGCCA G CCCUCUGA	719	UCAGAGGG GCCGAAAGGCGAGUCAAGGUCU UGGCUCUC 1304
2130	CCUCUGAC G UCCAUCAU	720	AUGAUGGA GCCGAAAGGCGAGUCAAGGUCU GUCAGAGG 1305
2146	UCUCUGCG G UGGUUGGC	721	GCCAACCA GCCGAAAGGCGAGUCAAGGUCU CGCAGAGA 1306
2149	CUGCGGUG G UUGGCAUU	722	AAUGCCAA GCCGAAAGGCGAGUCAAGGUCU CACCGCAG 1307 GCAGAAUG GCCGAAAGGCGAGUCAAGGUCU CAACCACC 1308
2153	GGUGGUUG G CAUUCUGC	723	
2164	UUCUGCUG G UCGUGGUC	724	GACCACGA GCCGAAAGGCGAGUCAAGGUCU CAGCAGAA 1309 CAAGACCA GCCGAAAGGCGAGUCAAGGUCU GACCAGCA 1310
2167	UGCUGGUC G UGGUCUUG	_	
2170	UGGUCGUG G UCUUGGGG	726	CCCCAAGA GCCGAAAGGCGAGUCAAGGUCU CACGACCA 1311 AAAGACCA GCCGAAAGGCGAGUCAAGGUCU CCCCAAGA 1312
2179	UCUUGGGG G UGGUCUUU	727	
2182	NGGGGGRG G NGNARGG	728	CCCAAAGA GCCGAAAGGCGAGUCAAGGUCU CACCCCCA 1313

Table 59

2202	CUCAUCAA G CGACGGCA	729	UGCCGUCG GCCGAAAGGCGAGUCAAGGUCU UUGAUGAG	1314
2208	AAGCGACG G CAGCAGAA	730	UUCUGCUG GCCGAAAGGCGAGUCAAGGUCU CGUCGCUU	1315
2211	CGACGGCA G CAGAAGAU	731	AUCUUCUG GCCGAAAGGCGAGUCAAGGUCU UGCCGUCG	1316
2226	AUCCGGAA G UACACGAU	732	AUCGUGUA GCCGAAAGGCGAGUCAAGGUCU UUCCGGAU	1317
2259	GAAACGGA G CUGGUGGA	733	UCCACCAG GCCGAAAGGCGAGUCAAGGUCU UCCGUUUC	1318
2263	CGGAGCUG G UGGAGCCG	734	OGGCUCCA GCCGAAAGGCGAGUCAAGGUCU CAGCUCCG	1319
2268	CUGGUGGA G CCGCUGAC	735	GUCAGCGG GCCGAAAGGCGAGUCAAGGUCU UCCACCAG	1320
2282	GACACCUA G CGGAGCGA	736	UCGCUCCG GCCGAAAGGCGAGUCAAGGUCU UAGGUGUC	1321
2287	CUAGCGGA G CGAUGCCC	737	GGGCAUCG GCCGAAAGGCGAGUCAAGGUCU UCCGCUAG	1322
2302	CCAACCAG G CGCAGAUG	738	CAUCUGCG GCCGAAAGGCGAGUCAAGGUCU CUGGUUGG	1323
2331	GAGACGGA G CUGAGGAA	739	UUCCUCAG GCCGAAAGGCGAGUCAAGGUCU UCCGUCUC	1324
2341	UGAGGAAG G UGAAGGUG	740	CACCUUCA GCCGAAAGGCGAGUCAAGGUCU CUUCCUCA	1325
2347	AGGUGAAG G UGCUUGGA	741	UCCAAGCA GCCGAAAGGCGAGUCAAGGUCU CUUCACCU	1326
2360	UGGAUCUG G CGCUUUUG	742	CAAAAGCG GCCGAAAGGCGAGUCAAGGUCU CAGAUCCA	1327
2369	CGCUUUUG G CACAGUCU	743	AGACUGUG GCCGAAAGGCGAGUCAAGGUCU CAAAAGCG	1328
2374	UUGGCACA G UCUACAAG	744	CUUGUAGA GCCGAAAGGCGAGUCAAGGUCU UGUGCCAA	1329
2384	CUACAAGG G CAUCUGGA	745	UCCAGAUG GCCGAAAGGCGAGUCAAGGUCU CCUUGUAG	1330
2422	AAAUUCCA G UGGCCAUC	746	GAUGGCCA GCCGAAAGGCGAGUCAAGGUCU UGGAAUUU	1331
2425	UUCCAGUG G CCAUCAAA	747	UUUGAUGG GCCGAAAGGCGAGUCAAGGUCU CACUGGAA	1332
2434	CCAUCAAA G UGUUGAGG	748	CCUCAACA GCCGAAAGGCGAGUCAAGGUCU UUUGAUGG	1333
2461	CCCCCAAA G CCAACAAA	749	UUUGUUGG GCCGAAAGGCGAGUCAAGGUCU UUUGGGGG	1334
2485	UAGACGAA G CAUACGUG	750	CACGUAUG GCCGAAAGGCGAGUCAAGGUCU UUCGUCUA	1335
2491	AAGCAUAC G UGAUGGCU	751	AGCCAUCA GCCGAAAGGCGAGUCAAGGUCU GUAUGCUU	1336
2497	ACGUGAUG G CUGGUGUG	752	CACACCAG GCCGAAAGGCGAGUCAAGGUCU CAUCACGU	1337
2501	GAUGGCUG G UGUGGGCU	753	AGCCCACA GCCGAAAGGCGAGUCAAGGUCU CAGCCAUC	1338
2507	UGGUGUGG G CUCCCCAU	754	AUGGGGAG GCCGAAAGGCGAGUCAAGGUCU CCACACCA	1339
2534	CCUUCUGG G CAUCUGCC	755	GGCAGAUG GCCGAAAGGCGAGUCAAGGUCU CCAGAAGG	1340
2554	CAUCCACG G UGCAGCUG	756	CAGCUGCA GCCGAAAGGCGAGUCAAGGUCU CGUGGAUG	1341
2559	ACGGUGCA G CUGGUGAC	757	GUCACCAG GCCGAAAGGCGAGUCAAGGUCU UGCACCGU	1342
2563	UGCAGCUG G UGACACAG	758	CUGUGUCA GCCGAAAGGCGAGUCAAGGUCU CAGCUGCA	1343
2571	GUGACACA G CUIJAUGCC	759	GGCAUAAG GCCGAAAGGCGAGUCAAGGUCU UGUGUCAC	1344
2585	GCCCUAUG G CUGCCUCU	760	AGAGGCAG GCCGAAAGGCGAGUCAAGGUCU CAUAGGGC	1345
2627	ACGCCUGG G CUCCCAGG	761	CCUGGGAG GCCGAAAGGCGAGUCAAGGUCU CCAGGCGU	1346
2649	CUGAACUG G UGUAUGCA	762	UGCAUACA GCCGAAAGGCGAGUCAAGGUCU CAGUUCAG	1347
2675	GGGGAUGA G CUACCUGG	763	CCAGGUAG GCCGAAAGGCGAGUCAAGGUCU UCAUCCCC	1348
2694	GAUGUGCG G CUCGUACA	764	UGUACGAG GCCGAAAGGCGAGUCAAGGUCU CGCACAUC	1349
2698	UGCGGCUC G UACACAGG	765	CCUGUGUA GCCGAAAGGCGAGUCAAGGUCU GAGCCGCA	1350
2713	GGGACUUG G CCGCUCGG	766	CCGAGCGG GCCGAAAGGCGAGUCAAGGUCU CAAGUCCC	1351
2725	CUCGGAAC G UGCUGGUC	767	GACCAGCA GCCGAAAGGCGAGUCAAGGUCU GUUCCGAG	1352
2731	ACGUGCUG G UCAAGAGU	768	ACUCUUGA GCCGAAAGGCGAGUCAAGGUCU CAGCACGU	1353
2738	GGUCAAGA G UCCCAACC	769	GGUUGGGA GCCGAAAGGCGAGUCAAGGUCU UCUUGACC	1354
2769	GACUTUCGG G CUGGCUCG	770	CGAGCCAG GCCGAAAGGCGAGUCAAGGUCU CCGAAGUC	1355
2773	UCGGGCUG G CUCGGCUG	771	CAGCCGAG GCCGAAAGGCGAGUCAAGGUCU CAGCCCGA	1356
2778	CUGGCUCG G CUGCUGGA	772	UCCAGCAG GCCGAAAGGCGAGUCAAGGUCU CGAGCCAG	1357
2802	GAGACAGA G UACCAUGC	773	GCAUGGUA GCCGAAAGGCGAGUCAAGGUCU UCUGUCUC	1358
2819	AGAUGGGG G CAAGGUGC	774	GCACCUUG GCCGAAAGGCGAGUCAAGGUCU CCCCAUCU	1359
2824	GGGGCAAG G UGCCCAUC	775	GAUGGGCA GCCGAAAGGCGAGUCAAGGUCU CUUGCCCC	1360

Table 59

2835	CCCAUCAA G UGGAUGGC	776	GCCAUCCA GCCGAAAGGCGAGUCAAGGUCU UUGAUGGG 1361
2842	AGUGGAUG G CGCUGGAG	777	CUCCAGCG GCCGAAAGGCGAGUCAAGGUCU CAUCCACU 1362
2850	GCGCUGGA G UCCAUUCU	778	AGAAUGGA GCCGAAAGGCGAGUCAAGGUCU UCCAGCGC 1363
2865	CUCCGCCG G OGGUUCAC	779	GUGAACCG GCCGAAAGGCGAGUCAAGGUCU CGGCGGAG 1364
2868	CGCCGGCG G UUCACCCA	780	UGGGUGAA GCCGAAAGGCGAGUCAAGGUCU CGCCGGCG 1365
2882	CCACCAGA G UGAUGUGU	781	ACACAUCA GCCGAAAGGCGAGUCAAGGUCU UCUGGUGG 1366
2894	UGUGUGGA G UUAUGGUG	782	CACCAUAA GCCGAAAGGCGAGUCAAGGUCU UCCACACA 1367
2900	GAGUUAUG G UGUGACUG	783	CAGUCACA GCCGAAAGGCGAGUCAAGGUCU CAUAACUC 1368
2916	GUGUGGGA G CUGAUGAC	784	GUCAUCAG GCCGAAAGGCGAGUCAAGGUCU UCCCACAC 1369
2932	CUUUUGGG G CCAAACCU	785	AGGUUUGG GCCGAAAGGCGAGUCAAGGUCU CCCAAAAG 1370
2956	GGAUCCCA G CCCGGGAG	786	CUCCCGGG GCCGAAAGGCGAGUCAAGGUCU UGGGAUCC 1371
2991	AAGGGGGA G CGGCUGCC	787	GGCAGCCG GCCGAAAGGCGAGUCAAGGUCU UCCCCCUU 1372
2994	GGGGAGCG G CUGCCCCA	788	UGGGGCAG GCCGAAAGGCGAGUCAAGGUCU CGCUCCCC 1373
3003	CUGCCCCA G CCCCCCAU	789	AUGGGGG GCCGAAAGGCGAGUCAAGGUCU UGGGGCAG 1374
3040	UGAUCAUG G UCAAAUGU	790	ACAUUUGA GCCGAAAGGCGAGUCAAGGUCU CAUGAUCA 1375
3072	GAAUGUCG G CCAAGAUU	791	AAUCUUGG GCCGAAAGGCGAGUCAAGGUCU CGACAUUC 1376
3087	UUCCGGGA G UUGGUGUC	792	GACACCAA GCCGAAAGGCGAGUCAAGGUCU UCCCGGAA 1377
3091	GGGAGUUG G UGUCUGAA	793	UUCAGACA GCCGAAAGGCGAGUCAAGGUCU CAACUCCC 1378
3112	CCCGCAUG G CCAGGGAC	794	GUCCCUGG GCCGAAAGGCGAGUCAAGGUCU CAUGCGGG 1379
3126	GACCCCCA G CGCUUUGU	795	ACAAAGCG GCCGAAAGGCGAGUCAAGGUCU UGGGGGUC 1380
3136	GCUUUGUG G UCAUCCAG	796	CUGGAUGA GCCGAAAGGCGAGUCAAGGUCU CACAAAGC 1381
3158	GGACUUGG G CCCAGCCA	797	UGGCUGGG GCCGAAAGGCGAGUCAAGGUCU CCAAGUCC 1382
3163	UGGGCCCA G CCAGUCCC	798	GGGACUGG GCCGAAAGGCGAGUCAAGGUCU UGGGCCCA 1383
3167	CCCAGCCA G UCCCUUGG	799	CCAAGGGA GCCGAAAGGCGAGUCAAGGUCU UGGCUGGG 1384
3179	CUUGGACA G CACCUUCU	800	AGAAGGUG GCCGAAAGGCGAGUCAAGGUCU UGUCCAAG 1385
3226	GGGACCUG G UGGAUGCU	801	AGCAUCCA GCCGAAAGGCGAGUCAAGGUCU CAGGUCCC 1386
3240	GCUGAGGA G UAUCUGGU	802	ACCAGAUA GCCGAAAGGCGAGUCAAGGUCU UCCUCAGC 1387
3247	AGUAUCUG G UACCCCAG	803	CUGGGGUA GCCGAAAGGCGAGUCAAGGUCU CAGAUACU 1388
3255	GUACCCCA G CAGGGCUU	804	AAGCCCUG GCCGAAAGGCGAGUCAAGGUCU UGGGGUAC 1389
3260	CCAGCAGG G CUUCUUCU	805	AGAAGAAG GCCGAAAGGCGAGUCAAGGUCU CCUGCUGG 1390
3287	UGCCCCGG G CGCUGGGG	806	CCCCAGCG GCCGAAAGGCGAGUCAAGGUCU CCGGGGCA 1391
3296	CGCUGGGG G CAUGGUCC	807	GGACCAUG GCCGAAAGGCGAGUCAAGGUCU CCCCAGCG 1392
3301	GGGGCAUG G UCCACCAC	808	GUGGUGGA GCCGAAAGGCGAGUCAAGGUCU CAUGCCCC 1393
3312	CACCACAG G CACCGCAG	809	CUGCGGUG GCCGAAAGGCGAGUCAAGGUCU CUGUGGUG 1394
3320	GCACCGCA G CUCAUCUA	810	UAGAUGAG GCCGAAAGGCGAGUCAAGGUCU UGCGGUGC 1395
3335	UACCAGGA G UGGCGGUG	811	CACCGCCA GCCGAAAGGCGAGUCAAGGUCU UCCUGGUA 1396
3338	CAGGAGUG G CGGUGGGG	812	CCCCACCG GCCGAAAGGCGAGUCAAGGUCU CACUCCUG 1397
3341	GAGUGGCG G UGGGGACC	813	GGUCCCCA GCCGAAAGGCGAGUCAAGGUCU CGCCACUC 1398
3360	ACACUAGG G CUGGAGCC	814	GGCUCCAG GCCGAAAGGCGAGUCAAGGUCU CCUAGUGU 1399
3366	GGGCUGGA G CCCUCUGA	815	UCAGAGGG GCCGAAAGGCGAGUCAAGGUCU UCCAGCCC 1400
3382	AAGAGGAG G CCCCCAGG	816	CCUGGGGG GCCGAAAGGCGAGUCAAGGUCU CUCCUCUU 1401
3390	GCCCCCAG G UCUCCACU	817	AGUGGAGA GCCGAAAGGCGAGUCAAGGUCU CUGGGGGC 1402
3400	CUCCACUG G CACCCUCC	818	GGAGGGUG GCCGAAAGGCGAGUCAAGGUCU CAGUGGAG 1403
3415	CCGAAGGG G CUGGCUCC	819	GGAGCCAG GCCGAAAGGCGAGUCAAGGUCU CCCUUCGG 1404
3419	AGGGGCUG G CUCCGAUG	820	CAUCGGAG GCCGAAAGGCGAGUCAAGGUCU CAGCCCCU 1405
3437	AUUUGAUG G UGACCUGG	821	CCAGGUCA GCCGAAAGGCGAGUCAAGGUCU CAUCAAAU 1406
3454	GAAUGGGG G CAGCCAAG	822	CUUGGCUG GCCGAAAGGCGAGUCAAGGUCU CCCCAUUC 1407

Table 59

			Tubic 33	
3457	UGGGGGCA G CCAAGGGG	823	CCCCUUGG GCCGAAAGGCGAGUCAAGGUCU UGCCCCCA	408
3465	GCCAAGGG G CUGCAAAG	824	CUUUGCAG GCCGAAAGGCGAGUCAAGGUCU CCCUUGGC :	1409
3473	GCUGCAAA G CCUCCCCA	825	UGGGGAGG GCCGAAAGGCGAGUCAAGGUCU UUUGCAGC :	L410
3494	UGACCCCA G CCCUCUAC	826	GUAGAGGG GCCGAAAGGCGAGUCAAGGUCU UGGGGUCA 1	1411
3504	CCUCUACA G CGGUACAG	827	CUGUACCG GCCGAAAGGCGAGUCAAGGUCU UGUAGAGG :	1412
3507	CUACAGCG G UACAGUGA	828	UCACUGUA GCCGAAAGGCGAGUCAAGGUCU CGCUGUAG :	L413
3512	GCGGUACA G UGAGGACC	829	GGUCCUCA GCCGAAAGGCGAGUCAAGGUCU UGUACCGC	1414
3526	ACCCCACA G UACCCCUG	830	CAGGGGUA GCCGAAAGGCGAGUCAAGGUCU UGUGGGGU	415
3551	GACUGAUG G CUACGUUG	831	CAACGUAG GCCGAAAGGCGAGUCAAGGUCU CAUCAGUC	416
3556	AUGGCUAC G UUGCCCCC	832	GGGGGCAA GCCGAAAGGCGAGUCAAGGUCU GUAGCCAU	1417
3575	GACCUGCA G CCCCCAGC	833	GCUGGGGG GCCGAAAGGCGAGUCAAGGUCU UGCAGGUC :	1418
3582	AGCCCCCA G CCUGAAUA	834	UAUUCAGG GCCGAAAGGCGAGUCAAGGUCU UGGGGGCU	419
3600	GUGAACCA G CCAGAUGU	835	ACAUCUGG GCCGAAAGGCGAGUCAAGGUCU UGGUUCAC :	1420
3612	GAUGUUCG G CCCCAGCC	836	GGCUGGGG GCCGAAAGGCGAGUCAAGGUCU CGAACAUC :	1421
3618	CGGCCCCA G CCCCCUUC	837	GAAGGGG GCCGAAAGGCGAGUCAAGGUCU UGGGGCCG :	1422
3638	CCGAGAGG G CCCUCUGC	838	GCAGAGGG GCCGAAAGGCGAGUCAAGGUCU CCUCUCGG	1423
3665	ACCUGCUG G UGCCACUC	839	GAGUGGCA GCCGAAAGGCGAGUCAAGGUCU CAGCAGGU	1424
3681	CUGGAAAG G CCCAAGAC	840	GUCUUGGG GCCGAAAGGCGAGUCAAGGUCU CUUUCCAG 1	L425
3712	AGAAUGGG G UCGUCAAA	841	UUUGACGA GCCGAAAGGCGAGUCAAGGUCU CCCAUUCU	1426
3715	AUGGGGUC G UCAAAGAC	842	GUCUUUGA GCCGAAAGGCGAGUCAAGGUCU GACCCCAU	1427
3724	UCAAAGAC G UUUUUUGCC	843	GGCAAAAA GCCGAAAGGCGAGUCAAGGUCU GUCUUUGA	1428
3740	CULUGGGG G UGCCGUGG	844	CCACGCA GCCGAAAGGCGAGUCAAGGUCU CCCCAAAG	1429
3745	GGGGUGCC G UGGAGAAC	845	GUUCUCCA GCCGAAAGGCGAGUCAAGGUCU GGCACCCC	430
3759	AACCCCGA G UACUUGAC	846	GUCAAGUA GCCGAAAGGCGAGUCAAGGUCU UCGGGGUU	1431
3781	AGGGAGGA G CUGCCCCU	847	AGGGGCAG GCCGAAAGGCGAGUCAAGGUCU UCCUCCCU	1432
3792	GCCCCUCA G CCCCACCC	848	GGGUGGGG GCCGAAAGGCGAGUCAAGGUCU UGAGGGGC	L433
3815	UGCCUUCA G CCCAGCCU	849	AGGCUGGG GCCGAAAGGCGAGUCAAGGUCU UGAAGGCA	1434
3820	UCAGCCCA G CCUUCGAC	850	GUCGAAGG GCCGAAAGGCGAGUCAAGGUCU UGGGCUGA	L435
3861	CCACCAGA G CGGGGGGC	851	GCCCCCCG GCCGAAAGGCGAGUCAAGGUCU UCUGGUGG 1	L436
3868	AGCGGGGG G CUCCACCC	852	GGGUGGAG GCCGAAAGGCGAGUCAAGGUCU CCCCCGCU :	L437
3878	UCCACCCA G CACCUUCA	853	UGAAGGUG GCCGAAAGGCGAGUCAAGGUCU UGGGUGGA	L438
3901	CACCUACG G CAGAGAAC	854	GUUCUCUG GCCGAAAGGCGAGUCAAGGUCU CGUAGGUG	L439
3915	AACCCAGA G UACCUGGG	855	CCCAGGUA GCCGAAAGGCGAGUCAAGGUCU UCUGGGUU	440
3923	GUACCUGG G UCUGGACG	856	CGUCCAGA GCCGAAAGGCGAGUCAAGGUCU CCAGGUAC 1	441
3931	GUCUGGAC G UGCCAGUG	857	CACUGGCA GCCGAAAGGCGAGUCAAGGUCU GUCCAGAC	442
3937	ACGUGCCA G UGUGAACC	858	GGUUCACA GCCGAAAGGCGAGUCAAGGUCU UGGCACGU	L443
3951	ACCAGAAG G CCAAGUCC	859	GGACUUGG GCCGAAAGGCGAGUCAAGGUCU CUUCUGGU	444
3956	AAGGCCAA G UCCGCAGA	860	UCUGCGGA GCCGAAAGGCGAGUCAAGGUCU UUGGCCUU	1445
3966	CCGCAGAA G CCCUGAUG	861	CAUCAGGG GCCGAAAGGCGAGUCAAGGUCU UUCUGCGG	446
3987	CUCAGGGA G CAGGGAAG	862	CUUCCCUG GCCGAAAGGCGAGUCAAGGUCU UCCCUGAG	447
3996	CAGGGAAG G CCUGACUU	863	AAGUCAGG GCCGAAAGGCGAGUCAAGGUCU CUUCCCUG	448
4011	UUCUGCUG G CAUCAAGA	864	UCUUGAUG GCCGAAAGGCGAGUCAAGGUCU CAGCAGAA	449
4021	AUCAAGAG G UGGGAGGG	865	CCCUCCCA GCCGAAAGGCGAGUCAAGGUCU CUCUUGAU 1	450
4029	GUGGGAGG G CCCUCCGA	866	UCGGAGGG GCCGAAAGGCGAGUCAAGGUCU CCUCCCAC	451
4100	CUGCUUGA G UUCCCAGA	867	UCUGGGAA GCCGAAAGGCGAGUCAAGGUCU UCAAGCAG 1	452
4111	CCCAGAUG G CUGGAAGG	868	CCUUCCAG GCCGAAAGGCGAGUCAAGGUCU CAUCUGGG 1	.453
4121	UGGAAGGG G UCCAGCCU	869	AGGCUGGA GCCGAAAGGCGAGUCAAGGUCU CCCUUCCA 1	454

Table 59

4126	GGGGUCCA G CCUCGUUG	870	CAACGAGG GCCGAAAGGCGAGUCAAGGUCU UGGACCCC	1455
4131	CCAGCCUC G UUGGAAGA	871	UCUUCCAA GCCGAAAGGCGAGUCAAGGUCU GAGGCUGG	1456
4146	GAGGAACA G CACUGGGG	872	CCCCAGUG GCCGAAAGGCGAGUCAAGGUCU UGUUCCUC	1457
4156	ACUGGGGA G UCUJUGUG	873	CACAAAGA GCCGAAAGGCGAGUCAAGGUCU UCCCCAGU	1458
4174	AUUCUGAG G CCCUGCCC	874	GGGCAGGG GCCGAAAGGCGAGUCAAGGUCU CUCAGAAU	1459
4197	ACUCUAGG G UCCAGUGG	875	CCACUGGA GCCGAAAGGCGAGUCAAGGUCU CCUAGAGU	1460
4202	AGGGUCCA G UGGAUGCC	876	GGCAUCCA GCCGAAAGGCGAGUCAAGGUCU UGGACCCU	1461
4214	AUGCCACA G CCCAGCUU	877	AAGCUGGG GCCGAAAGGCGAGUCAAGGUCU UGUGGCAU	1462
4219	ACAGCCCA G CUUGGCCC	878	GGGCCAAG GCCGAAAGGCGAGUCAAGGUCU UGGGCUGU	1463
4224	CCAGCUUG G CCCUUUCC	879	GGAAAGGG GCCGAAAGGCGAGUCAAGGUCU CAAGCUGG	1464
4246	GAUCCUGG G UACUGAAA	880	UUUCAGUA GCCGAAAGGCGAGUCAAGGUCU CCAGGAUC	1465
4255	UACUGAAA G CCUUAGGG	881	CCCUAAGG GCCGAAAGGCGAGUCAAGGUCU UUUCAGUA	1466
4266	UUAGGGAA G CUGGCCUG	882	CAGGCCAG GCCGAAAGGCGAGUCAAGGUCU UUCCCUAA	1467
4270	GGAAGCUG G CCUGAGAG	883	CUCUCAGG GCCGAAAGGCGAGUCAAGGUCU CAGCUUCC	1468
4284	GAGGGGAA G CGGCCCUA	884	UAGGGCCG GCCGAAAGGCGAGUCAAGGUCU UUCCCCUC	1469
4287	GGGAAGCG G CCCUAAGG	885	CCUUAGGG GCCGAAAGGCGAGUCAAGGUCU CGCUUCCC	1470
4298	CUAAGGGA G UGUCUAAG	886	CUUAGACA GCCGAAAGGCGAGUCAAGGUCU UCCCUUAG	1471
4314	GAACAAAA G CGACCCAU	887	AUGGGUCG GCCGAAAGGCGAGUCAAGGUCU UUUUGUUC	1472
4346	GAAACCUA G UACUGCCC	888	GGGCAGUA GCCGAAAGGCGAGUCAAGGUCU UAGGUUUC	1473
4372	AAGGAACA G CAAUGGUG	889	CACCAUUG GCCGAAAGGCGAGUCAAGGUCU UGUUCCUU	1474
4378	CAGCAAUG G UGUCAGUA	890	UACUGACA GCCGAAAGGCGAGUCAAGGUCU CAUUGCUG	1475
4384	UGGUGUCA G UAUCCAGG	891	CCUGGAUA GCCGAAAGGCGAGUCAAGGUCU UGACACCA	1476
4392	GUAUCCAG G CUUUGUAC	892	GUACAAAG GCCGAAAGGCGAGUCAAGGUCU CUGGAUAC	1477
4404	UGUACAGA G UGCUUUUC	893	GAAAAGCA GCCGAAAGGCGAGUCAAGGUCU UCUGUACA	1478
4419	UCUGUUUA G UUUUUACU	894	AGUAAAAA GCCGAAAGGCGAGUCAAGGUCU UAAACAGA	1479

Input Sequence = HSERB2R. Cut Site = G/Y

Stem Length = 8 . Core Sequence = GCcgaaagGCGaGuCaaGGuCu

HSERB2R (Human c-erb-B-2 mRNA; 4473 bp)

WO 01/16312 PCT/US00/23998

Table 60: Substrate Specificity for Class I Ribozymes

Substrate sequence	1-9t mutation	krel
5'-GCCGU G GGUUGCAC ACCUUUCC-3'	w.t.	1.00
5'-GCCGU G GGUUGCAC ACCUUUCC-3'	A57G	2.5
5'-GCCGA G GGUUGCAC ACCUUUCC-3'	A57U	0.24
5'-GCCGC G GGUUGCAC ACCUUUCC-3'	A57G	0.66
5'-GCCGG G GGUUGCAC ACCUUUCC-3'	A57C	0.57
5'-GCCGU U GGUUGCAC ACCUUUCC-3'	w.t	0.17
5'-GCCGU A GGUUGCAC ACCUUUCC-3'	w.t.	n.d.
5'-GCCGU C GGUUGCAC ACCUUUCC-3'	w.t.	n.d.
5'-GCCGU G GGUUGCAC ACCUUUCC-3'	C16U	0.98
5'-GCCGU G UGUUGCAC ACCUUUCC-3'	C16G	n.d.
5'-GCCGU G UGUUGCAC ACCUUUCC-3'	C16A	0.65
5'-GCCGU G AGUUGCAC ACCUUUCC-3'	C16U	0.45
5'-GCCGU G CGUUGCAC ACCUUUCC-3'	C16G	0.73
5'-GCCGU G GGUUGCAC ACCUUU-3'	w.t.	0.89
5'-GCCGU G GGUUGCAC ACCU-3'	w.t.	1.0
5'-GCCGU G GGUUGCAC AC-3'	w.t.	0.67

Table 61

Table 61: Random region alignments/mutations for Class I ribozyme

	죍	1.01	9.8	1.0	6.0	0.8	9.6	9.0	0.7	9.8	0.2	0.1	0.0	0.6	0.2	0.9	0.78	7.	0.84	0.31	0.81	0.36	0.6	1.1	0.98	0.86	1.51	0.22	-	96.0	0.44	0.27	0.97
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												2.13															3.26				4.19		

Table 62: Human Her2 Class II Ribozyme and Target Sequence

	Substrate	GI Bes	Ribozyme Sequence	Sed ID
	acucanc a cucacaa	7	მ ენინიინ ი უ ინნინინინენნიან ენინ ⁸ ი ⁸ ი გა	1480
1	GCUCAUC G CUCACAA	-	9°segueg u <u>O</u> ngaegagagagagagagagagagagagagagagagagaga	1481
1	coeccue e conecco	22	ც ნგენდი ი <mark>ე</mark> ინმომინდნენმციდინ ნნც ^გ ე ⁸ ნ ⁸ ნ ⁸ ი	1482
1	coccoe e conecco	22	გ მოენმო ი ე იტეომიმდე ე მმომომამ მამიში მ	1483
1	UGAGCU G CACUGC	2.2	g earcha agunda gcodasagag Gogagagaganga garana B	1484
	UGAGOU G CACUGO	27	g eznobe n <u>O</u> negagagagagagagagagagagagagagagagagagaga	1485
1	UGAGCU G CACUGC	2.7	8 පාත්රිය අධ්ය පුරු පුරු පුරු පුරු පුරු පුරු පුරු පුර	1486
1	DEAGCU 6 CACUGC	27	გ მითიანი ი ე იტეინინენმიცინენ მით ⁸ 6 ⁸ ი ⁸ ე ⁸ ნ	1487
ĺ.	DGAGCU G CACUGC	27	gnn 6ne ono 6en 7ng ge6 n6e576 6ee e6o o66 een nn ⁸ 6 ⁸ e ⁸ o ⁸ 6	1488
1	UGAGCU G CACUGC	27	gs sas gs usu ang usa agg cog asa gGC gag uga GGu Cua gcu cau guu uB	1489
ı	UGAGCU G CACUGC	2.2	g nnn eôn ean age ngu gge ghôeógge eag acidae ean an ann g	1490
1	UGAGOU G CACUGO	27	მ აიიანა იპინეციმინენაციმი მიზი ^ზ ი ^ზ იზი	1491
1	UGAGCU G CACUGC	27	g _s c _s a _s g _s ug gcc P ggCgagugaGguCu agcuca B	1492
	UGAGCU G CACUGC	27	მ აიიენი ი <u>ე</u> იტემიენიტენ გამე ⁸ ეზე მეიიდი ც	1493
ı	UGAGCU G CACUGC	27	g _{cc} a _g g _{cus} us usus a _g ag gcc gaa agg <u>Cga</u> gug aGG u <u>C</u> u agc uca uga uuu B	1494
1	UGAGCU G CACUGC	27	g csag gsusus ususas as a ga go co gaa agg Cga gug aGG uCu agc uca uga uuu B	1495
ı	UGAGCU G CACUGC	27	g eznose n o ngesonsesoossennsoos sin ⁸ 6 ⁸ e ⁸ 0 ⁸ 6	1496
1	UGAGCU 6 CACUGC	27	მ ^გ ავ _მ ენ მივემიმ გამ გამ მიზი გამ	1497
	UGAGCU G CACUGC	27	g csasgerg GccgaaagGCGaGnGaGGnCn agcnca B	1498
ı	UGAGCU G CACUGC	2.1	g especial GeogaaagGGGaGnGaGGuGu agonca B	1499
1	UGAGCU G CACUGC	27	მ ლიომი ი ე იტეიმიმიშემმიმიმიში მმომიზიზი გამი	1500
	UGAGCU G CACUGC	27	მ დეობდ ი <mark>პ</mark> იტეცმიმიმე <u>ნ</u> მიმიმიმიმიმიმიმიმიმიმიმიმიმიმიმიმიმიმი	1501
l	UGAGCU G CACUGC	27	g _{scs} a _g g _g ug gccgaaaggCgagugaGGuCu agcuca B	1502
l	UGAGCU G CACUGC	27	მ აიიმი ი პ იტეცმიმიმენმამიმიმიმიმიში მმიზიზი აზ	1503
	UGAGCU G CACUGC	27	ම පොත්ස හ ි ගලිපුම්බර්ධ පත්ත වී සම පුම්බර්ධ පත්තය ප	1504
1	UGAGCU G CACUGC	27	gscsasgaug g uuuu <u>C</u> gagugaGGu <u>C</u> u agcuca B	1505
	UGAGCU G CACUGC	2.7	g eorobe nongebababababababababababababababababababa	1506
ı	UGAGCU G CACUGC	2.1	g ⁸ c ⁸ a ⁸ g ⁸ ng g noca <u>C</u> gaguga GGu <u>C</u> n agonca B	1507
	UGAGCU G CACUGC	27	g eorobe n <mark>o</mark> nggebnbebon eron 6 bn ⁸ 6 ⁸ e ⁸ o ⁸ 6	1508
ı	UGAGCU G CACUGC	27	q_c_a_q_uq q quaa CqaquqaGGuCu aqcuca B	1509

Table 62

21454	972	UGAGCU G CACUGC	27	g.c.a.g.ug g aau CgagugaGGuCu agcuca B	1510
21455	972	UGAGCU G CACUGC	27	9 _S c _S a _S g _S ug g aag <u>C</u> gagugaGGu <u>C</u> u agcuca B	1511
21456	972	UGAGCU G CACUGC	27	მ ⁸ ა ⁸ ე ⁸ მ მ ი მმმენიშენი მმიინი გ	1512
21457	972	UGAGCU G CACUGC	27	8 පාෆරිස බටුබලලස්බන් වී රිසි සිස හ රී සින් පිළිතු මේ පැමිණිය ම	1513
21458	972	UGAGCU G CACUGC	27	g _{scs} gggggggggggggggggggggggggggggggggg	1514
21459	972	UGAGCU G CACUGC	27	8 spoose <u>15</u> 000 ac guua gg <u>C</u> aguga Guga Guga g	1515
19954	1292	UUGGGA G CCUGGC	34	მ ecocan ი <u>ე</u> ინნინინინინინინინინი მნ ⁸ ი ⁸ ი ⁸ ი	1516
3062R	1202	DESCRIPT OF THE PROPERTY.	3.4	n c c a no GeorgaanGCGaGiiGaiGai Incesa B	1517

lower case = 2'-O-methyl
U, C = 2'-deoxy-2'-amino U, = 2'-deoxy-2'-amino C
G,A= ribo G, A
B = inverted deoxyabasic
P= polyechyme g/yool 18 (PEG 18) linker

Table 63: Human PKCa NCH Ribozyme and Substrate Sequence

Pos	Substrate	Seq ID	Ribozyme	Rz Seq ID
27	GGGGGGAC C AUGGCUGA		UCAGCCAU CUGAUGAG X CGAA IUCCCCCC	
28	GGGGGACC A UGGCUGAC		GUCAGCCA CUGAUGAG X CGAA IGUCCCCC	
33	ACCAUGGC U GACGUUUU		AAAACGUC CUGAUGAG X CGAA ICCAUGGU	
43	ACGUUUUC C CGGGCAAC		GUUGCCCG CUGAUGAG X CGAA IAAAACGU	
44	CGUUUUCC C GGGCAACG		CGUUGCCC CUGAUGAG X CGAA IGAAAACG	
49	UCCCGGGC A ACGACUCC		GGAGUCGU CUGAUGAG X CGAA ICCCGGGA	
55	GCAACGAC U CCACGGCG		CGCCGUGG CUGAUGAG X CGAA IUCGUUGC	
57	AACGACUC C ACGGCGUC		GACGCCGU CUGAUGAG X CGAA IAGUCGUU	T
58	ACGACUCC A CGGCGUCU		AGACGCCG CUGAUGAG X CGAA IGAGUCGU	
66	ACGGCGUC U CAGGACGU		ACGUCCUG CUGAUGAG X CGAA IACGCCGU	
68	GGCGUCUC A GGACGUGG		CCACGUCC CUGAUGAG X CGAA IAGACGCC	
78	GACGUGGC C AACCGCUU		AAGCGGUU CUGAUGAG X CGAA ICCACGUC	
79	ACGUGGCC A ACCGCUUC		GAAGCGGU CUGAUGAG X CGAA IGCCACGU	
82	UGGCCAAC C GCUUCGCC		GGCGAAGC CUGAUGAG X CGAA IUUGGCCA	1
85	CCAACCGC U UCGCCCGC		GCGGGCGA CUGAUGAG X CGAA ICGGUUGG	
90	CGCUUCGC C CGCAAAGG		CCUUUGCG CUGAUGAG X CGAA ICGAAGCG	
91	GCUUCGCC C GCAAAGGG		CCCUUUGC CUGAUGAG X CGAA IGCGAAGC	
94	UCGCCCGC A AAGGGGCG		CGCCCCUU CUGAUGAG X CGAA ICGGGCGA	
104	AGGGGCGC U GAGGCAGA		UCUGCCUC CUGAUGAG X CGAA ICGCCCCU	
110	GCUGAGGC A GAAGAACG		CGUUCUUC CUGAUGAG X CGAA ICCUCAGC	
122	GAACGUGC A CGAGGUGA		UCACCUCG CUGAUGAG X CGAA ICACGUUC	1
136	UGAAGGAC C ACAAAUUC		GAAUUUGU CUGAUGAG X CGAA IUCCUUCA	
137	GAAGGACC A CAAAUUCA		UGAAUUUG CUGAUGAG X CGAA IGUCCUUC	
139	AGGACCAC A AAUUCAUC		GAUGAAUU CUGAUGAG X CGAA IUGGUCCU	
145	ACAAAUUC A UCGCGCGC		GCGCGCGA CUGAUGAG X CGAA IAAUUUGU	
154	UCGCGCGC U UCUUCAAG		CUUGAAGA CUGAUGAG X CGAA ICGCGCGA	
157	CGCGCUUC U UCAAGCAG		CUGCUUGA CUGAUGAG X CGAA IAAGCGCG	
160	GCUUCUUC A AGCAGCCC		GGGCUGCU CUGAUGAG X CGAA IAAGAAGC	
164	CUUCAAGC A GCCCACCU		AGGUGGGC CUGAUGAG X CGAA ICUUGAAG	
167	CAAGCAGC C CACCUUCU		AGAAGGUG CUGAUGAG X CGAA ICUGCUUG	
168	AAGCAGCC C ACCUUCUG		CAGAAGGU CUGAUGAG X CGAA IGCUGCUU	
169	AGCAGCCC A CCUUCUGC		GCAGAAGG CUGAUGAG X CGAA IGGCUGCU	
171	CAGCCCAC C UUCUGCAG		CUGCAGAA CUGAUGAG X CGAA IUGGGCUG	
172	AGCCCACC U UCUGCAGC		GCUGCAGA CUGAUGAG X CGAA IGUGGGCU	
175	CCACCUUC U GCAGCCAC		GUGGCUGC CUGAUGAG X CGAA IAAGGUGG	
178	CCUUCUGC A GCCACUGC		GCAGUGGC CUGAUGAG X CGAA ICAGAAGG	
181	UCUGCAGC C ACUGCACC		GGUGCAGU CUGAUGAG X CGAA ICUGCAGA	
182	CUGCAGCC A CUGCACCG		CGGUGCAG CUGAUGAG X CGAA IGCUGCAG	
184	GCAGCCAC U GCACCGAC		GUCGGUGC CUGAUGAG X CGAA IUGGCUGC	
187	GCCACUGC A CCGACUUC		GAAGUCGG CUGAUGAG X CGAA ICAGUGGC	
189	CACUGCAC C GACUUCAU		AUGAAGUC CUGAUGAG X CGAA IUGCAGUG	
193	GCACCGAC U UCAUCUGG		CCAGAUGA CUGAUGAG X CGAA IUCGGUGC	
196	CCGACUUC A UCUGGGGG		CCCCCAGA CUGAUGAG X CGAA IAAGUCGG	
199	ACUUCAUC U GGGGGUUU		AAACCCCC CUGAUGAG X CGAA IAUGAAGU	
215	UGGGAAAC A AGGCUUCC		GGAAGCCU CUGAUGAG X CGAA IUUUCCCA	
220	AACAAGGC U UCCAGUGC		GCACUGGA CUGAUGAG X CGAA ICCUUGUU	T
223	AAGGCUUC C AGUGCCAA		UUGGCACU CUGAUGAG X CGAA IAAGCCUU	

Table 63

224	AGGCUUCC A GUGCCAAG	CUUGGCAC CUGAUGAG X CGAA IGAAGCCU
229	UCCAGUGC C AAGUUUGC	GCAAACUU CUGAUGAG X CGAA ICACUGGA
230	CCAGUGCC A AGUUUGCU	AGCAAACU CUGAUGAG X CGAA IGCACUGG
238	AAGUUUGC U GUUUUGUG	CACAAAAC CUGAUGAG X CGAA ICAAACUU
250	UUGUGGUC C ACAAGAGG	CCUCUUGU CUGAUGAG X CGAA IACCACAA
251	UGUGGUCC A CAAGAGGU	ACCUCUUG CUGAUGAG X CGAA IGACCACA
253	UGGUCCAC A AGAGGUGC	GCACCUCU CUGAUGAG X CGAA IUGGACCA
262	AGAGGUGC C AUGAAUUU	AAAUUCAU CUGAUGAG X CGAA ICACCUCU
263	GAGGUGCC A UGAAUUUG	CAAAUUCA CUGAUGAG X CGAA IGCACCUC
276	UUUGUUAC U UUUUCUUG	CAAGAAAA CUGAUGAG X CGAA IUAACAAA
282	ACUUUUUC U UGUCCGGG	CCCGGACA CUGAUGAG X CGAA IAAAAAGU
287	UUCUUGUC C GGGUGCGG	CCGCACCC CUGAUGAG X CGAA IACAAGAA
305	UAAGGGAC C CGACACUG	CAGUGUCG CUGAUGAG X CGAA IUCCCUUA
306	AAGGGACC C GACACUGA	UCAGUGUC CUGAUGAG X CGAA IGUCCCUU
310	GACCCGAC A CUGAUGAC	GUCAUCAG CUGAUGAG X CGAA IUCGGGUC
312	CCCGACAC U GAUGACCC	GGGUCAUC CUGAUGAG X CGAA IUGUCGGG
319	CUGAUGAC C CCAGGAGC	GCUCCUGG CUGAUGAG X CGAA IUCAUCAG
320	UGAUGACC C CAGGAGCA	UGCUCCUG CUGAUGAG X CGAA IGUCAUCA
321	GAUGACCC C AGGAGCAA	UUGCUCCU CUGAUGAG X CGAA IGGUCAUC
322	AUGACCCC A GGAGCAAG	CUUGCUCC CUGAUGAG X CGAA IGGGUCAU
328	CCAGGAGC A AGCACAAG	CUUGUGCU CUGAUGAG X CGAA ICUCCUGG
332	GAGCAAGC A CAAGUUCA	UGAACUUG CUGAUGAG X CGAA ICUUGCUC
334	GCAAGCAC A AGUUCAAA	UUUGAACU CUGAUGAG X CGAA IUGCUUGC
340	ACAAGUUC A AAAUCCAC	GUGGAUUU CUGAUGAG X CGAA IAACUUGU
346	UCAAAAUC C ACACUUAC	GUAAGUGU CUGAUGAG X CGAA IAUUUUGA
347	CAAAAUCC A CACUUACG	CGUAAGUG CUGAUGAG X CGAA IGAUUUUG
349	AAAUCCAC A CUUACGGA	UCCGUAAG CUGAUGAG X CGAA IUGGAUUU
351	AUCCACAC U UACGGAAG	CUUCCGUA CUGAUGAG X CGAA IUGUGGAU
361	ACGGAAGC C CCACCUUC	GAAGGUGG CUGAUGAG X CGAA ICUUCCGU
362	CGGAAGCC C CACCUUCU	AGAAGGUG CUGAUGAG X CGAA IGCUUCCG
363	GGAAGCCC C ACCUUCUG	CAGAAGGU CUGAUGAG X CGAA IGGCUUCC
364	GAAGCCCC A CCUUCUGC	GCAGAAGG CUGAUGAG X CGAA IGGGCUUC
366	AGCCCCAC C UUCUGCGA	UCGCAGAA CUGAUGAG X CGAA IUGGGGCU
367	GCCCCACC U UCUGCGAU	AUCGCAGA CUGAUGAG X CGAA IGUGGGGC
370	CCACCUUC U GCGAUCAC	GUGAUCGC CUGAUGAG X CGAA TAAGGUGG
377	CUGCGAUC A CUGUGGGU	ACCCACAG CUGAUGAG X CGAA IAUCGCAG
379	GCGAUCAC U GUGGGUCA	UGACCCAC CUGAUGAG X CGAA IUGAUCGC
387	UGUGGGUC A CUGCUCUA	UAGAGCAG CUGAUGAG X CGAA IACCCACA
389	UGGGUCAC U GCUCUAUG	CAUAGAGC CUGAUGAG X CGAA IUGACCCA
392	GUCACUGC U CUAUGGAC	GUCCAUAG CUGAUGAG X CGAA ICAGUGAC
394	CACUGCUC U AUGGACUU	AAGUCCAU CUGAUGAG X CGAA IAGCAGUG
401	CUAUGGAC U UAUCCAUC	GAUGGAUA CUGAUGAG X CGAA IUCCAUAG
406	GACUUAUC C AUCAAGGG	CCCUUGAU CUGAUGAG X CGAA IAUAAGUC
407	ACUUAUCC A UCAAGGGA	UCCCUUGA CUGAUGAG X CGAA IGAUAAGU
410	UAUCCAUC A AGGGAUGA	UCAUCCCU CUGAUGAG X CGAA IAUGGAUA
427	AAUGUGAC A CCUGCGAU	AUCGCAGG CUGAUGAG X CGAA IUCACAUU
429	UGUGAÇAC C UGCGAUAU	AUAUCGCA CUGAUGAG X CGAA IUGUCACA
430	GUGACACC U GCGAUAUG	CAUAUCGC CUGAUGAG X CGAA IGUGUCAC
446	GAACGUUC A CAAGCAAU	AUUGCUUG CUGAUGAG X CGAA IAACGUUC
448	ACGUUCAC A AGCAAUGC	GCAUUGCU CUGAUGAG X CGAA IUGAACGU
452	UCACAAGC A AUGCGUCA	UGACGCAU CUGAUGAG X CGAA ICUUGUGA
	- I III I I I I I I I I I I I I I I I I	TELEGORIA COMPANIA

Table 63

460	AAUGCGUC A UCAAUGUC	GACAUUGA CUGAUGAG X CGAA IACGCAUU
463	GCGUCAUC A AUGUCCCC	GGGGACAU CUGAUGAG X CGAA IAUGACGC
469	UCAAUGUC C CCAGCCUC	GAGGCUGG CUGAUGAG X CGAA IACAUUGA
470	CAAUGUCC C CAGCCUCU	AGAGGCUG CUGAUGAG X CGAA IGACAUUG
471	AAUGUCCC C AGCCUCUG	CAGAGGCU CUGAUGAG X CGAA IGGACAUU
472	AUGUCCCC A GCCUCUGC	GCAGAGGC CUGAUGAG X CGAA IGGGACAU
475	UCCCCAGC C UCUGCGGA	UCCGCAGA CUGAUGAG X CGAA ICUGGGGA
476	CCCCAGCC U CUGCGGAA	UUCCGCAG CUGAUGAG X CGAA IGCUGGGG
478	CCAGCCUC U GCGGAAUG	CAUUCCGC CUGAUGAG X CGAA IAGGCUGG
491	AAUGGAUC A CACUGAGA	UCUCAGUG CUGAUGAG X CGAA IAUCCAUU
493	UGGAUCAC A CUGAGAAG	CUUCUCAG CUGAUGAG X CGAA IUGAUCCA
495	GAUCACAC U GAGAAGAG	CUCUUCUC CUGAUGAG X CGAA IUGUGAUC
517	GGAUUUAC C UAAAGGCU	AGCCUUUA CUGAUGAG X CGAA IUAAAUCC
518	GAUUUACC U AAAGGCUG	CAGCCUUU CUGAUGAG X CGAA IGUAAAUC
525	CUAAAGGC U GAGGUUGC	GCAACCUC CUGAUGAG X CGAA ICCUUUAG
534	GAGGUUGC U GAUGAAAA	UUUUCAUC CUGAUGAG X CGAA ICAACCUC
545	UGAAAAGC U CCAUGUCA	UGACAUGG CUGAUGAG X CGAA ICUUUUCA
547	AAAAGCUC C AUGUCACA	UGUGACAU CUGAUGAG X CGAA IAGCUUUU
548	AAAGCUCC A UGUCACAG	CUGUGACA CUGAUGAG X CGAA IGAGCUUU
553	UCCAUGUC A CAGUACGA	UCGUACUG CUGAUGAG X CGAA IACAUGGA
555	CAUGUCAC A GUACGAGA	UCUCGUAC CUGAUGAG X CGAA IUGACAUG
567	CGAGAUGC A AAAAAUCU	AGAUUUUU CUGAUGAG X CGAA ICAUCUCG
575	AAAAAAUC U AAUCCCUA	UAGGGAUU CUGAUGAG X CGAA IAUUUUUU
580	AUCUAAUC C CUAUGGAU	AUCCAUAG CUGAUGAG X CGAA IAUUAGAU
581	UCUAAUCC C UAUGGAUC	GAUCCAUA CUGAUGAG X CGAA IGAUUAGA
582	CUAAUCCC U AUGGAUCC	GGAUCCAU CUGAUGAG X CGAA IGGAUUAG
590	UAUGGAUC C AAACGGGC	GCCCGUUU CUGAUGAG X CGAA IAUCCAUA
591	AUGGAUCC A AACGGGCU	AGCCCGUU CUGAUGAG X CGAA IGAUCCAU
599	AAACGGGC U UUCAGAUC	GAUCUGAA CUGAUGAG X CGAA ICCCGUUU
603	GGGCUUUC A GAUCCUUA	UAAGGAUC CUGAUGAG X CGAA IAAAGCCC
608	UUCAGAUC C UUAUGUGA	UCACAUAA CUGAUGAG X CGAA IAUCUGAA
609	UCAGAUCC U UAUGUGAA	UUCACAUA CUGAUGAG X CGAA IGAUCUGA
620	UGUGAAGC U GAAACUUA	UAAGUUUC CUGAUGAG X CGAA ICUUCACA
626	GCUGAAAC U UAUUCCUG	CAGGAAUA CUGAUGAG X CGAA IUUUCAGC
632	ACUUAUUC C UGAUCCCA	UGGGAUCA CUGAUGAG X CGAA IAAUAAGU
633	CUUAUUCC U GAUCCCAA	UUGGGAUC CUGAUGAG X CGAA IGAAUAAG
638	UCCUGAUC C CAAGAAUG	CAUUCUUG CUGAUGAG X CGAA IAUCAGGA
639	CCUGAUCC C AAGAAUGA	UCAUUCUU CUGAUGAG X CGAA IGAUCAGG
640	CUGAUCCC A AGAAUGAA	UUCAUUCU CUGAUGAG X CGAA IGGAUCAG
652	AUGAAAGC A AGCAAAAA	UUUUUGCU CUGAUGAG X CGAA ICUUUCAU
656	AAGCAAGC A AAAAACCA	UGGUUUUU CUGAUGAG X CGAA ICUUGCUU
663	CAAAAAAC C AAAACCAU	AUGGUUUU CUGAUGAG X CGAA IUUUUUUG
664	AAAAAACC A AAACCAUC	GAUGGUUU CUGAUGAG X CGAA IGUUUUUU
669	ACCAAAAC C AUCCGCUC	GAGCGGAU CUGAUGAG X CGAA IUUUUGGU
670	CCAAAACC A UCCGCUCC	GGAGCGGA CUGAUGAG X CGAA IGUUUUGG
673	AAACCAUC C GCUCCACA	UGUGGAGC CUGAUGAG X CGAA IAUGGUUU
676	CCAUCCGC U CCACACUA	UAGUGUGG CUGAUGAG X CGAA ICGGAUGG
678	AUCCGCUC C ACACUAAA	UUUAGUGU CUGAUGAG X CGAA IAGCGGAU
679	UCCGCUCC A CACUAAAU	AUJUAGUG CUGAUGAG X CGAA IGAGCGGA
681	CGCUCCAC A CUAAAUCC	GGAUUUAG CUGAUGAG X CGAA IUGGAGCG
683	CUCCACAC U AAAUCCGC	GCGGAUUU CUGAUGAG X CGAA IUGUGGAG

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689	ACUAAAUC C GCAGUGGA	UCCACUGC CUGAUGAG X CGAA IAUUUAGU
692	AAAUCCGC A GUGGAAUG	CAUUCCAC CUGAUGAG X CGAA IAGUUAGU
705	AAUGAGUC C UUUACAUU	AAUGUAAA CUGAUGAG X CGAA IACUCAUU
705	AUGAGUCC U UUACAUUC	GAAUGUAA CUGAUGAG X CGAA IGACUCAU
711	UCCUUUAC A UUCAAAUU	AAUUUGAA CUGAUGAG X CGAA TUAAAGGA
715	UUACAUUC A AAUUGAAA	UUUCAAUU CUGAUGAG X CGAA IAAUGUAA
725	AUUGAAAC C UUCAGACA	UGUCUGAA CUGAUGAG X CGAA IUUUCAAU
726	UUGAAACC U UCAGACAA	UUGUCUGA CUGAUGAG X CGAA IGUUUCAA
729	AAACCUUC A GACAAAGA	UCUUUGUC CUGAUGAG X CGAA IAAGGUUU
733	CUUCAGAC A AAGACCGA	UCGGUCUU CUGAUGAG X CGAA IUCUGAAG
739	ACAAAGAC C GACGACUG	CAGUCGUC CUGAUGAG X CGAA IUCUUUGU
746	CCGACGAC U GUCUGUAG	CUACAGAC CUGAUGAG X CGAA IUCGUCGG
750	CGACUGUC U GUAGAAAU	AUJUCUAC CUGAUGAG X CGAA IACAGUCG
760	UAGAAAUC U GGGACUGG	CCAGUCCC CUGAUGAG X CGAA IACAGCG
766	UCUGGGAC U GGGAUCGA	UCGAUCCC CUGAUGAG X CGAA IAUUCCAGA
777	GAUCGAAC A ACAAGGAA	UUCCUIGU CUGAUGAG X CGAA IUUCGAUC
780	CGAACAAC A ACAAGGAA CGAACAAC A AGGAAUGA	UCAUUCCU CUGAUGAG X CGAA IUUGUUCG
790	GGAAUGAC U UCAUGGGA	UCCCAUGA CUGAUGAG X CGAA IUCAUUCC
793	AUGACUUC A UGGGAUCC	GGAUCCCA CUGAUGAG X CGAA IAAGUCAU
801	AUGGGAUC C CUUUCCUU	AAGGAAAG CUGAUGAG X CGAA IAUCCCAU
802	UGGGAUCC C UUUCCUUU	AAAGGAAA CUGAUGAG X CGAA IGAUCCCA
803	GGGAUCCC U UUCCUUUG	CAAAGGAA CUGAUGAG X CGAA IGGAUCCC
807	UCCCUUUC C UUUGGAGU	ACUCCAAA CUGAUGAG X CGAA IAAAGGGA
808	CCCUTUCC U UUGGAGUU	AACUCCAA CUGAUGAG X CGAA IGAAAGGG
824	UUCGGAGC U GAUGAAGA	UCUUCAUC CUGAUGAG X CGAA ICUCCGAA
836	GAAGAUGC C GGCCAGUG	CACUGGCC CUGAUGAG X CGAA ICAUCUUC
840	AUGCCGGC C AGUGGAUG	CAUCCACU CUGAUGAG X CGAA ICCGGCAU
841	UGCCOGCC A GUGGAUGG	CCAUCCAC CUGAUGAG X CGAA IGCCGGCA
853	GAUGGUAC A AGUUGCUU	AAGCAACU CUGAUGAG X CGAA IUACCAUC
860	CAAGUUGC U UAACCAAG	CUUGGUUA CUGAUGAG X CGAA ICAACUUG
865	UGCUUAAC C AAGAAGAA	UUCUUCUU CUGAUGAG X CGAA IUUAAGCA
866	GCUUAACC A AGAAGAAG	CUUCUUCU CUGAUGAG X CGAA IGUUAAGC
883	GUGAGUAC U ACAACGUA	UACGUUGU CUGAUGAG X CGAA IUACUCAC
886	AGUACUAC A ACGUACCC	GGGUACGU CUGAUGAG X CGAA IUAGUACU
893	CAACGUAC C CAUUCCGG	CCGGAAUG CUGAUGAG X CGAA IUACGUUG
894	AACGUACC C AUUCCGGA	UCCGGAAU CUGAUGAG X CGAA IGUACGUU
895	ACGUACCC A UUCCGGAA	UUCCGGAA CUGAUGAG X CGAA IGGUACGU
899	ACCCAUUC C GGAAGGGG	CCCCUUCC CUGAUGAG X CGAA IAAUGGGU
922	AAGGAAAC A UGGAACUC	GAGUUCCA CUGAUGAG X CGAA IUUUCCUU
929	CAUGGAAC U CAGGCAGA	UCUGCCUG CUGAUGAG X CGAA IUUCCAUG
931	UGGAACUC A GGCAGAAA	UUUCUGCC CUGAUGAG X CGAA IAGUUCCA
935	ACUCAGGC A GAAAUUCG	CGAAUUUC CUGAUGAG X CGAA ICCUGAGU
951	GAGAAAGC C AAACUUGG	CCAAGUUU CUGAUGAG X CGAA ICUUUCUC
952	AGAAAGCC A AACUUGGC	GCCAAGUU CUGAUGAG X CGAA IGCUUUCU
956	AGCCAAAC U UGGCCCUG	CAGGGCCA CUGAUGAG X CGAA IUUUGGCU
961	AACUUGGC C CUGCUGGC	GCCAGCAG CUGAUGAG X CGAA ICCAAGUU
962	ACUUGGCC C UGCUGGCA	UGCCAGCA CUGAUGAG X CGAA IGCCAAGU
963	CUUGGCCC U GCUGGCAA	UUGCCAGC CUGAUGAG X CGAA IGGCCAAG
966	GGCCCUGC U GGCAACAA	UUGUUGCC CUGAUGAG X CGAA ICAGGGCC
970	CUGCUGGC A ACAAAGUC	GACUUUGU CUGAUGAG X CGAA ICCAGCAG
973	CUGGCAAC A AAGUCAUC	GAUGACUU CUGAUGAG X CGAA IUUGCCAG

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979	ACAAAGUC A UCAGUCCC	GGGACUGA CUGAUGAG X CGAA IACUUUGU
982	AAGUCAUC A GUCCCUCU	AGAGGGAC CUGAUGAG X CGAA IAUGACUU
986	CAUCAGUC C CUCUGAAG	CUUCAGAG CUGAUGAG X CGAA IACUGAUG
987	AUCAGUCC C UCUGAAGA	UCUUCAGA CUGAUGAG X CGAA IGACUGAU
988	UCAGUCCC U CUGAAGAC	GUCUUCAG CUGAUGAG X CGAA IGGACUGA
990	AGUCCCUC U GAAGACAG	CUGUCUUC CUGAUGAG X CGAA IAGGGACU
997	CUGAAGAC A GGAAACAA	UUGUUUCC CUGAUGAG X CGAA IUCUUCAG
1004	CAGGAAAC A ACCUUCCA	UGGAAGGU CUGAUGAG X CGAA IUUUCCUG
1007	GAAACAAC C UUCCAACA	UGUUGGAA CUGAUGAG X CGAA IUUGUUUC
1008	AAACAACC U UCCAACAA	UUGUUGGA CUGAUGAG X CGAA IGUUGUUU
1011	CAACCUUC C AACAACCU	AGGUUGUU CUGAUGAG X CGAA LAAGGUUG
1012	AACCUUCC A ACAACCUU	AAGGUUGU CUGAUGAG X CGAA IGAAGGUU
1015	CUUCCAAC A ACCUUGAC	GUCAAGGU CUGAUGAG X CGAA IUUGGAAG
1018	CCAACAAC C UUGACCGA	UCGGUCAA CUGAUGAG X CGAA IUUGUUGG
1019	CAACAACC U UGACCGAG	CUCGGUCA CUGAUGAG X CGAA IGUUGUUG
1024	ACCUUGAC C GAGUGAAA	UUUCACUC CUGAUGAG X CGAA IUCAAGGU
1034	AGUGAAAC U CACGGACU	AGUCCGUG CUGAUGAG X CGAA IUUUCACU
1036	UGAAACUC A CGGACUUC	GAAGUCCG CUGAUGAG X CGAA IAGUUUCA
1042	UCACGGAC U UCAAUUUC	GAAAUUGA CUGAUGAG X CGAA IUCCGUGA
1045	CGGACUUC A AUUUCCUC	GAGGAAAU CUGAUGAG X CGAA IAAGUCCG
1051	UCAAUUUC C UCAUGGUG	CACCAUGA CUGAUGAG X CGAA IAAAUUGA
1052	CAAUUUCC U CAUGGUGU	ACACCAUG CUGAUGAG X CGAA IGAAAUUG
1054	AUUUCCUC A UGGUGUUG	CAACACCA CUGAUGAG X CGAA IAGGAAAU
1091	GGUGAUGC U UGCCGACA	UGUCGGCA CUGAUGAG X CGAA ICAUCACC
1095	AUGCUUGC C GACAGGAA	UUCCUGUC CUGAUGAG X CGAA ICAAGCAU
1099	UUGCCGAC A GGAAGGGC	GCCCUUCC CUGAUGAG X CGAA IUCGGCAA
1108	GGAAGGGC A CAGAAGAA	UUCUUCUG CUGAUGAG X CGAA ICCCUUCC
1110	AAGGGCAC A GAAGAACU	AGUUCUUC CUGAUGAG X CGAA IUGCCCUU
1118	AGAAGAAC U GUAUGCAA	UUGCAUAC CUGAUGAG X CGAA IUUCUUCU
1125	CUGUAUGC A AUCAAAAU	AUUUUGAU CUGAUGAG X CGAA ICAUACAG
1129	AUGCAAUC A AAAUCCUG	CAGGAUUU CUGAUGAG X CGAA IAUUGCAU
1135	UCAAAAUC C UGAAGAAG	CUUCUUCA CUGAUGAG X CGAA IAUUUUGA
1136	CAAAAUCC U GAAGAAGG	CCUUCUUC CUGAUGAG X CGAA IGAUUUUG
1157	GGUGAUUC A GGAUGAUG	CAUCAUCC CUGAUGAG X CGAA IAAUCACC
1177	UGGAGUGC A CCAUGGUA	UACCAUGG CUGAUGAG X CGAA ICACUCCA
1179	GAGUGCAC C AUGGUAGA	UCUACCAU CUGAUGAG X CGAA IUGCACUC
1180	AGUGCACC A UGGUAGAA	UUCUACCA CUGAUGAG X CGAA IGUGCACU
1198	AGCGAGUC U UGGCCCUG	CAGGGCCA CUGAUGAG X CGAA IACUCGCU
1203	GUCUUGGC C CUGCUUGA	UCAAGCAG CUGAUGAG X CGAA ICCAAGAC
1204	UCUUGGCC C UGCUUGAC	GUCAAGCA CUGAUGAG X CGAA IGCCAAGA
1205	CUUGGCCC U GCUUGACA	UGUCAAGC CUGAUGAG X CGAA IGGCCAAG
1208	GGCCCUGC U UGACAAAC	GUUUGUCA CUGAUGAG X CGAA ICAGGGCC
1213	UGCUUGAC A AACCCCCG	CGGGGGUU CUGAUGAG X CGAA IUCAAGCA
1217	UGACAAAC C CCCGUUCU	AGAACGGG CUGAUGAG X CGAA IUUUGUCA
1218	GACAAACC C CCGUUCUU	AAGAACGG CUGAUGAG X CGAA IGUUUGUC
1219	ACAAACCC C CGUUCUUG	CAAGAACG CUGAUGAG X CGAA IGGUUUGU
1220	CAAACCCC C GUUCUUGA	UCAAGAAC CUGAUGAG X CGAA IGGGUUUG
1225	CCCCGUUC U UGACGCAG	CUGCGUCA CUGAUGAG X CGAA IAACGGGG
1232	CUUGACGC A GCUGCACU	AGUGCAGC CUGAUGAG X CGAA ICGUCAAG
1235	GACGCAGC U GCACUCCU	AGGAGUGC CUGAUGAG X CGAA ICUGCGUC
1238	GCAGCUGC A CUCCUGCU	AGCAGGAG CUGAUGAG X CGAA ICAGCUGC
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1240	AGCUGCAC U CCUGCUUC	GAAGCAGG CUGAUGAG X CGAA IUGCAGCU
1242	CUGCACUC C UGCUUCCA UGCACUCC U GCUUCCAG	UGGAAGCA CUGAUGAG X CGAA IAGUGCAG
1243		CUGGAAGC CUGAUGAG X CGAA IGAGUGCA
1246	ACUCCUGC U UCCAGACA	UGUCUGGA CUGAUGAG X CGAA ICAGGAGU
1249	CCUGCUUC C AGACAGUG	CACUGUCU CUGAUGAG X CGAA IAAGCAGG
1250	CUGCUUCC A GACAGUGG	CCACUGUC CUGAUGAG X CGAA IGAAGCAG
1254	UUCCAGAC A GUGGAUCG	CGAUCCAC CUGAUGAG X CGAA IUCUGGAA
1265	GGAUCGGC U GUACUUCG	CGAAGUAC CUGAUGAG X CGAA ICCGAUCC
1270	GGCUGUAC U UCGUCAUG	CAUGACGA CUGAUGAG X CGAA IUACAGCC
1276	ACUUCGUC A UGGAAUAU	AUAUUCCA CUGAUGAG X CGAA IACGAAGU
1288	AAUAUGUC A ACGGUGGG	CCCACCGU CUGAUGAG X CGAA IACAUAUU
1300	GUGGGGAC C UCAUGUAC	GUACAUGA CUGAUGAG X CGAA IUCCCCAC
1301	UGGGGACC U CAUGUACC	GGUACAUG CUGAUGAG X CGAA IGUCCCCA
1303	GGGACCUC A UGUACCAC	GUGGUACA CUGAUGAG X CGAA IAGGUCCC
1309	UCAUGUAC C ACAUUCAG	CUGAAUGU CUGAUGAG X CGAA IUACAUGA
1310	CAUGUACC A CAUUCAGC	GCUGAAUG CUGAUGAG X CGAA IGUACAUG
1312	UGUACCAC A UUCAGCAA	UUGCUGAA CUGAUGAG X CGAA IUGGUACA
1316	CCACAUUC A GCAAGUAG	CUACUUGC CUGAUGAG X CGAA IAAUGUGG
1319	CAUUCAGC A AGUAGGAA	UUCCUACU CUGAUGAG X CGAA ICUGAAUG
1340	UAAGGAAC C ACAAGCAG	CUGCUUGU CUGAUGAG X CGAA IUUCCUUA
1341	AAGGAACC A CAAGCAGU	ACUGCUUG CUGAUGAG X CGAA IGUUCCUU
1343	GGAACCAC A AGCAGUAU	AUACUGCU CUGAUGAG X CGAA IUGGUUCC
1347	CCACAAGC A GUAUUCUA	UAGAAUAC CUGAUGAG X CGAA ICUUGUGG
1354	CAGUAUUC U AUGCGGCA	UGCCGCAU CUGAUGAG X CGAA IAAUACUG
1362	UAUGCGGC A GAGAUUUC	GAAAUCUC CUGAUGAG X CGAA ICCGCAUA
1371	GAGAUUUC C AUCGGAUU	AAUCCGAU CUGAUGAG X CGAA IAAAUCUC
1372	AGAUUUCC A UCGGAUUG	CAAUCCGA CUGAUGAG X CGAA IGAAAUCU AUGAAGAA CUGAUGAG X CGAA IAACAAUC
1384	GAUUGUUC U UUCUUCAU	
1388	GUUCUUUC U UCAUAAAA CUUUCUUC A UAAAAGAG	UUUUAUGA CUGAUGAG X CGAA IAAAGAAC CUCUUUUA CUGAUGAG X CGAA IAAGAAAG
1391	GAGGAAUC A UUUAUAGG	CCUAUAAA CUGAUGAG X CGAA TAAGAAAG CCUAUAAA CUGAUGAG X CGAA TAUUCCUC
1418	UAGGGAUC U GAAGUUAG	CUAACUUC CUGAUGAG X CGAA IAUCCCUA
1418	AUAACGUC A UGUUGGAU	AUCCAACA CUGAUGAG X CGAA TAUCCCUA
1446	UUGGAUUC A GAAGGACA	UGUCCUUC CUGAUGAG X CGAA IAAUCCAA
1454	AGAAGGAC A UAUCAAAA	UUUUGAUA CUGAUGAG X CGAA IAAUCCAA
1454	GACAUAUC A AAAUUGCU	AGCAAUUU CUGAUGAG X CGAA TAUAUGUC
1467	AAAAUUGC U GACUUUGG	CCAAAGUC CUGAUGAG X CGAA IAUAUGUC
1471	UUGCUGAC U UUGGGAUG	CAUCCCAA CUGAUGAG X CGAA ICAAUUUU
1483	GGAUGUGC A AGGAACAC	GUGUUCCU CUGAUGAG X CGAA ICACAUCC
1490	CAAGGAAC A CAUGAUGG	CCAUCAUG CUGAUGAG X CGAA IUUCCUUG
1490	AGGAACAC A UGAUGGAU	AUCCAUCA CUGAUGAG X CGAA IUGUUCCU
1507	AUGGAGUC A CGACCAGG	CCUGGUCG CUGAUGAG X CGAA IACUCCAU
1512	GUCACGAC C AGGACCUU	AAGGUCCU CUGAUGAG X CGAA TUCGUGAC
1512	UCACGACC A GGACCUUC	GAAGGUCC CUGAUGAG X CGAA IGUCGUGA
1513	ACCAGGAC C UUCUGUGG	CCACAGAA CUGAUGAG X CGAA IUCCUGGU
1519	CCAGGACC U UCUGUGGG	CCCACAGA CUGAUGAG X CGAA IGUCCUGG
1522	GGACCUUC U GUGGGACU	AGUCCCAC CUGAUGAG X CGAA IAAGGUCC
1522	UGUGGGAC U CCAGAUUA	UAAUCUGG CUGAUGAG X CGAA IAAGGUCC
1530	UGGGACUC C AGAUUAUA	UAUAAUCU CUGAUGAG X CGAA IAGUCCCA
1532	GGGACUCC A GAUUAUAU	AUAUAAUC CUGAUGAG X CGAA IAGUCCCA AUAUAAUC CUGAUGAG X CGAA IGAGUCCC
1545	UAUAUCGC C CCAGAGAU	AUCUCUGG CUGAUGAG X CGAA IGAGUCCC
1545	UAUAUCGC C CCAGAGAU	AUCUCUGG CUGADGAG X CGAA ICGAUAUA

Table 63

1546	AUAUCGCC C CAGAGAUA	UAUCUCUG CUGAUGAG X CGAA IGCGAUAU
1547	UAUCGCCC C AGAGAUAA	UUAUCUCU CUGAUGAG X CGAA IGGCGAUA
1548	AUCGCCCC A GAGAUAAU	AUUAUCUC CUGAUGAG X CGAA IGGGCGAU
1560	AUAAUCGC U UAUCAGCC	GGCUGAUA CUGAUGAG X CGAA ICGAUUAU
1565	CGCUUAUC A GCCGUAUG	CAUACGGC CUGAUGAG X CGAA IAUAAGCG
1568	UUAUCAGC C GUAUGGAA	UUCCAUAC CUGAUGAG X CGAA ICUGAUAA
1581	GGAAAAUC U GUGGACUG	CAGUCCAC CUGAUGAG X CGAA IAUUUUCC
1588	CUGUGGAC U GGUGGGCC	GGCCCACC CUGAUGAG X CGAA IUCCACAG
1596	UGGUGGGC C UAUGGCGU	ACGCCAUA CUGAUGAG X CGAA ICCCACCA
1597	GGUGGGCC U AUGGCGUC	GACGCCAU CUGAUGAG X CGAA IGCCCACC
1606	AUGGCGUC C UGUUGUAU	AUACAACA CUGAUGAG X CGAA IACGCCAU
1607	UGGCGUCC U GUUGUAUG	CAUACAAC CUGAUGAG X CGAA IGACGCCA
1622	UGAAAUGC U UGCCGGGC	GCCCGGCA CUGAUGAG X CGAA ICAUUUCA
1626	AUGCUUGC C GGGCAGCC	GGCUGCCC CUGAUGAG X CGAA ICAAGCAU
1631	UGCCGGGC A GCCUCCAU	AUGGAGGC CUGAUGAG X CGAA ICCCGGCA
1634	CGGGCAGC C UCCAUUUG	CAAAUGGA CUGAUGAG X CGAA ICUGCCCG
1635	GGGCAGCC U CCAUUUGA	UCAAAUGG CUGAUGAG X CGAA IGCUGCCC
1637	GCAGCCUC C AUUUGAUG	CAUCAAAU CUGAUGAG X CGAA IAGGCUGC
1638	CAGCCUCC A UUUGAUGG	CCAUCAAA CUGAUGAG X CGAA IGAGGCUG
1664	AGACGAGC U AUUUCAGU	ACUGAAAU CUGAUGAG X CGAA ICUCGUCU
1670	GCUAUUUC A GUCUAUCA	UGAUAGAC CUGAUGAG X CGAA IAAAUAGC
1674	UUUCAGUC U AUCAUGGA	UCCAUGAU CUGAUGAG X CGAA IACUGAAA
1678	AGUCUAUC A UGGAGCAC	GUGCUCCA CUGAUGAG X CGAA IAUAGACU
1685	CAUGGAGC A CAACGUUU	AAACGUUG CUGAUGAG X CGAA ICUCCAUG
1687	UGGAGCAC A ACGUUUCC	GGAAACGU CUGAUGAG X CGAA IUGCUCCA
1695	AACGUUUC C UAUCCAAA	UUUGGAUA CUGAUGAG X CGAA IAAACGUU
1696	ACGUUUCC U AUCCAAAA	UUUUGGAU CUGAUGAG X CGAA IGAAACGU
1700	UUCCUAUC C AAAAUCCU	AGGAUUUU CUGAUGAG X CGAA IAUAGGAA
1701	UCCUAUCC A AAAUCCUU	AAGGAUUU CUGAUGAG X CGAA IGAUAGGA
1707	CCAAAAUC C UUGUCCAA	UUGGACAA CUGAUGAG X CGAA IAUUUUGG
1708	CAAAAUCC U UGUCCAAG	CUUGGACA CUGAUGAG X CGAA IGAUUUUG
1713	UCCUUGUC C AAGGAGGC	GCCUCCUU CUGAUGAG X CGAA IACAAGGA
1714	CCUUGUCC A AGGAGGCU	AGCCUCCU CUGAUGAG X CGAA IGACAAGG
1722	AAGGAGGC U GUUUCUAU	AUAGAAAC CUGAUGAG X CGAA ICCUCCUU
1728	GCUGUUUC U AUCUGCAA	UUGCAGAU CUGAUGAG X CGAA IAAACAGC
1732	UUUCUAUC U GCAAAGGA	UCCUUUGC CUGAUGAG X CGAA IAUAGAAA
1735	CUAUCUGC A AAGGACUG	CAGUCCUU CUGAUGAG X CGAA ICAGAUAG
1742	CAAAGGAC U GAUGACCA	UGGUCAUC CUGAUGAG X CGAA IUCCUUUG
1749	CUGAUGAC C AAACACCC	GGGUGUUU CUGAUGAG X CGAA IUCAUCAG
1750	UGAUGACC A AACACCCA	UGGGUGUU CUGAUGAG X CGAA IGUCAUCA
1754	GACCAAAC A CCCAGCCA	UGGCUGGG CUGAUGAG X CGAA IUUUGGUC
1756	CCAAACAC C CAGCCAAG	CUUGGCUG CUGAUGAG X CGAA IUGUUUGG
1757	CAAACACC C AGCCAAGC	GCUUGGCU CUGAUGAG X CGAA IGUGUUUG
1758	AAACACCC A GCCAAGCG	CGCUUGGC CUGAUGAG X CGAA IGGUGUUU
1761	CACCCAGC C AAGCGGCU	AGCCGCUU CUGAUGAG X CGAA ICUGGGUG
1762	ACCCAGCC A AGCGGCUG	CAGCCGCU CUGAUGAG X CGAA IGCUGGGU
1769	CAAGCGGC U GGGCUGUG	CACAGCCC CUGAUGAG X CGAA ICCGCUUG
1774	GGCUGGGC U GUGGGCCU	AGGCCCAC CUGAUGAG X CGAA ICCCAGCC
1781	CUGUGGGC C UGAGGGGG	CCCCCUCA CUGAUGAG X CGAA ICCCACAG
1782	UGUGGGCC U GAGGGGGA	UCCCCCUC CUGAUGAG X CGAA IGCCCACA
1808	GAGAGAGC A UGCCUUCU	AGAAGGCA CUGAUGAG X CGAA ICUCUCUC
1000		

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1812	GAGCAUGC C UUCUUCCG	CGGAAGAA CUGAUGAG X CGAA ICAUGCUC
1813	AGCAUGCC U UCUUCCGG	CCGGAAGA CUGAUGAG X CGAA IGCAUGCU
1816	AUGCCUUC U UCCGGAGG	CCUCCGGA CUGAUGAG X CGAA IAAGGCAU
1819	CCUUCUUC C GGAGGAUC	GAUCCUCC CUGAUGAG X CGAA IAAGAAGG
1831	GGAUCGAC U GGGAAAAA	UUUUUCCC CUGAUGAG X CGAA IUCGAUCC
1841	GGAAAAAC U GGAGAACA	UGUUCUCC CUGAUGAG X CGAA IUUUUUCC
1849	UGGAGAAC A GGGAGAUC	GAUCUCCC CUGAUGAG X CGAA IUUCUCCA
1858	GGGAGAUC C AGCCACCA	UGGUGGCU CUGAUGAG X CGAA IAUCUCCC
1859	GGAGAUCC A GCCACCAU	AUGGUGGC CUGAUGAG X CGAA IGAUCUCC
1862	GAUCCAGC C ACCAUUCA	UGAAUGGU CUGAUGAG X CGAA ICUGGAUC
1863	AUCCAGCC A CCAUUCAA	UUGAAUGG CUGAUGAG X CGAA IGCUGGAU
1865	CCAGCCAC C AUUCAAGC	GCUUGAAU CUGAUGAG X CGAA IUGGCUGG
1866	CAGCCACC A UUCAAGCC	GGCUUGAA CUGAUGAG X CGAA IGUGGCUG
1870	CACCAUUC A AGCCCAAA	UUUGGGCU CUGAUGAG X CGAA IAAUGGUG
1874	AUUCAAGC C CAAAGUGU	ACACUUUG CUGAUGAG X CGAA ICUUGAAU
1875	UUCAAGCC C AAAGUGUG	CACACUUU CUGAUGAG X CGAA IGCUUGAA
1876	UCAAGCCC A AAGUGUGU	ACACACUU CUGAUGAG X CGAA IGGCUUGA
1888	UGUGUGGC A AAGGAGCA	UGCUCCUU CUGAUGAG X CGAA ICCACACA
1896	AAAGGAGC A GAGAACUU	AAGUUCUC CUGAUGAG X CGAA ICUCCUUU
1903	CAGAGAAC U UUGACAAG	CUUGUCAA CUGAUGAG X CGAA IUUCUCUG
1909	ACUUUGAC A AGUUCUUC	GAAGAACU CUGAUGAG X CGAA IUCAAAGU
1915	ACAAGUUC U UCACACGA	UCGUGUGA CUGAUGAG X CGAA IAACUUGU
1918	AGUUCUUC A CACGAGGA	UCCUCGUG CUGAUGAG X CGAA IAAGAACU
1920	UUCUUCAC A CGAGGACA	UGUCCUCG CUGAUGAG X CGAA IUGAAGAA
1928	ACGAGGAC A GCCCGUCU	AGACGGGC CUGAUGAG X CGAA IUCCUCGU
1931	AGGACAGC C CGUCUUAA	UUAAGACG CUGAUGAG X CGAA ICUGUCCU
1932	GGACAGCC C GUCUUAAC	GUUAAGAC CUGAUGAG X CGAA IGCUGUCC
1936	AGCCCGUC U UAACACCA	UGGUGUUA CUGAUGAG X CGAA IACGGGCU
1941	GUCUUAAC A CCACCUGA	UCAGGUGG CUGAUGAG X CGAA IUUAAGAC
1943	CUUAACAC C ACCUGAUC	GAUCAGGU CUGAUGAG X CGAA IUGUUAAG
1944	UUAACACC A CCUGAUCA	UGAUCAGG CUGAUGAG X CGAA IGUGUUAA
1946	AACACCAC C UGAUCAGC	GCUGAUCA CUGAUGAG X CGAA IUGGUGUU
1947	ACACCACC U GAUCAGCU	AGCUGAUC CUGAUGAG X CGAA IGUGGUGU
1952	ACCUGAUC A GCUGGUUA	UAACCAGC CUGAUGAG X CGAA IAUCAGGU
1955	UGAUCAGC U GGUUAUUG	CAAUAACC CUGAUGAG X CGAA ICUGAUCA
1965	GUUAUUGC U AACAUAGA	UCUAUGUU CUGAUGAG X CGAA ICAAUAAC
1969	UUGCUAAC A UAGACCAG	CUGGUCUA CUGAUGAG X CGAA IUUAGCAA
1975	ACAUAGAC C AGUCUGAU	AUCAGACU CUGAUGAG X CGAA IUCUAUGU
1976	CAUAGACC A GUCUGAUU	AAUCAGAC CUGAUGAG X CGAA IGUCUAUG
1980	GACCAGUC U GAUUUUGA	UCAAAAUC CUGAUGAG X CGAA IACUGGUC
1996	AAGGGUUC U CGUAUGUC	GACAUACG CUGAUGAG X CGAA IAACCCUU
2005	CGUAUGUC A ACCCCCAG	CUGGGGGU CUGAUGAG X CGAA IACAUACG
2008	AUGUCAAC C CCCAGUUU	AAACUGGG CUGAUGAG X CGAA IUUGACAU
2009	UGUCAACC C CCAGUUUG	CAAACUGG CUGAUGAG X CGAA IGUUGACA
2010	GUCAACCC C CAGUUUGU	ACAAACUG CUGAUGAG X CGAA IGGUUGAC
2011	UCAACCCC C AGUUUGUG	CACAAACU CUGAUGAG X CGAA IGGGUUGA
2012	CAACCCCC A GUUUGUGC	GCACAAAC CUGAUGAG X CGAA IGGGGUUG
2021	GUUUGUGC A CCCCAUCU	AGAUGGGG CUGAUGAG X CGAA ICACAAAC
2023	UUGUGCAC C CCAUCUUA	UAAGAUGG CUGAUGAG X CGAA IUGCACAA
2024	UGUGCACC C CAUCUUAC	GUAAGAUG CUGAUGAG X CGAA IGUGCACA
2025	GUGCACCC C AUCUUACA	UGUAAGAU CUGAUGAG X CGAA IGGUGCAC
2323	STOCKES C HOOVENIA	TOTAL TELEVISION AND A TOTAL T

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2026	UGCACCCC A UCUUACAG	CUGUAAGA CUGAUGAG X CGAA IGGGUGCA
2029	ACCCCAUC U UACAGAGU	ACUCUGUA CUGAUGAG X CGAA IAUGGGGU
2033	CAUCUUAC A GAGUGCAG	CUGCACUC CUGAUGAG X CGAA IUAAGAUG
2040	CAGAGUGC A GUAUGAAA	UUUCAUAC CUGAUGAG X CGAA ICACUCUG
2050	UAUGAAAC U CACCAGCG	CGCUGGUG CUGAUGAG X CGAA IUUUCAUA
2052	UGANACUC A CCAGCGAG	CUCGCUGG CUGAUGAG X CGAA IAGUUUCA
2054	AAACUCAC C AGCGAGAA	UUCUCGCU CUGAUGAG X CGAA IUGAGUUU
2055	AACUCACC A GCGAGAAC	GUUCUCGC CUGAUGAG X CGAA IGUGAGUU
2064	GCGAGAAC A AACACCUC	GAGGUGUU CUGAUGAG X CGAA IUUCUCGC
2068	GAACAAAC A CCUCCCCA	UGGGGAGG CUGAUGAG X CGAA IUUUGUUC
2070	ACAAACAC C UCCCCAGC	GCUGGGGA CUGAUGAG X CGAA IUGUUUGU
2071	CAAACACC U CCCCAGCC	GGCUGGGG CUGAUGAG X CGAA IGUGUUUG
2073	AACACCUC C CCAGCCCC	GGGGCUGG CUGAUGAG X CGAA IAGGUGUU
2074	ACACCUCC C CAGCCCCC	GGGGGCUG CUGAUGAG X CGAA IGAGGUGU
2075	CACCUCCC C AGCCCCCA	UGGGGGCU CUGAUGAG X CGAA IGGAGGUG
2076	ACCUCCCC A GCCCCCAG	CUGGGGC CUGAUGAG X CGAA IGGGAGGU
2079	UCCCCAGC C CCCAGCCC	GGGCUGGG CUGAUGAG X CGAA ICUGGGGA
2080	CCCCAGCC C CCAGCCCU	AGGGCUGG CUGAUGAG X CGAA IGCUGGGG
2081	CCCAGCCC C CAGCCCUC	GAGGGCUG CUGAUGAG X CGAA IGGCUGGG
2082	CCAGCCCC C AGCCCUCC	GGAGGGCU CUGAUGAG X CGAA IGGGCUGG
2083	CAGCCCCC A GCCCUCCC	GGGAGGGC CUGAUGAG X CGAA IGGGGCUG
2086	CCCCCAGC C CUCCCCGC	GCGGGGAG CUGAUGAG X CGAA ICUGGGGG
2087	CCCCAGCC C UCCCCGCA	UGCGGGGA CUGAUGAG X CGAA IGCUGGGG
2088	CCCAGCCC U CCCCGCAG	CUGCGGGG CUGAUGAG X CGAA IGGCUGGG
2090	CAGCCCUC C CCGCAGUG	CACUGCGG CUGAUGAG X CGAA IAGGGCUG
2091	AGCCCUCC C CGCAGUGG	CCACUGCG CUGAUGAG X CGAA IGAGGGCU
2092	GCCCUCCC C GCAGUGGA	UCCACUGC CUGAUGAG X CGAA IGGAGGGC
2095	CUCCCCGC A GUGGAAGU	ACUUCCAC CUGAUGAG X CGAA ICGGGGAG
2109	AGUGAAUC C UUAACCCU	AGGGUUAA CUGAUGAG X CGAA IAUUCACU
2110	GUGAAUCC U UAACCCUA	UAGGGUUA CUGAUGAG X CGAA IGAUUCAC
2115	UCCUUAAC C CUAAAAUU	AAUUUUAG CUGAUGAG X CGAA IUUAAGGA
2116	CCUUAACC C UAAAAUUU	AAAUUUUA CUGAUGAG X CGAA IGUUAAGG
2117	CUUAACCC U AAAAUUUU	AAAAUUUU CUGAUGAG X CGAA IGGUUAAG
2131	UUUAAGGC C ACGCCUUG	CAAGCCGU CUGAUGAG X CGAA ICCUUAAA
2132	UUAAGGCC A CGGCUUGU	ACAAGCCG CUGAUGAG X CGAA IGCCUUAA
2137	GCCACGGC U UGUGUCUG	CAGACACA CUGAUGAG X CGAA ICCGUGGC
2144	CUUGUGUC U GAUUCCAU	AUGGAAUC CUGAUGAG X CGAA IACACAAG
2150	UCUGAUUC C AUAUGGAG	CUCCAUAU CUGAUGAG X CGAA IAAUCAGA
2151	CUGAUUCC A UAUGGAGG	CCUCCAUA CUGAUGAG X CGAA IGAAUCAG
2161	AUGGAGGC C UGAAAAUU	AAUUUUCA CUGAUGAG X CGAA ICCUCCAU
2162	UGGAGGCC U GAAAAUUG	CAAUUUUC CUGAUGAG X CGAA IGCCUCCA
2185	UAUUAGUC C AAAUGUGA	UCACAUUU CUGAUGAG X CGAA IACUAAUA
2186	AUUAGUCC A AAUGUGAU	AUCACAUU CUGAUGAG X CGAA IGACUAAU
2196	AUGUGAUC A ACUGUUCA	UGAACAGU CUGAUGAG X CGAA IAUCACAU
2199	UGAUCAAC U GUUCAGGG	CCCUGAAC CUGAUGAG X CGAA IUUGAUCA
2204	AACUGUUC A GGGUCUCU	AGAGACCC CUGAUGAG X CGAA IAACAGUU
2210	UCAGGGUC U CUCUCUUA	UAAGAGAG CUGAUGAG X CGAA IACCCUGA
2212	AGGGUCUC U CUCUUACA	UGUAAGAG CUGAUGAG X CGAA IAGACCCU
2214	GGUCUCUC U CUUACAAC	GUUGUAAG CUGAUGAG X CGAA IAGAGACC
2216	UCUCUCUC U UACAACCA	UGGUUGUA CUGAUGAG X CGAA IAGAGAGA
2220	UCUCUUAC A ACCAAGAA	UUCUUGGU CUGAUGAG X CGAA IUAAGAGA
		l l

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Table 63

2223 CUUACAAC C AAGAACAU	AUGUUCUU CUGAUGAG X CGAA IUUGUAAG
2224 UUACAACC A AGAACAUU	AAUGUUCU CUGAUGAG X CGAA IGUUGUAA
2230 CCAAGAAC A UUAUCUUA	UAAGAUAA CUGAUGAG X CGAA IUUCUUGG
2236 ACAUUAUC U UAGUGGAA	UUCCACUA CUGAUGAG X CGAA IAUAAUGU

Input Sequence = PRKCA. Cut Site = CH/.

Stem Length = 8 . Core Sequence = CUGAUGAG X CGAA (X = GCCGUUAGGC or other stem II) PRKCA (Homo sapiens protein kinase C, alpha (PRKCA) mRNA.; 2245 bp)

Table 64

Table 64: Activity of ribozyme core substituted analogues

A

RYH/ All ribo I-15.1 G-5, A-6, G-8, G-12, I-15.1 r			G-12, I-15.1 ribo	
	Kobs (min-1)	2'-O-allyl environment Kobs (min-1)		
		U-4=ribo U	U-4=2'-amino U	U-4=2'-O-alkyl U
GCA	0.39	0.10	0.08	0.02
GCC	0.19	0.03	0.01	0.003
GCU	0.028	0.025	0.013	0.002

В

RYH/	All ribo A-15.1 K _{obs} (min ⁻¹)	G-5, A-6, G-8, G-12, A-15.1 ribo 2'-O-allyl environment K _{obs} (min ⁻¹)		
		U-4=ribo U	U-4=2'-amino U	U-4=2'-O-alkyl U
GUA	0.12	0.06	0.04	0.01
GUC	0.15	0.015	0.014	0.001
GUU	0.04	0.031	0.012	0.008

Comparison of single turnover cleavage rates for GCH and GUH substrates with I-15.1 and A-15.1 ribozymes and ribozyme analogs. Conditions: Single turnover (250 nM substrate, $2.5 \mu M$ ribozyme) pH 6.0, 37 C, 10 mM Mg⁺⁺

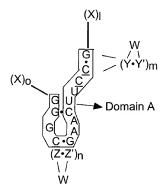
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Claims:

We claim:

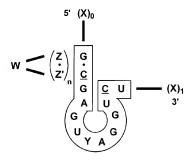
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5 1. An enzymatic nucleic acid molecule having formula 4 namely:



wherein each X, Y, and Z represents independently a nucleotide which may be the same or different; I is an integer greater than or equal to 3; m is an integer greater than 10 1; n is an integer greater than 1; 0 is an integer greater than or equal to 3; Z' is a nucleotide complementary to Z; Y' is a nucleotide complementary to Y; each X(I) and X(o) are oligonucleotides which are of sufficient length to stably interact independently with a target nucleic acid sequence; W is a linker of ≥ 2 nucleotides; A, U, G, and C represent nucleotides; C is 2'-amino; and ____ represents a chemical linkage.

An enzymatic nucleic acid molecule having formula 5 namely:



- 5 wherein each X, Y, and Z represents independently a nucleotide which may be the same or different; 1 is an integer greater than or equal to 3; n is an integer greater than 1; 0 is an integer greater than or equal to 3; Z' is a nucleotide complementary to Z; each X₍₁₎ and X₍₀₎ are oligonucleotides which are of sufficient length to stably interact independently with a target nucleic acid sequence; W is a linker of ≥ 2 nucleotides in length or may be a non-nucleotide linker; A, U, G, and C represent nucleotides; C is 2'-amino; and represents a chemical linkage.
 - The enzymatic nucleic acid molecule of claims 1 or 2, wherein 1 is selected from the group consisting of 4, 5, 6, 7, 8, 9, 10, 11, 12, and 15.
 - The enzymatic nucleic acid molecule of claim 1, wherein m is selected from the group consisting of 2, 3, 4, 5, 6, and 7.

- 5. The enzymatic nucleic acid molecule of claims 1 or 2, wherein n is selected from the group consisting of 2, 3, 4, 5, 6, and 7.
- The enzymatic nucleic acid molecule of claims 1 or 2, wherein o is selected from the group consisting of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, and 15.

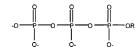
- The enzymatic nucleic acid molecule of claims 1 or 2, wherein 1 and 0 are of the same length.
- The enzymatic nucleic acid molecule of claims 1 or 2, wherein 1 and 0 are of different length.
- The enzymatic nucleic acid molecule of claims 1 or 2, wherein the target nucleic acid sequence is selected from the group consisting of an RNA, DNA and RNA/DNA mixed polymer.
 - 10. The enzymatic nucleic acid molecule of claims 1 or 2, wherein said chemical linkage is selected from the group consisting of phosphate ester linkage, amide linkage, phosphorothioate, and phosphorodithioate.
 - The enzymatic nucleic acid molecule of claims 1 or 2, wherein said <u>Clis</u> selected from the group consisting of 2'-deoxy-2'-NH₂ and 2'-deoxy-2'-O-NH₂.
 - 12. A method for inhibiting expression of a gene in a cell, comprising the step of administering to said cell the enzymatic nucleic acid molecule of claims 1 or 2 under conditions suitable for said inhibition.
 - 13. A method of cleaving a separate RNA molecule comprising, contacting the enzymatic nucleic acid molecule of claims 1 or 2 with said separate RNA molecule under conditions suitable for the cleavage of said separate RNA molecule.
 - 14. The method of claim 13, wherein said cleavage is carried out in the presence of a divalent cation.
 - 15. The method of claim 14, wherein said divalent cation is Mg2+.

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- 16. The enzymatic nucleic acid molecule of claims 1 or 2, wherein said enzymatic nucleic acid molecule is chemically synthesized.
- 17. The enzymatic nucleic acid molecule of claims 1 or 2, wherein said enzymatic nucleic acid molecule comprises at least one ribonucleotide.
- 18. The enzymatic nucleic acid molecule of claims 1 or 2, wherein said enzymatic nucleic acid molecule comprises no ribonucleotide residues.
- 19. The enzymatic nucleic acid molecule of claims 1 or 2, wherein said enzymatic nucleic acid molecule comprises at least one 2-amino modification.

- 20. The enzymatic nucleic acid molecule of claims 1 or 2, wherein said enzymatic nucleic acid molecule comprises at least three phosphorothioate modifications.
- 21. The enzymatic nucleic acid molecule of claim 20, wherein said phosphorothioate modification is at the 5'-end of said enzymatic nucleic acid molecule.
- 22. The enzymatic nucleic acid molecule of claims 1 or 2, wherein said enzymatic nucleic acid molecule comprises a 5'-cap or a 3'-cap or both a 5'-cap and a 3'-cap.
 - 23. The enzymatic nucleic acid molecule of claim 22, wherein said 5-cap is phosphorothioate modification.
 - 24. The enzymatic nucleic acid molecule of claim 22, wherein said 3'-cap is an inverted abasic moiety.
 - 25. A compound having the formula 3:



wherein R is independently any nucleoside selected from the group consisting of 2'-Omethyl-2,6-diaminopurine riboside: 2'-deoxy-2'amino-2,6-diaminopurine riboside: 2'-15 (N-alanyl) amino-2'-deoxy-uridine; 2'-(N-phenylalanyl)amino-2'-deoxy-uridine; 2'deoxy -2'-(N-β-alanyl) amino; 2'-deoxy-2'-(lysiyl) amino uridine; 2'-C-allyl uridine; 2'-O-amino-uridine; 2'-O-methylthiomethyl adenosine; 2'-O-methylthiomethyl cytidine; 2'-O-methylthiomethyl guanosine; 2'-O-methylthiomethyl-uridine; 2'deoxy-2'-(N-histidyl) amino uridine; 2'-deoxy-2'-amino-5-methyl cytidine; 2'-(N-βcarboxamidine-β-alanyl)amino-2'-deoxy-uridine; 2'-deoxy-2'-(N-β-alanyl)-guanosine; 20 2'-O-amino-adenosine; 2'-(N-1ysyl)amino-2'-deoxy-cytidine; 2'-Deoxy -2'-(Lhistidine) amino Cytidine; 5-Imidazoleacetic acid 2'-deoxy uridine, 5-[3-(N-4imidazoleacetyl)aminopropynyl]-2'-O-methyl uridine, 5-(3-aminopropynyl)-2'-Omethyl uridine. 5-(3-aminopropyl)-2'-O-methyl uridine. 5-[3-(N-4imidazoleacetyl)aminopropyl]-2'-O-methyl uridine, 5-(3-aminopropyl)-2'-deoxy-2fluoro uridine, 2'-Deoxy-2'-(B-alanyl-L-histidyl)amino uridine, 2'-deoxy-2'-Balaninamido-uridine. 3-(2'-deoxy-2'-fluoro-\(\theta\)-ribofuranosyl)piperazino[2.3-Dlpyrimidine-2-one. 5-[3-(N-4-imidazoleacetyl)aminopropyl]-2'-deoxy-2'-fluoro uridine, 5-[3-(N-4-imidazoleacetyl)aminopropynyl]-2'-deoxy-2'-fluoro uridine, 5-E- (2-carboxyvinyl-2'-deoxy-2'-fluoro uridine, 5-[3-(N-4-aspartyl)aminopropynyl-2'-fluoro uridine, 5-(3-aminopropyl)-2'-deoxy-2-fluoro cytidine, and 5-[3-(N-4-succynyl)aminopropyl-2'-deoxy-2-fluoro cytidine.

26. A process for incorporation of the compounds of claim 25 into an oligonucleotide comprising the step of contacting said compound with a mixture comprising a nucleic acid template, an RNA polymerase enzyme, and an enhancer of modified nucleotide triphosphate incorporation, under conditions suitable for the incorporation of said compound into said oligonucleotide.

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- 27. The process of claim 26, wherein said RNA polymerase is a T7 RNA polymerase.
- 0 28. The process of claim 26, wherein said RNA polymerase is a mutant T7 RNA polymerase.
 - 29. The process of claim 26, wherein said RNA polymerase is a SP6 RNA polymerase.
 - The process of claim 26, wherein said RNA polymerase is a mutant SP6 RNA polymerase.
- 31. The process of claim 26, wherein said RNA polymerase is a T3 RNA polymerase.
 - 32. The process of claim 26, wherein said RNA polymerase is a mutant T3 RNA polymerase.
 - 33. The process of claim 26, wherein said enhancer of modified nucleotide triphosphate incorporation is selected from the group consisting of LiCl, methanol, polyethylene glycol, diethyl ether, propanol, methylamine, and ethanol.
 - 34. A process for the synthesis of a pyrimidine nucleotide triphosphate comprising the steps of:
- a. monophosphorylation, wherein a pyrimidine nucleoside is contacted with a mixture comprising a phosphorylating reagent, a trialkyl phosphate and 25 dimethylaminopyridine, under conditions suitable for the formation of a pyrimidine nucleotide monophosphate; and

b. pyrophosphorylation, wherein said pyrimidine monophosphate from step (a) is contacted with a pyrophosphorylating reagent under conditions suitable for the formation of said pyrimidine nucleotide triphosphate.

- 35. The process of claim 34, wherein said pyrimidine nucleoside triphosphate is uridine triphosphate.
- The process of claim 34, wherein said uridine triphosphate has a 2'-sugar modification.
- 37. The process of claim 36, wherein said uridine triphosphate is 2*-O-methylthiomethyl uridine triphosphate.
 - 38. The process of claim 34, wherein said phosphorylating agent is selected from the group consisting of phosphorus oxychloride, phospho-tris-triazolides and phosphotris-triimidazolides.
- 10 39. The process of claim 34, wherein said trialkylphosphate is triethyl phosphate.
 - The process of claim 34, wherein said pyrophosphorylating reagent is tributyl ammonium pyrophosphate.
 - 41. The process of claim 26, wherein said oligonucleotide is RNA.
- 42. The process of claim 26, wherein said oligonucleotide is an enzymatic nucleic acid molecule.
 - 43. The process of claim 26, wherein said oligonucleotide is an aptamer.
 - 44. A kit for synthesis of an oligonucleotide comprising an RNA polymerase, an enhancer of modified nucleotide triphosphate incorporation and at least one compound of claim 25.
- 45. A kit for synthesis of an oligonucleotide comprising a DNA polymerase, an enhancer of modified nucleotide triphosphate incorporation and at least one compound of claim 25.
 - 46. The kit of claim 44, wherein said RNA polymerase is a bacteriophage T7 RNA polymerase.
- 47. The kit of claim 44, wherein said RNA polymerase is a bacteriophage SP6 RNA polymerase.
 - The kit of claim 44, wherein said RNA polymerase is a bacteriophage T3 RNA polymerase.

- The kit of claim 44, wherein said RNA polymerase is a mutant T7 RNA polymerase.
- 50. The kit of claim 44 or 45, wherein said kit comprises at least two different compounds of claim 25.
- 5 51. A nucleic acid catalyst comprising a histidyl modification, wherein said nucleic acid catalyst is able to catalyze an endonuclease reaction in the absence of a metal ion co-factor.
 - 52. The nucleic acid catalyst of claim 51, wherein said catalyst is able to cleave a separate nucleic acid molecule.
- 53. The nucleic acid catalyst of claim 52, wherein said separate nucleic acid molecule is an RNA molecule.
 - 54. The nucleic acid catalyst of claim 52, wherein said separate nucleic acid molecule is a DNA molecule.
 - 55. The nucleic acid catalyst of claim 51, wherein said nucleic acid catalyst comprises at least one ribonucleotide.
 - 56. The enzymatic nucleic acid molecule of claim 2, wherein said nucleic acid molecule has an endonuclease activity to cleave RNA of HER2 gene.
 - 57. The enzymatic nucleic acid molecule of claim 56, wherein said nucleic acid molecule comprises sequences complementary to any of substrate sequences defined as Target sequence in Tables 58, 59 and 62.
 - 58. The enzymatic nucleic acid molecule of claim 56, wherein said nucleic acid molecule comprises any of ribozyme sequences defined as Ribozyme sequence in Tables 58, 59 and 62.
 - A method for treating cancer using the enzymatic nucleic acid molecule of claim
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 - 60. The method of claim 59, wherein said cancer is breast cancer.

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61. A method for treating conditions associated with the level of HER2 gene using the enzymatic nucleic acid molecule of claim 56.

- 62. The enzymatic nucleic acid molecule of claim 56, wherein said enzymatic nucleic acid molecule comprises a substrate binding region which has between 5 and 30 nucleotides complementary to the RNA.
- 63. The enzymatic nucleic acid molecule of claim 56, wherein said enzymatic nucleic acid molecule comprises a substrate binding region which has between 7 and 12 nucleotides complementary to the RNA.

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- 64. A mammalian cell including the enzymatic nucleic acid molecule of claim 56.
- 65. The mammalian cell of claim 64, wherein said mammalian cell is a human cell.
- 66. A mammalian cell including the enzymatic nucleic acid molecule of claims 1 or 2.
- 67. The mammalian cell of claim 66, wherein said mammalian cell is a human cell.
 - 68. A method for inhibiting expression of HER2 gene in a cell, comprising the step of administering to said cell the enzymatic nucleic acid molecule of claim 56 under conditions suitable for said inhibition.
- 69. A method of cleaving RNA derived from HER2 gene comprising, contacting the enzymatic nucleic acid molecule of claim 56 with said RNA molecule under conditions suitable for the cleavage of said RNA molecule.
 - 70. A pharmaceutical composition comprising the enzymatic nucleic acid molecule of any of claims 1 or 2.
- A pharmaceutical composition comprising the enzymatic nucleic acid molecule of claim 56.
- 72. A method of treatment of a patient having a condition associated with the level of HER2, wherein said patient is administered the enzymatic nucleic acid molecule of claim 56 under conditions suitable for said treatment.
- 73. The method of claim 72, wherein said method is performed in conjunction with one or more other therapies.
- 74. The method of claim 59, wherein said enzymatic nucleic acid molecule is used in conjunction with one or more other therapies.
- 75. The enzymatic nucleic acid molecule of claim 56, wherein said enzymatic nucleic acid molecule comprises at least one sugar modification.

- 76. The enzymatic nucleic acid molecule of claim 56, wherein said enzymatic nucleic acid molecule comprises at least one nucleic acid base modification.
- 77. The enzymatic nucleic acid molecule of claim 56, wherein said enzymatic nucleic acid molecule comprises at least one phosphate backbone modification.
- 5 78. The enzymatic nucleic acid molecule of claim 56, wherein said phosphate backbone modification is selected from the group consisting of phosphorothioate, phosphorodithioate and amide.
 - 79. An enzymatic nucleic acid molecule which down regulates expression of genes selected from the group consisting of beta site APP-cleaving enzyme (BACE) and telomerase reverse transcintase (TERT) genes.

- The enzymatic nucleic acid molecule of claim 79, wherein said gene is the beta site APP-cleaving enzyme (BACE).
- 81. The enzymatic nucleic acid molecule of claim 79, wherein said gene is the telomerase reverse transcriptase (TERT).
- 5 82. A nucleic acid molecule which down regulates expression of genes selected from the group consisting of protein-tyrosine phosphatase-1B (PTP-1B), methionine aminopeptidase (MetAP-2), hepatitis B virus (HBV), phospholamban (PLN), and presentilin (ns-2) genes.
 - 83. The nucleic acid molecule of claim 82, wherein said nucleic acid molecule is an enzymatic nucleic acid molecule.
 - 84. The nucleic acid molecule of claim 82, wherein said nucleic acid molecule is an antisense nucleic acid molecule.
 - 85. The nucleic acid molecule of any of claims 82-84, wherein said gene is the proteintyrosine phosphatase-1B (PTP-1B).
- 86. The nucleic acid molecule of any of claims 82-84, wherein said gene is the methionine aminopeptidase (MetAP-2).
 - The nucleic acid molecule of any of claims 82-84, wherein said gene is the hepatitis B virus (HBV).

- 88. The nucleic acid molecule of any of claims 82-84, wherein said gene is the phospholamban (PLN).
- The nucleic acid molecule of any of claims 82-84, wherein said gene is the presenilin (ps-2).
- 5 90. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule is adapted for use to treat diseases and conditions related to the expression of genes selected from the group consisting of beta site APP-cleaving enzyme (BACE), telomerase reverse transciptase (TERT), proteintyrosine phosphatase-1B (PTP-1B), methionine aminopeptidase (MetAP-2), hepatitis B virus (HBV), phospholamban (PLN), and presenilin (ps-2) genes.
 - 91. The nucleic acid molecule of claim 82, wherein said nucleic acid molecule is adapted for use to treat diseases and conditions related to the expression of genes selected from the group consisting of protein-tyrosine phosphatase-1B (PTP-1B), methionine aminopeptidase (MetAP-2), hepatitis B virus (HBV), phospholamban (PLN), and presentlin (ps-2) genes.

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- 92. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule has an endonuclease activity to cleave RNA encoded by said beta site APP-cleaving enzyme (BACE), telomerase reverse transciptase (TERT), protein-tyrosine phosphatase-1B (PTP-1B), methionine aminopeptidase (MetAP-2), hepatitis B virus (HBV), phospholamban (PLN), and presenilin (ps-2) genes.
- 93. The enzymatic nucleic acid of any of claims 79 or 83, wherein a binding arm of said enzymatic nucleic acid molecule comprise sequences complementary to any of the sequences defined as Target or Substrate sequence in Tables 3-30, and 36-43.
- 94. The enzymatic nucleic acid molecule of any of claims 79 or 83 wherein said enzymatic nucleic acid molecule comprises any of the sequences defined as Ribozyme or DNAzyme sequence in Tables 3-29, and 37-43.
- 95. The nucleic acid molecule of claim 84, wherein said antisense nucleic acid molecule comprises sequence complementary to any of the sequences defined as Target or Substrate sequence in Tables 3-12, 24-30, and 36-43.

- 96. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule is in a hammerhead (HH) motif.
- The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule is in a zinzyme (Class II) motif.
- 98. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule is in a amberzyme (Class 1) motif.
 - 99. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule is in a hairpin, hepatitis Delta virus, group I intron. VS nucleic acid. or RNAse P nucleic acid motif.
- 10 100. The enzymatic nucleic acid molecule of claim 97, wherein said zinzyme motif comprises sequences complementary to any of the substrate sequences shown in Tables 21, 27 and 40.
 - 101. The enzymatic nucleic acid molecule of claim 98, wherein said amberzyme motif comprises sequences complementary to any of the substrate sequences shown in Tables 23, 29, and 42.

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- 102. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule is in a NCH motif.
- 103. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule is in a G-cleaver motif.
- 20 104. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule is a DNAzyme.
 - 105. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule comprises between 12 and 100 bases complementary to the RNA of genes selected from the group consisting of beta site APP-cleaving enzyme (BACE), telomerase reverse transciptase (TERT), protein-tyrosine phosphatase-1B (PTP-1B), methionine aminopeptidase (MetAP-2), hepatitis B virus (HBV), phospholamban (PLN), and presentlin (ps-2) genes.
 - 106. The enzymatic nucleic acid of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule comprises between 14 and 24 bases complementary to the RNA of genes selected from the group consisting of beta site APP-cleaving enzyme (BACE), telomerase reverse transciptase (TERT), protein-tyrosine

- phosphatase-1B (PTP-1B), methionine aminopeptidase (MetAP-2), hepatitis B virus (HBV), phospholamban (PLN), and presenilin (ps-2) genes.
- 107. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid is chemically synthesized.
- 108. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid comprises at least one 2'-sugar modification.
 - 109. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid comprises at least one nucleic acid base modification.
- 110. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid comprises at least one phosphate backbone modification.

- 111. A mammalian cell including the enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said mammalian cell is not a living human.
- The mammalian cell of claim 111, wherein said mammalian cell is a human cell.
- 15 113. The antisense nucleic acid molecule of claim 84, wherein said antisense nucleic acid is chemically synthesized.
 - 114. The antisense nucleic acid molecule of claim 84, wherein said antisense nucleic acid comprises at least one 2'-sugar modification.
 - 115. The antisense nucleic acid molecule of claim 84, wherein said antisense nucleic acid comprises at least one nucleic acid base modification.
 - 116. The antisense nucleic acid molecule of claim 84, wherein said antisense nucleic acid comprises at least one phosphate backbone modification.
 - 117. A mammalian cell including the antisense nucleic acid molecule of claim 84, wherein said mammalian cell is not a living human.
- 25 118. The mammalian cell of claim 117, wherein said mammalian cell is a human cell
 - 119. A method of reducing BACE activity in a cell, comprising the step of contacting said cell with the enzymatic nucleic acid molecule of claim 80, under conditions suitable for said inhibition.

- 120. A method of reducing TERT activity in a cell, comprising the step of contacting said cell with the enzymatic nucleic acid molecule of claim 81, under conditions suitable for said inhibition.
- 121. A method of reducing PTP-1B activity in a cell, comprising the step of contacting said cell with the nucleic acid molecule of claim 85, under conditions suitable for said inhibition.
 - 122. A method of reducing MetAP-2 activity in a cell, comprising the step of contacting said cell with the nucleic acid molecule of claim 86, under conditions suitable for said inhibition.
- 10 123. A method of reducing HBV activity in a cell, comprising the step of contacting said cell with the nucleic acid molecule of claim 87, under conditions suitable for said inhibition.
 - 124. A method of reducing phospholamban (PLN) activity in a cell, comprising the step of contacting said cell with the nucleic acid molecule of claim 88, under conditions suitable for said inhibition.

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- 125. A method of reducing presenilin-2 (ps-2) activity in a cell, comprising the step of contacting said cell with the nucleic acid molecule of claim 89, under conditions suitable for said inhibition.
- 126. A method of treatment of a patient having a condition associated with the level of BACE, comprising contacting cells of said patient with the enzymatic nucleic acid molecule of claim 80, under conditions suitable for said treatment.
- 127. A method of treatment of a patient having a condition associated with the level of TERT, comprising contacting cells of said patient with the enzymatic nucleic acid molecule of claim 81, under conditions suitable for said treatment.
- 25 128. A method of treatment of a patient having a condition associated with the level of PTP-1B, comprising contacting cells of said patient with the nucleic acid molecule of claim 85, under conditions suitable for said treatment.
 - 129. A method of treatment of a patient having a condition associated with the level of MetAP-2, comprising contacting cells of said patient with the nucleic acid molecule of claim 86, under conditions suitable for said treatment.

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- 130. A method of treatment of a patient having a condition associated with the level of HBV, comprising contacting cells of said patient with the nucleic acid molecule of claim 87, under conditions suitable for said treatment.
- 131. A method of treatment of a patient having a condition associated with the level of phospholamban (PLN), comprising contacting cells of said patient with the nucleic acid molecule of claim 88, under conditions suitable for said treatment.
 - A method of treatment of a patient having a condition associated with the level of presenilin-2 (ps-2), comprising contacting cells of said patient with the nucleic acid molecule of claim 89, under conditions suitable for said treatment.
- 133. The method of any of claims 126-132 further comprising the use of one or more drug therapies under conditions suitable for said treatment.
 - 134. A method of cleaving RNA of BACE gene, comprising, contacting the enzymatic nucleic acid molecule of claim 80, with said RNA under conditions suitable for the cleavage of said RNA.
- 15 135. A method of cleaving RNA of TERT gene, comprising, contacting the enzymatic nucleic acid molecule of claim 81, with said RNA under conditions suitable for the cleavage of said RNA.
 - 136. A method of cleaving RNA of PTP-1B gene, comprising, contacting the enzymatic nucleic acid molecule of claim 85, with said RNA under conditions suitable for the cleavage of said RNA.

- A method of cleaving RNA of MetAP-2 gene, comprising, contacting the enzymatic nucleic acid molecule of claim 86, with said RNA under conditions suitable for the cleavage of said RNA.
- 138. A method of cleaving RNA of HBV gene, comprising, contacting the enzymatic nucleic acid molecule of claim 87, with said RNA under conditions 25 suitable for the cleavage of said RNA.
 - 139. A method of cleaving RNA of phospholamban (PLN) gene, comprising, contacting the enzymatic nucleic acid molecule of claim 88, with said RNA under conditions suitable for the cleavage of said RNA.

- 140. A method of cleaving RNA of presenilin-2 (ps-2) gene, comprising, contacting the enzymatic nucleic acid molecule of claim 89, with said RNA under conditions suitable for the cleavage of said RNA.
- 141. The method of any of claims 134-140, wherein said cleavage is carried out in the presence of a divalent cation.
 - The method of claim 141, wherein said divalent cation is Mg2+.

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- 143. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid comprises a cap structure, wherein the cap structure is at the 5'-end or 3'-end or both the 5'-end and the 3'-end
- 144. The antisense nucleic acid molecule of claim 84, wherein said antisense nucleic acid comprises a cap structure, wherein the cap structure is at the 5'-end or 3'-end or both the 5'-end and the 3'-end.
 - 145. The enzymatic nucleic acid molecule of claim 96, wherein said hammerhead motif comprises sequences complementary to any of sequences defined as Target or Substrate sequences in Tables 3, 9, 13, 18, 24, and 37.
 - 146. The enzymatic nucleic acid molecule of claim 102, wherein said NCH motif comprises sequences complementary to any of sequences defined as Target or Substrate sequences in Tables 4, 10, 14, 19, 25, and 38.
 - The enzymatic nucleic acid molecule of claim 103, wherein said G-cleaver motif comprises sequences complementary to any of sequences defined as Target or Substrate sequences in Tables 5, 11, 15, 20, 26, and 39.
 - 148. The enzymatic nucleic acid molecule of claim 104, wherein said DNAzyme comprises sequences complementary to any of sequences defined as Target or Substrate sequences in Tables 6, 16, 22, 28, and 41.
- 5 149. The method of any of claims 119-125 or 133, wherein said enzymatic nucleic acid molecule is in a hammerhead motif.
 - 150. The method of any of claims 119-125 or 133, wherein said nucleic acid molecule is a DNAzyme.

- 151. An expression vector comprising nucleic acid sequence encoding at least one enzymatic nucleic acid molecule of any of claims 79 or 83, in a manner which allows expression of that enzymatic nucleic acid molecule.
- 152. An expression vector comprising nucleic acid sequence encoding at least one antisense nucleic acid molecule of claim 84, in a manner which allows expression of that antisense nucleic acid molecule.

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- 153. A mammalian cell including an expression vector of any of claims 151 or 152, wherein said mammalian cell is not a living human.
- 154. The mammalian cell of claim 153, wherein said mammalian cell is a human cell
- 155. The expression vector of claim 151, wherein said enzymatic nucleic acid molecule is in a hammerhead motif.
- 156. The expression vector of claim 151, wherein said expression vector further comprises a sequence for an antisense nucleic acid molecule complementary to the RNA of genes selected from the group consisting of beta site APP-cleaving enzyme (BACE), telomerase reverse transciptase (TERT), protein-tyrosine phosphatase-1B (PTP-1B), methionine aminopeptidase (MetAP-2), hepatitis B virus (HBV), phospholamban (PLN), and presentlin (ps-2) genes.
- 157. The expression vector of claim 151, wherein said expression vector comprises sequence encoding at least two said enzymatic nucleic acid molecules, which may be same or different.
 - 158. The expression vector of claim 157, wherein one said expression vector further comprises sequence encoding antisense nucleic acid molecule complementary to the RNA of genes selected from the group consisting of beta site APP-cleaving enzyme (BACE), telomerase reverse transciptase (TERT), protein-tyrosine phosphatase-1B (PTP-1B), methionine aminopeptidase (MetAP-2), hepatitis B virus (HBV), phospholamban (PLN), and presenilin (ps-2) genes.
- 159. A method for treatment of Alzheimer's disease comprising the step of administering to a patient the enzymatic nucleic acid molecule of claim 80 under conditions suitable for said treatment.

- The method of claim 159, wherein said treatment of Alzheimer's disease is treatment of dementia
- A method for treatment of Alzheimer's disease comprising the step of administering to a patient the antisense nucleic acid molecule of claim 89 under conditions suitable for said treatment.
- A method for treatment of diabetes comprising the step of administering to a natient the nucleic acid molecule of claim 85 under conditions suitable for said treatment.
- The method of claim 162, wherein said diabetes is type I diabetes.
- 164. The method of claim 162, wherein said diabetes is type II diabetes.
 - 165. A method for treatment of diabetes comprising the step of administering to a patient the antisense nucleic acid molecule of claim 85 under conditions suitable for said treatment.
 - A method for treatment of obesity comprising the step of administering to a patient the nucleic acid molecule of claim 85 under conditions suitable for said treatment.
 - A method for treatment of obesity comprising the step of administering to a patient the antisense nucleic acid molecule of claim 85 under conditions suitable for said treatment
- A method for treatment of heart disease comprising the step of administering to a patient the nucleic acid molecule of claim 88 under conditions suitable for said treatment.
 - 169 The method of claim 168, wherein said heart disease is heart failure.
 - 170. The method of claim 168, wherein said heart disease is congestive heart failure.
- 25 171. A method for treatment of pressure overload hypertrophy, or dilated cardiomyopathy, or both, comprising the step of administering to a patient the nucleic acid molecule of claim 88 under conditions suitable for said treatment.

- 172. A method for treatment of cancer comprising the step of administering to a patient the nucleic acid molecule of claim 86 under conditions suitable for said treatment.
- 173. A method for treatment of hepatitis comprising the step of administering to a patient the nucleic acid molecule of claim 87 under conditions suitable for said treatment.

- 174. A method for treatment of hepatocellular carcinoma comprising the step of administering to a patient the nucleic acid molecule of claim 87 under conditions suitable for said treatment.
- 0 175. The method of claim 159, wherein said enzymatic nucleic acid molecule is in a hammerhead motif
 - 176. The method of claim 159, wherein said method further comprises administering to said patient the enzymatic nucleic acid molecule in conjunction with one or more of other therapies.
- 5 177. The method of any of claims 162, 165-168, or 171-174, wherein said nucleic acid molecule is an enzymatic nucleic acid molecule.
 - 178. The method of any of claims 162, 166-168, or 171-174, wherein said nucleic acid molecule is an antisense nucleic acid molecule.
- 179. The method of any of claims 162, 165-168, or 171-174, wherein said method further comprises administering to said patient the nucleic acid molecule in conjunction with one or more of other therapies.
 - 180. The enzymatic nucleic acid molecule of any of claims 79 or 83, wherein said enzymatic nucleic acid molecule comprises at least five ribose residues; at least ten 2'-O-methyl modifications, and a 3'- end modification.
 - 5 181. The enzymatic nucleic acid molecule of claim 180, wherein said enzymatic nucleic acid molecule further comprises phosphorothioate linkages on at least three of the 5' terminal nucleotides.
 - 182. The enzymatic nucleic acid molecule of claim 180, wherein said 3'- end modification is 3'-3' inverted abasic moiety.

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- The enzymatic nucleic acid molecule of claim 104, wherein said DNAzyme comprises at least ten 2'-O-methyl modifications and a 3'-end modification.
- 184. The enzymatic nucleic acid molecule of claim 183, wherein said DNAzyme further comprises phosphorothioate linkages on at least three of the 5' terminal nucleotides.
- 185. The enzymatic nucleic acid molecule of claim 183, wherein said 3'- end modification is 3'-3' inverted abasic moiety.
- 186. An enzymatic nucleic acid molecule having formula 1:

$$L \xrightarrow{(N)} {}_{n-(N)p-A-G-N-A-G-U-C-E-s}$$

wherein N represents independently a nucleotide or a non-nucleotide linker, which may be same or different; D and E are independently oligonucleotides of length sufficient to stably interact with a target RNA molecule; o and n are integers independently greater than or equal to 1, wherein if (N)o and (N)n are nucleotides. (N)o and (N)n are optionally able to interact by hydrogen bond interaction; • indicates base-paired interaction; L is a linker which may be present or absent, but when present, is a nucleotide linker, a non-nucleotide linker, or a combination of nucleotide and a non-nucleotide linker; p is an integer 0 or 1; represents a chemical linkage; and A. U. I. C and G represent adenosine, uridine, inosine, cytidine and guanosine nucleotides, respectively.

187. An enzymatic nucleic acid molecule having formula 2:

$$L \xrightarrow{(N) \ n} G^{-}(N)_{p}^{-}A^{-}G^{-}N^{-}A^{-}G^{-}U^{-}C^{-}E^{-}s^{-}$$

wherein N represents independently a nucleotide or a non-nucleotide linker, which may be same or different: D and E are independently oligonucleotides of length sufficient to stably interact with a target RNA molecule; o and n are integers independently greater than or equal to 0, wherein if (N)o and (N)n are nucleotides,

- (N)o and (N)n are optionally able to interact by hydrogen bond interaction; indicates base-paired interaction; L is a linker which may be present or absent, but when present, is a nucleotide linker, a non-nucleotide linker, or a combination of nucleotide and a non-nucleotide linker; p is an integer 0 or 1; represents a chemical linkage; and A, U, I, C and G represent adenosine, uridine, inosine, cytidine and
- guanosine nucleotides, respectively.
 - 188. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said D and E are independently of length selected from the group consisting of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, and 20 nucleotides.
- 189. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said D and E are of the same length.
 - 190. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said D and E are of different length.
 - 191. The enzymatic nucleic acid molecule of claim 186, wherein said o and n are independently integers selected from the group consisting of 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, and 50.

- 192. The enzymatic nucleic acid molecule of claim 187, wherein said o and n are independently integers selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, and 50.
- 20 193. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said (N)o and (N)n comprise nucleotides that are complementary to each other.
 - 194. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said (N)o and (N)n are of the same length.
- 195. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said (N)o and (N)n are of different length.
 - The enzymatic nucleic acid molecule of claims 186 or 187, wherein said L is a nucleotide linker.
 - 197. The enzymatic nucleic acid molecule of claim 196, wherein said nucleotide linker is of length between 3-50 nucleotides.

- 198. The enzymatic nucleic acid molecule of claim 196, wherein said nucleotide linker is an antamer.
- 199. The enzymatic nucleic acid molecule of claim 196 wherein said nucleotide linker is selected from the group consisting of 5'-GAAA-3' and 5'-GUUA-3'.
- 200. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said L is a non-nucleotide linker.
 - 201. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said chemical linkage is independently or in combination selected from the group consisting of phosphate ester linkage, amide linkage, phosphorothioate, arabino, arabinofluoro, and phosphorodithioate.
 - 202. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said p is 1.

- 203. The enzymatic nucleic acid molecule of claim 202, wherein said N of (N)p is independently selected from the group consisting of adenosine, uridine, and cytidine.
- 15 204. The enzymatic nucleic acid molecule of claims 186 or 187 wherein said enzymatic nucleic acid molecule is chemically synthesized.
 - 205. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said enzymatic nucleic acid molecule comprises at least three ribonucleotide residues.
 - 206. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said enzymatic nucleic acid molecule comprises at least four ribonucleotide residues.
 - 207. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said enzymatic nucleic acid molecule comprises at least five ribonucleotide residues.
 - 208. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said I is selected from the group consisting of ribo-inosine and xylo-inosine.
- 25 209. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said enzymatic nucleic acid molecule comprises at least one sugar modification.
 - 210. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said enzymatic nucleic acid molecule comprises at least nucleic acid base modification.

- 211. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said enzymatic nucleic acid molecule comprises at least one phosphate backbone modification.
- 212. The enzymatic nucleic acid molecule of claim 209, wherein said sugar modification is selected from the group consisting of 2'-H, 2'-O-methyl, 2'-O-allyl, and 2'-deoxy-2'-amino.
 - 213. The enzymatic nucleic acid molecule of claim 211, wherein said phosphate backbone modification is selected from the group consisting of phosphorothioate, phosphorodithioate and amide.
- 214. The enzymatic nucleic acid molecule of claims 186 or 187 wherein said enzymatic nucleic acid molecule comprises a 5'-cap or a 3'-cap or both a 5'-cap and a 3'-cap.
 - 215. The enzymatic nucleic acid molecule of claim 214, wherein said 5'-cap is a phosphorothioate modification of at least one 5'-terminal nucleotide in said enzymatic nucleic acid molecule.

- 216. The enzymatic nucleic acid molecule of claim 214, wherein said 5'-cap is a phosphorothioate modification of at least two 5'-terminal nucleotide in said enzymatic nucleic acid molecule.
- 217. The enzymatic nucleic acid molecule of claim 214, wherein said 5'-cap is a phosphorothioate modification of at least three 5'-terminal nucleotide in said enzymatic nucleic acid molecule.
 - 218. The enzymatic nucleic acid molecule of claim 214, wherein said 3'-cap is a 3'-3' inverted abasic moiety.
- 219. The enzymatic nucleic acid molecule of claim 214, wherein said 3'-cap is a 3' 3' inverted nucleotide moiety.
 - 220. A method for inhibiting expression of a gene in a cell, comprising the step of administering to said cell the enzymatic nucleic acid molecule of claims 186 or 187 under conditions suitable for said inhibition.
- 221. A method of cleaving a separate RNA molecule comprising, contacting the enzymatic nucleic acid molecule of claims 186 or 187 with said separate RNA

molecule under conditions suitable for the cleavage of said separate RNA molecule.

- 222. The method of claim 221, wherein said cleavage is carried out in the presence of a divalent cation.
- 223. The method of claim 222, wherein said divalent cation is Mg2+.
 - 224. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said enzymatic nucleic acid molecule has an endonuclease activity to cleave RNA derived from HER2 gene.
- 225. The enzymatic nucleic acid molecule of claim 224, wherein said enzymatic nucleic acid molecule comprises sequences complementary to any of NCH substrate sequence of Table 34.
 - 226. The enzymatic nucleic acid molecule of claim 224, wherein said enzymatic nucleic acid molecule comprises any of the NCH ribozyme sequences shown in Table 34.
 - 5 227. The enzymatic nucleic acid molecule of claim 224, wherein said enzymatic nucleic acid molecule is used to treat cancer.
 - 228. The enzymatic nucleic acid molecule of claim 224, wherein said cancer is breast cancer.
- 229. The enzymatic nucleic acid molecule of claim 224, wherein said enzymatic nucleic acid molecule is used to treat conditions associated with the level of HER2 gene.
 - 230. An enzymatic nucleic acid molecule, wherein said enzymatic nucleic acid molecule comprises any of sequence shown as NCH ribozyme sequence in Table 31.
- 231. The enzymatic nucleic acid molecule of claim 224, wherein said enzymatic nucleic acid molecule comprises a substrate binding region which has between 5 and 30 nucleotides complementary to the RNA.
 - 232. The enzymatic nucleic acid molecule of claim 224, wherein said enzymatic nucleic acid molecule comprises a substrate binding region which has between 7 and 12 nucleotides complementary to the RNA.

- 233. A mammalian cell including the enzymatic nucleic acid molecule of claim 224, wherein said mammalian cell is not a living human.
- 234. The mammalian cell of claim 233, wherein said mammalian cell is a human cell
- 235. A mammalian cell including the enzymatic nucleic acid molecule of claims 186 or 187, wherein said mammalian cell is not a living human.
 - 236. The mammalian cell of claim 235, wherein said mammalian cell is a human cell
- 237. A method for inhibiting expression of HER2 gene in a cell, comprising the step of administering to said cell the enzymatic nucleic acid molecule of claim 224 under conditions suitable for said inhibition.
 - 238. A method of cleaving RNA derived from HER2 gene comprising, contacting the enzymatic nucleic acid molecule of claim 224 with said RNA molecule under conditions suitable for the cleavage of said RNA molecule.
 - 339. A pharmaceutical composition comprising the enzymatic nucleic acid molecule of any of claims 186 or 187.
 - A pharmaceutical composition comprising the enzymatic nucleic acid molecule of claim 224.
 - 241. A method of treatment of a patient having a condition associated with the level of HER2, wherein said patient is administered the enzymatic nucleic acid molecule of claim 224 under conditions suitable for said treatment.

- 242. The method of claim 241, wherein said method is performed in conjunction with one or more other therapies.
- 243. The enzymatic nucleic acid molecule of claim 227, wherein said enzymatic nucleic acid molecule is used in conjunction with one or more other therapies.
- 244. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said nucleic acid molecule comprises at least five ribose residues; a 2'-C-allyl modification at position No. 4 of said enzymatic nucleic acid; at least ten 2'-O-alkyl modifications, and a 3'- can structure.

- 245. The enzymatic nucleic acid molecule of claim 244, wherein said 2'-O-alkyl
- modifications is selected from the group consisting of 2'-O-methyl and 2'-O-allyl.

 246. The enzymatic nucleic acid molecule of claim 244, wherein said 3'-cap is 3'-3' inverted abasic moiety.
- 247. The enzymatic nucleic acid molecule of claim 244, wherein said 3'-cap is 3'-3' inverted nucleotide.
 - 248. The enzymatic nucleic acid molecule of claim 244, wherein said enzymatic nucleic acid comprises phosphorothioate linkages in at least three of the 5' terminal nucleotides.
- 10 249. The enzymatic nucleic acid molecule of claims 186 or 187, wherein said nucleic acid molecule comprises at least five ribose residues; a 2'-deoxy-2'-amino modification at position Nos. 4 and 7 of said enzymatic nucleic acid; at least ten 2'-O-alkyl modifications, and a 3'- cap structure.
 - 250. The enzymatic nucleic acid molecule of claim 249, wherein said 2'-O-alkyl modifications is selected from the group consisting of 2'-O-methyl and 2'-O-allyl.

- 251. The enzymatic nucleic acid molecule of claim 249, wherein said 3'-cap is 3'-3' inverted abasic moiety.
- 252. The enzymatic nucleic acid molecule of claim 249, wherein said 3'-cap is 3'-3' inverted nucleotide.
- 20 253. The enzymatic nucleic acid molecule of claim 249, wherein said enzymatic nucleic acid comprises phosphorothioate linkages in at least three of the 5' terminal nucleotides.
 - 254. The enzymatic nucleic acid molecule of claim 224, wherein said enzymatic nucleic acid molecule comprises at least one sugar modification.
- 25 255. The enzymatic nucleic acid molecule of claim 224, wherein said enzymatic nucleic acid molecule comprises at least one nucleic acid base modification.
 - 256. The enzymatic nucleic acid molecule of claim 224, wherein said enzymatic nucleic acid molecule comprises at least one phosphate backbone modification.

- 257. The enzymatic nucleic acid molecule of claim 224, wherein said phosphate backbone modification is selected from the group consisting of phosphorothioate, phosphorodithioate and amide.
- 258. The enzymatic nucleic acid molecule of claim 224, wherein said nucleic acid molecule comprises at least five ribose residues; a 2'-C-allyl modification at position No. 4 of said enzymatic nucleic acid; at least ten 2'-O-alkyl modifications, and a 3'- can structure.

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- 259. The enzymatic nucleic acid molecule of claim 258, wherein said 2'-O-alkyl modifications is selected from the group consisting of 2'-O-methyl and 2'-O-allyl.
- 10 260. The enzymatic nucleic acid molecule of claim 258, wherein said 3'-cap is 3'-3' inverted abasic moiety.
 - 261. The enzymatic nucleic acid molecule of claim 258, wherein said 3'-cap is 3'-3' inverted nucleotide.
 - 262. The enzymatic nucleic acid molecule of claim 258, wherein said enzymatic nucleic acid comprises phosphorothioate linkages in at least three of the 5' terminal nucleotides.
 - 263. The enzymatic nucleic acid molecule of claim 224, wherein said nucleic acid molecule comprises at least five ribose residues; a 2-deoxy-2-amino modification at position Nos. 4 and 7 of said enzymatic nucleic acid; at least ten 2-O-alkyl modifications, and a 3- cap structure.
 - 264. The enzymatic nucleic acid molecule of claim 263, wherein said 2'-O-alkyl modifications is selected from the group consisting of 2'-O-methyl and 2'-O-allyl.
 - 265. The enzymatic nucleic acid molecule of claim 263, wherein said 3'-cap is 3'-3' inverted abasic moiety.
- 25 266. The enzymatic nucleic acid molecule of claim 263, wherein said 3'-cap is 3'-3' inverted nucleotide.
 - 267. The enzymatic nucleic acid molecule of claim 263, wherein said enzymatic nucleic acid comprises phosphorothioate linkages in at least three of the 5' terminal nucleotides.

- 268. The enzymatic nucleic acid molecule of claim 186, wherein said enzymatic nucleic acid molecule is capable of down-regulating the expression of protein kinase C alpha (PKC alpha) eene.
- 269. A method for inhibiting expression of a PKC alpha gene in a cell, comprising the step of administering to said cell the enzymatic nucleic acid molecule of claim 268 under conditions suitable for said inhibition.
 - 270. A method of cleaving a PKC alpha RNA molecule comprising, contacting the enzymatic nucleic acid molecule of claim 268 with said separate PKC alpha RNA molecule under conditions suitable for the cleavage of said PKC alpha RNA molecule.
 - 271. The method of claim 270, wherein said cleavage is carried out in the presence of a divalent cation
 - 272. The method of claim 271, wherein said divalent cation is Mg2+.

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- 273. The enzymatic nucleic acid molecule of claim 268, wherein said enzymatic nucleic acid molecule has an endonuclease activity to cleave RNA derived from PKC alpha gene.
 - 274. The enzymatic nucleic acid molecule of claim 273, wherein said enzymatic nucleic acid molecule comprises sequences complementary to any of NCH substrate sequence of Table 63.
- 275. The enzymatic nucleic acid molecule of claim 273 wherein said enzymatic nucleic acid molecule comprises any of the NCH ribozyme sequences shown in Table 63.
 - 276. The enzymatic nucleic acid molecule of claim 268, wherein said enzymatic nucleic acid molecule is used to treat cancer.
- 5 277. The enzymatic nucleic acid molecule of claim 276, wherein said cancer is selected from the group consisting of lung, breast, colon, prostate, bladder, ovary, melanoma, and glioblastoma cancer.
 - 278. The enzymatic nucleic acid molecule of claim 268, wherein said enzymatic nucleic acid molecule is used to treat conditions associated with the level of PKC alpha gene.

- 279. The enzymatic nucleic acid molecule of claim 268, wherein said D and E independently has between 5 and 30 nucleotides complementary to the RNA.
- 280. The enzymatic nucleic acid molecule of claim 268, wherein said D and E independently has between 7 and 12 nucleotides complementary to the RNA.
- A mammalian cell including the enzymatic nucleic acid molecule of claim 268, wherein said mammalian cell is not a living human.
 - The mammalian cell of claim 281, wherein said mammalian cell is a human cell.
- A pharmaceutical composition comprising the enzymatic nucleic acid molecule
 of claim 238,
 - A pharmaceutical composition comprising the enzymatic nucleic acid molecule of claim 273.
 - 285. A method of treatment of a patient having a condition associated with the level of PKC alpha, wherein said patient is administered the enzymatic nucleic acid molecule of claim 268 under conditions suitable for said treatment.

- 286. The method of claim 285, wherein said method is performed in conjunction with one or more other therapies.
- 287. The enzymatic nucleic acid molecule of claim 286, wherein said enzymatic nucleic acid molecule is used in conjunction with one or more other therapies.
- 288. An antisense nucleic acid molecule comprising sequence complementary to any of substrate sequence in Tables 13-23.
 - 289. The antisense nucleic acid molecule of claim 288, wherein said enzymatic nucleic acid is chemically synthesized.
 - 290. The antisense nucleic acid molecule of claim 288, wherein said antisense nucleic acid comprises at least one 2'-sugar modification.
 - 291. The antisense nucleic acid molecule of claim 288, wherein said antisense nucleic acid comprises at least one nucleic acid base modification.
 - 292. The antisense nucleic acid molecule of claim 288, wherein said antisense nucleic acid comprises at least one phosphate backbone modification.

- 293. A mammalian cell including the antisense nucleic acid molecule of claim 288, wherein said mammalian cell is not a living human.
- 294. The mammalian cell of claim 293, wherein said mammalian cell is a human cell.

Figure 1: Ribozyme Motifs

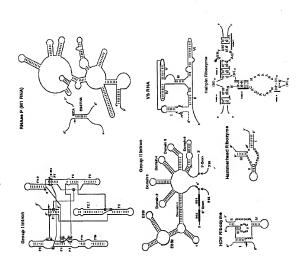


Figure 2: Examples of Nuclease Stable Ribozyme Motifs

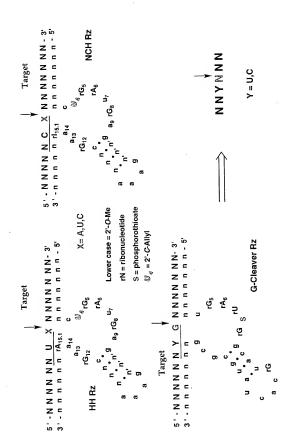


Figure 3: 2'-O-Me substituted Amberzyme Enzymatic Nucleic Acid Motif

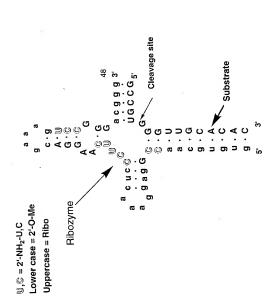


Figure 4: Stabilized Zinzyme Ribozyme Motif

Zinzyme A-motif RZ

page

Uppercase indicates natural ribo residues

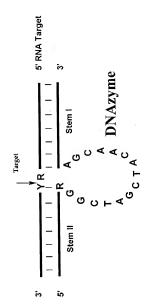
C indicates 2' - d-NH₂-C

Lowercase: 2'-0- Me

Subscript s indicates phosphothioate linkage

B: 3'-3' abasic moiety

Figure 5: DNAzyme Motif



Y=UorC R=AorG

Legend

Figure 6: Ribozyme Motifs

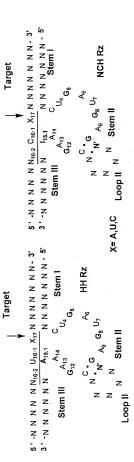


Figure 7: Examples of Nuclease Stable Ribozyme Motifs

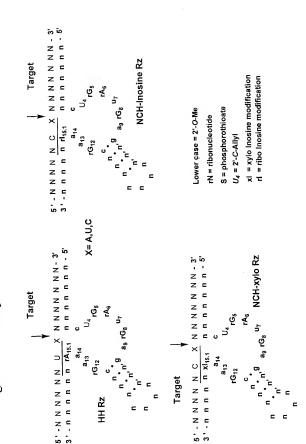


Figure 8: Inhibition of Cell Proliferation by Anti-Her2 Ribozymes

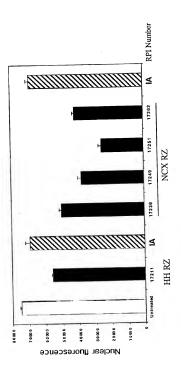


Figure 9: Synthesis of b-D-xylofuranosyl hypoxantine 3'-phosphoramidite

Beagants and Conditions: (i) MMT-CVPyr-DMSO, rt, 48 h; (ii) TBDMS-CI/AgNO₃/Pyr/THF; (iii) CrO₃/Pyr/Ac₂C/DCM, rt, 1 h; (iv) NaB(OAo)₃H/EtOH, rt, overnight; (v) 2-Cyanoethyl-N,N-diisopropylchlorophosphoramidite/1-Melm/DIPEA/DCM, rt, 2 h.

MMT = 4-methoxytriphenylmethyl

TBDMS = t-butyldimethylsilyl

Figure 10: One-Pot Formation of Nucleoside-5'-triphosphates

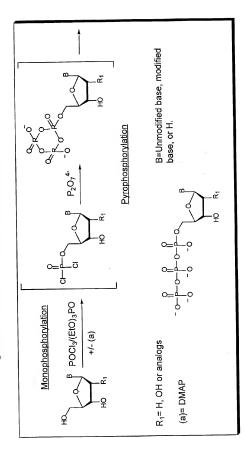
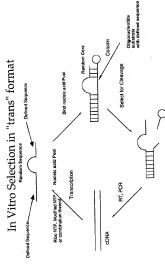


Figure 11



In Vitro Selection of Trans Acting Nucleic Acid Catalysts

Figure 12. Removal of "parasitic RNA" using a Second Selection column

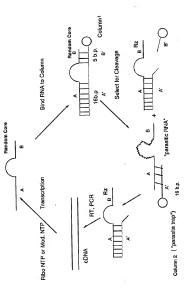


Figure 13. 2'-O-Me Stabilization of a Class I Enzymatic Nucleic Acid Motif

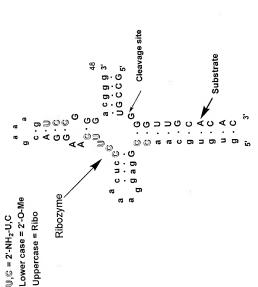


FIGURE 14. Dual Reporter System for Cytoplasmic HCV Target

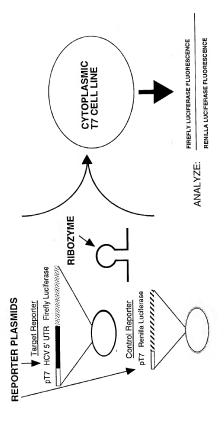


Figure 15. Dose-dependent inhibition of HCV-IRES

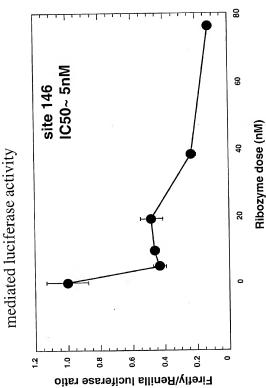
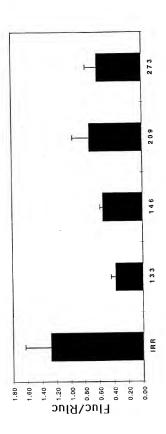


Figure 16. Efficacious Ribozymes Targeting 5'UTR HCV RNA



Site Numbers

Sequence and chemical compositions for site numbers are given in table XII

Figure 17. Characterized Class II Enzymatic Nucleic Acid Motifs

	CONCRETE CONTROL	Faremette NA	POSTERO PARTICIPANTO PARTICIPAN	Faromatic NA	STATE OF STA									(7) and not	d in the	ymatie NA		
, , , , , , , , , , , , , , , , , , ,	CONTROL OF STREET, OF STROTTED	* } , , , ,	TOTO S ANDONNO TO THE PARTY OF	**************************************	SOMEONIA DOSSESSIONES									These six motifs can all cleave with minimizations in the binding arms (7/7) and not	significantly affect rate. All eytosine residues are 2: NH; modified. The arrows in	diagrams shown above indicate the cleavage site within the substrate. Enzymatic NA		
Fayrmanie NA	SELECTORECEASURE FOR	Environtin NA	SOURCES CONTROL OF THE PROPERTY OF THE PROPERT	Feromalic NA	go to ito poeticipenco	Required NTP		2'-NH ₂ -CTP	2'-NB ₁ -CTP	2'-NH-CIP	2"-NH-CTP	2.NH-CTP	2'-NH ₂ -CTP	cleave with minimizal	di cytosine residues are	ndicate the cleavage sit	refers to the enzymatic nucleie soid malecule	
333			30 Sales	£ 200		Rate (min-1)	(Suboptimal)	0.05	60'0	0 11	1.0	90.0	10'0	x motifs can al	nly affect rate.	avods muons a	the enzymation	
337	Contenos		opposite a		CONTRACTOR STORY	,	_	₹	AS	32	98	823	S	There	significa	diagram	refers to	

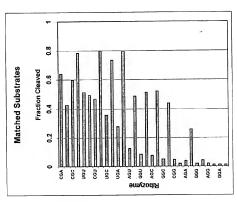
Figure 18: Chemically Stabilized Class II Motif

```
gugçeng geegege-B³
CAC GGAY, G YGGC GCG §
                                                                                                                                                                                                                               Subscript s Indicates phosphothioate linkage
                                                                                                                                     Uppercase indicates natural ribo residues
                                                                                                                                                              © indicates 2' - d·NH₂-C
                                                                                                                                                                                                                                                                                                                       G' can be G, ca, or caa
                                                                                                                                                                                                Lowercase: 2'- O- Me
                                                                                                                                                                                                                                                             B: 3'-3' abasic moiety
                                                                                                                                                                                                                                                                                          Y=Uorc
                                                                                                             regend
```

The gaaa tetraloop can be replaced by 18 atom polyethylene glycol (Spacer)

All ribo G's can be replaced with 2'- 0-methy! G

Figure 19: Substrate specificities of Class II (zinzyme) ribozymes



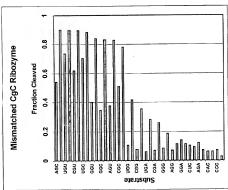
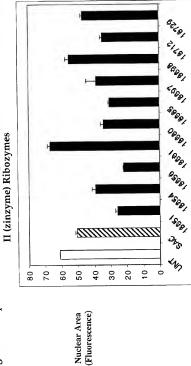


Figure 20: Representative data of HER2 cell proliferation primary screen of Class



Treatment (RPI number)

SKBR3 breast carcinoma cells 2 µg/mL RPI.9649 (lipid)

200 nM ribozymes 120 hour timepoint

120 hour timepoir UNT = untreated

SAC = scrambled attenuated control

Figure 21: Synthesis of 5-[3-aminopropynyl(propyl)]uridine 5'-triphosphates and 4-imidazoleacetic acid conjugates

Reagents and Conditions: (1) N-TFA propargy lamine, Cul, tetrakis (Ph3P)Pd(0), Et3N, DMF, 16 h, (ii) aq NaOH, pyr, MeOH, 0°C, 1 h, (iii) POCl₃. Proton-Sponge, (EtO)₃PO, 2 h, (iv) n-Bu₃N PPi, MeCN, 15 min.,

(v) ІМЕВ, МІТНСО, пьел ИНДОН, 16 h, (б) Нъ, 5% Рас., 24 h, 40 рsi, (vii) 40% МеNНъ, 3 h, (viii) NНДОН, 4 °С, 16 h, (ix) ІмАА РРС, ЕВСНСІ, DМЕ, 16 h.

Figure 22: Synthesis of 5-[3-(N-4-imidazoleacetyl0aminopropynyl(propyl)]uridine 5'-triphosphates

9a,b 11a,b

Reagents and Conditions. (I) DMT-Cl, pyr, 16 h, (ii) Ac₂O, pyr, 2 h, (iii) 3%TCA, CH₂Cl₂, 2 h, (iv) 2-Cl-4H-1,3,2-benzo-dioxaphosphorin-4-one, pyr, dioxane, 30 min., (v) n-Bu₃N PPi, DMF, 30 min. (vi) I₂, pyr-H₂O, 20 min., (vii) NH₄OH, 2 h.

Figure 23: Synthesis of Carboxylate tethered uridine 5'-triphosphoates

Reagents and Conditions: (1) methyl acrylate, Ph.P. Pd(II)acctate, Bi,N, dioxane, 30 min., reflux, (ii) DMT-Cl. pyr, 16 h. (iii) Ac,O, pyr, 3 h. (iv) 3% TCA, CH₂Cl₂, 1 h. (v) 2.CL-4H-1,3,2-benzodioxaphosphorin-4-one, pyr, dioxane, 30 min. (vi) n-Bu₃N PPi, DMF, 30 min. (vii) I₂, pyr-H₂O, 20 min. (vii) 1N MoOH, 50 min. (vii) I₃, pyr-H₂O, 20 min. (viii) IN NaOH, 5 h.

(ix) Fmoc-Asp-OFm NHS-ester, DMF-0.1M Na₂B₄O₇, 16 h, then Et₂NH, 3 h.

Figure 24: Synthesis of 5-(3-aminoalkyl) and 5-[3(N-succinyl)aminopropyl] functionalized cytidines

(v) DMT-Cl, pyr, 16 h, (vii) Ac,O, pyr, 3 h, (viii) 3% TCA, CH,Cl, 3 h, (ix) HO₃, L, AcOH, CCl₀, H₂O, 45 °C, 4 h, (x) A-TFA propargylamine, Cul, tetrakis(Ph,P)Pd(0), Et₃N, DMF, 16 h, (x) H₃, Sw, Pd-C, MeOH, 72 h, 40 psi, (xii) POCl₃, Proton-Sponge, (MeO)₃PO, 2 h, (xiii) n-Bu₃N PPi, MeCN, 15 min., (xiv) NH₄OH, 4 °C, 16 h, Reagents and Conditions: (i) H₂, 5% Pd-C, 24 h, 40 psi, (ii) POCl₃, 1,24-tria²Sole, Et₃N, McCN, 16 h, (iii), NH,OH, dioxane, 16 h, (iv) CF3COOEt, Et3N, MeOH, reflux, 3 h, (v) Bz2O, EtOH, reflux, 5 h,

(xv) succinic anhydride, DMF-0.1M $\mathrm{Na_2B_4O_7}$ 1:1, 16 h.

Figure 25: Class I ribozyme stem truncation/loop replacement

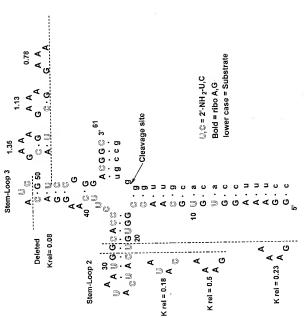


Figure 26: Class I ribozyme Stem truncation and Loop replacement

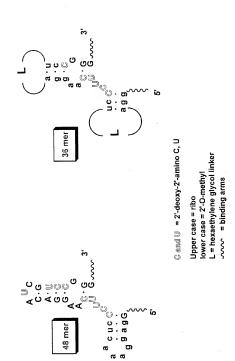


Figure 27: Non ribo Class II (zinzyme) motifs

A A G A G G G G G G G G G G G G G G G G	Substrate is the Kras site 521	۷	fackaya Agcuca · iB¹ ° cevcac _f o vcaagu f	Substrate is the HER2 site 972
Figure 27a		Figure 27b		

LASTIC TO THE CONTROL OF T

Figure 28: Non ribo Class II (zinzyme) cleavage reactions

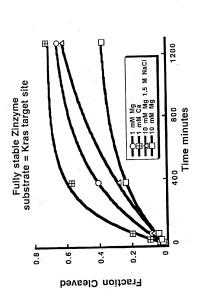
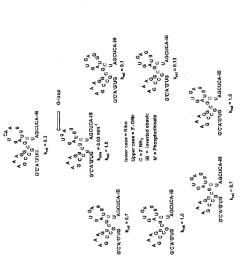


Figure 29: Positional testing of ribose positions in Class II (zinzyme) nucleic acid catalysts targeting HER2 site 972



All assays done under selection conditions - physiological buffer 1 mM Mg, 1 mM Ca 37° C Susbstrate 15-mer HER2 site 972

Figure 30: RPI 18656 Mediated Decrease in HER2 RNA site 972 vs SAC

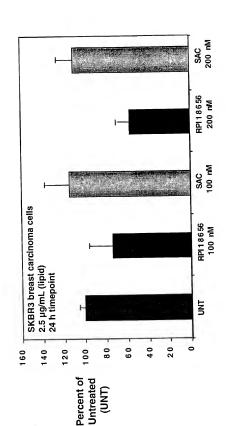


Figure 31: Dose Response of RPI 18656 Against Site 972 in Antiproliferation Assay

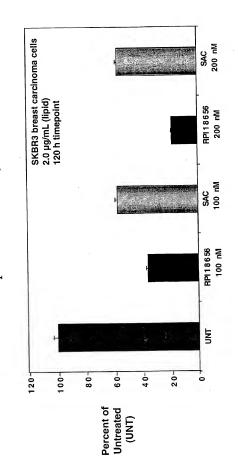


Figure 32: Dose-Dependent HER2 RNA Reduction after

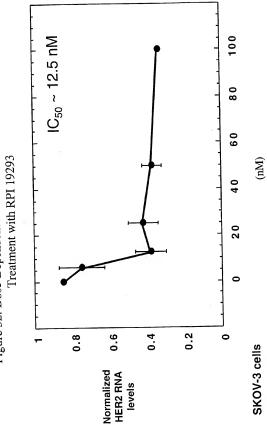


Figure 33: Dose-Dependent HER2 RNA Reduction & Inhibition of Cell Proliferation (RPI.19293)

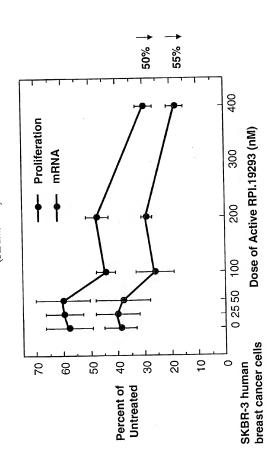


Figure 34: Zinzyme CA →G loop (7-ribo)

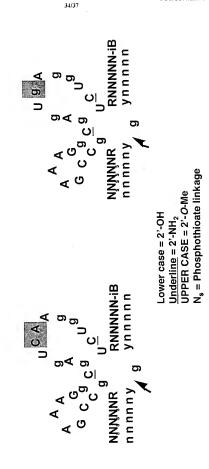


Figure 35: Screen of Zinzymes (containing ribose-G reductions) for Anti-proliferative Activity

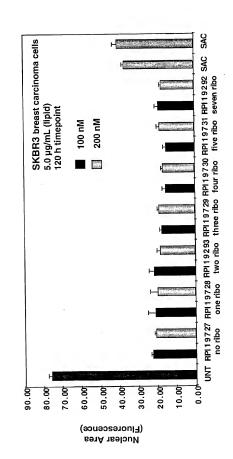


Figure 37: Effect of substitutions at Hammerhead Ribozyme position 15.1

Sim and One 1902, Bellevin Bellevin Bellevin St. (2016) 6709
 Lidholing et al., 1903, Muckein Acids Res., 35, 2779-2286.
 Seela et al., 1903, Muckein Acids Res., 35, 2779-2286.
 Seela et al., 1903, Hombolin Acids Res., 28, 1010-1018.
 Nig et al., 1904, Bellevin Michael Acids Res., 28, 1010, 1018.
 Bellevin St. Age Bellevin Michael Acids Res., 28, 1010, 1018.
 Bellevin St. 1905, Bellevin Michael Acids Res., 28, 1010, 1018.
 Bellevin St. 1905, Bellevin Michael Acids Res., 28, 1010, 1018.

kral values describe the cleavage rate relative to A-15.1 activity